

Query Match 46.0%; Score 617.6; DB 24; Length 6904;
 Best Local Similarity 76.4%; Pred. No. 7.7e-114;
 Matches 758; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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QY 1 ATGAGCAGCAGAGACCCCTACTCCGTGAGGCGACAGAGGCGCATAGGCGGCGCATCACC 60
DB 1904 ATAAACGACCAAAACCCCTACTCCGTGACAAACGACGACATTAAGAGACCATCACC 1845
QY 61 TTCTCTATCTCTTACCATCTTTGGGCAAGCCTGTGATCTCTGGGTGTGTACCAAC 120
DB 1844 TTCTCTATCTCTTACCATCTTTGACAAACGCTTAATCACTTAATTAATTAACCAAC 1785
QY 121 CGCTGCTGCGGCGCCCTCAGAACCTGTTCTGTGTGTGCGGCGCGCGCATCTG 180
DB 1784 CGCTGCTGCGGCGCCCTCAGAACCTTAATCTTAATGTGCTTAACGCGCGCGCATCTTA 1725
QY 181 GTGCGCAGCTCATCATCTCTTTCTGTGTGCGCAACGAGCTGTGGGCTACTGTACTTC 240
DB 1724 ATAAACGACGCTCATCATCTCTTTCTGTGTGCAACGAACTAACTAATATCTTC 1665
QY 241 CGGCGCAGCTGTGCGAGGTATCTGCGGCTGCAAGCTCTTCTGCACTCTGTCATC 300
DB 1664 CGAGCAGGTATAGAAATTAACCTTAAGCTGACGTAATCTTCTACCTGTCATC 1605
QY 301 GTGCACTGTGCGCATCAGCCTGAGACGCTACTGAGCGCGCGCTGAGATAC 360
DB 1604 GTACACCTATAGCGCATTAACCTTAACCGCTACTTAACCGTAAACCGCGCTAAATAC 1545
QY 361 AACTCCAGCGCAGCCCGCGCGCATCAAGTCATCATCTGCTGTGTGCTATGCC 420
DB 1544 AACTCCAGCGCAGCCCGCGCGCATCAATATATCATCTCTCAATATATATCATGCC 1485
QY 421 GCGGTATCTGCGCGCGCGCGCGCGCATCAAGGCGCGCGCGCGCGCGCGCGG 480
DB 1484 GCGGTATCTGCGCGCGCGCGCGCGCGCATCAAGGCGCGCGCGCGCGCGCGG 1425
QY 481 CGCCCGCAGTGCAGCTCAACAGAGGCGCTGTATCTGCGCGCTCAGCATGATCT 540
DB 1424 CGCCCGCAGTGCAGCTCAACAGAGGCGCTGTATCTGCGCGCTCAGCATGATCT 1365
QY 541 TTCTTTGCTCTGCTCTCATCATCTGTTGTCTAAGCTGCGCATCTGATGCCAA 600
DB 1364 TTCTTTGCTCTGCTCTCATCATCTGTTGTCTAAGCTGCGCATCTGATGCCAA 1305
QY 601 CGGAGCAACGCGCAAGGTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGG 660
DB 1304 CGGAGCAACGCGCAAGGTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGG 1245
QY 661 CCGCGACCGCAGCATGTGTGCGCTTTGGCTCAGCCAACTGCCAGCGCTGTGTG 720
DB 1244 CCGCGACCGCAGCATGTGTGCGCTTTGGCTCAGCCAACTGCCAGCGCTGTGTG 1185
QY 721 GCTTCTGCGAGAGGTCAAGCACTGCAAGTCTGAGGGAAGAGAGAGGCGGAG 780
DB 1184 ACTTCTGCGAGAGGTCAAGCACTGCAAGTCTGAGGGAAGAGAGAGGCGGAG 1125
QY 781 ACCCTGAGATCATGCGGACCGCGGCGCTGCGCAACCGTGTGGGCTTCCCAATCA 840
DB 1124 ACCCTGAGATCATGCGGACCGCGGCGCTGCGCAACCGTGTGGGCTTCCCAATCA 1065
QY 841 GCGCAGGCGCAGAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 1064 AACCAAAACCAAAATATATATATATATATATATATATATATATATATATATAT 1005
QY 901 GAGAGAGAGAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
DB 1004 AAAAAAATATATATATATATATATATATATATATATATATATATATATATAT 945
QY 961 AGCGCGCGCTGAGCAGCAGCAGGCGCGG 992
DB 944 AACCGCGCTTACAGACAGCAAACTCCG 913

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RESULT 13

ABL32074 standard; DNA; 6904 BP.

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XX ID ABL32074
XX AC ABL32074;
XX DT 26-MAR-2002 (first entry)
XX DE Human immune system associated gene SEQ ID NO: 47.
XX KW Human; immune system disease; cytosine methylation; antiaesthetic;
XX KW antiarteriosclerotic; antianaemic; cyostatic; nootropic;
XX KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX KW antihemematic; antiarthritic; antidiabetic; antipsoriatic;
XX KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
XX KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO200200928-A2.
XX PD 03-JAN-2002.
XX PF 02-JUL-2001; 2001MO-EP07537.
XX PR 30-JUN-2000; 2000DE-1032529.
XX PR 01-SEP-2000; 2000DE-1043826.
XX PA (EPig-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2002-130909/17.
XX PT Nucleic acid comprising fragment of chemically modified gene, useful
XX PT for diagnosis and treatment of diseases associated with abnormal
XX PT cytosine methylation.
XX PS Claim 1; SEQ ID NO 47; 32pp + Sequence Listing; German.
XX CC The present invention provides a number of human immune system associated
XX CC genes which are modified by the methylation of cytosines. The sequences
XX CC can be used in the diagnosis and treatment of immune system disorders,
XX CC including eye diseases such as retinopathy, neovascular glaucoma and
XX CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX CC diseases. The present sequence is a gene of the invention.
XX SQ Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 1 other;

Query Match 39.6%; Score 531.6; DB 24; Length 6904;
Best Local Similarity 70.9%; Pred. No. 1.1e-96;
Matches 705; Conservative 0; Mismatches 289; Indels 0; Gaps 0;

QY 1 ATGAGCAGCAGAGACCCCTACTCCGTGAGGCGACAGAGGCGCATAGGCGGCGCATCACC 60
DB 5001 ATGAGATTAATAGATTTATTTATTTGTTAGGTTAGCGGTTATAGCGGCGGTTATTATT 5060
QY 61 TTCTCTATCTCTTACCATCTTTGGGCAAGCCTGTGATCTCTGGGTGTGTACCAAC 120
DB 5061 TTTTATTTTATTTTATTTATTTTGGGTAACGTTTGGTATTTTGTGTGTGATTAAT 5120
QY 121 CGCTGCTGCGGCGCCCTCAGAACCTGTTCTGTGTGTGCGGCGCGCGCATCTG 180
DB 5121 CGTGTGCTGCGGCTTTTATTAATTTGTTTGGTGTGTGTGTGTGTGTGTGTGTGTGT 5180
QY 181 GTGCGCAGCTCATCATCTCTTTCTGTGTGCGCAACGAGCTGTGGGCTACTGTACTTC 240
DB 5181 GTGCTTACCTTATTAATTTTATTTTGTGTGTGTTAAGAGTGTGTGTGTATTTT 5240

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QY 241 CGGCGACGTGTGCGAGGTGTACCTGGCCCTGACGTCCTCTTTCGACCTCGTCATC 300
DB 5241 CGGCGTACGTGTGCGAGGTGTATTTGGCGTTGACGTTGTTTTTTTGTATTTGTTATTC 5300
QY 301 GTGCACTGTGGCCCATCAGCCTGTGACCGCTACCTGGCCGCTGAGCCGCTGGATAC 360
DB 5301 GTGTATTTGTGCGTTATTAATTTGTGATCGTTATTTGGGTGCTGATCCGGGTGGAGTAT 5360
QY 361 AACTCCAAAGCGACCCCGCCGATCATGATCATCTCCATGCTGATGCTCATGCTCC 420
DB 5361 AATTATTAAGCGTATTTGCGCTGATTAAGTATTAATTTTATTTGTGTGTTATTCGTC 5420
QY 421 GCGGTATCTGCTGCGCCCTCATCTACAGGCGACAGGCGCCCGACCGCGCGG 480
DB 5421 GTGCTATTTTGTGTGCTTTTATTTATTAAGGCGATTAAGGTTTTTATGTCGCGGG 5480
QY 481 CGGCCCCAGTGCAGCTCAACAGAGGCGCTGTACATCTGCGCTTCAGATCGATCT 540
DB 5481 CGTTTTTATGTATGTTAATTAAGAGGTTGGTATTTTGTGTTTATGATCGGATTT 5540
QY 541 TTCTTGTCTCTTCCCTCATCATGATCTGTCTACTGCGGATCTACCTGATCGCCAA 600
DB 5541 TTTTGTGTTTTTGTATTATTAATTAATTTGTTATTTGCGTATTAATTTGATCGTTAA 5600
QY 601 CGCAGCAACCGCAGAGGTCCAGGCGCCAGGCGGCGCTGCGCAGGCTGATCCAGACG 660
DB 5601 CGTAGTATGTAGAGGTTTAAAGGTTAAAGGCGGCTTGGTAGGCTGATTAAGTAA 5660
QY 661 CCCGACCGCAGCATGTGTGGGCTTTGGCTCAGCCAACTGCGACGCTGCGCTCTG 720
DB 5661 TTTTGATTCATTAATGCTGGGCTTTGGTTTATGTTAAATGTTAGTTTGTGTTTGTG 720
QY 721 GCTTCGCGAGAGGTGCACAGGACTCGAAGTCCAGTGGGAGAGAGAGGAGGAGG 780
DB 5721 GTTTTGTATGAAGGTTAAAGGATTCAGAGTTATTTGGGAGAGAGAGGAGGAGG 5780
QY 781 ACCCTGAAAGATCTGGGACCCGCGCTTGCACCCAGTTGGGCTGCTTCCCACTCA 840
DB 5781 ATTTTGAAGATATTTGGGATTCGCGGTTTGTATTAATTTAGTTGTTTATTTTAA 5840
QY 841 GCGCAGGCGCAGAGAGGCTTTTGTGGGCACTTCAGAGAGATGAAGCTGAAGAGAG 900
DB 5841 GGTATGAGGTAAAGAGGAGGCTTTGTGGGCTATTTTAAAGATGAAGTTGAAGAGAG 5900
QY 901 GAGCAGAGAGAGAGAGGTGTGAACCCAGGAGAGTGCAGTCTCGGCTCAGCTTCG 960
DB 5901 GAGCAGAGAGAGAGAGATGTGAATTTTAAAGTATGTAGTGTTCGTTTAAAGTTGT 5960
QY 961 AGCCCCCGCTGACAGCAGCAGGCTCCCGG 994
DB 5961 AGTTTTTCTTTGTATGATTAAGGTTTTCGGG 5994
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RESULT 14
AAD28364
AAD28364 standard; DNA: 6904 BP.

AC AAD28364;
DT 22-APR-2002 (first entry)
DE Human chemically created genomic DNA #5.
XX Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
XX adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
XX behavioral disorder; neurological; psychiatric; cancer; schizophrenia;
XX Tourette's syndrome; smoking; human immunodeficiency virus dementia;
XX drug abuse; migraine, de.
OS Homo sapiens.
XX
XX
XX MO200202809-A2.

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PD 10-JAN-2002.  
XX  
XX 02-JUL-2001; 2001MO-BP07540.  
PF  
XX 30-JUN-2000; 2000DE-1032529.  
PR 01-SEP-2000; 2000DE-1043826.  
XX  
XX (EPiG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2002-154759/20.  
DR  
XX  
XX Novel nucleic acid useful for diagnosis and therapy of behavioral  
PT disorder, neurological disorder and cancer, comprises a sequence of a  
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor  
PT gene -  
XX  
XX Claim 1; Page 40-44; 190pp; English.  
XX  
XX The invention relates to nucleic acids comprising a segment of chemically  
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also  
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers  
CC useful for detecting cytosine methylations. The pretreated DNA is useful  
CC for the diagnosis or therapy of behavioural disorders, neurological  
CC disorders and cancer, in particular major depressive disorder, Tourette's  
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,  
CC drug abuse, alcoholism, personality traits, compulsive gambling, human  
CC immunodeficiency virus dementia, migraine, behaviour in schizophrenia  
CC and schizoaffective patients, and suicidal behaviour in patients with  
CC schizophrenia. The nucleic acid is useful for detecting the methylation  
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms  
CC (SNPs). The present sequence is human chemically treated genomic DNA.  
XX  
SQ Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 1 other;  
Query Match 39.6%; Score 531.6; DB 24; Length 6904;  
Best Local Similarity 70.9%; Pred. No. 1,1e-96;  
Matches 705; Conservative 0; Mismatches 289; Indels 0; Gaps 0;  
QY 1 ATGACACACAGAGACCCCTAATCTCGTCAGAGCCAGCGCCATAGCGGCGCATCAC 60  
DB 5001 ATGATATTAATTAAGATTTTATTTATTCGTAGTTATAGCGGTATTAACCGGCGTTATAT 5060  
QY 61 TTCTCATTTCTCTTACCATCTTGGCAAGCTCTGTGTCATCTGCTGTGTGACACG 120  
DB 5061 TTTTATTTTATTTTATTTATTTTCGTAACGTTTGTGTTATTTGTTGTGATTAAT 5120  
QY 121 CGCTGCTGCGGCGCCCTCAGAACCTGTTCTGTGTCGTGCGCGCGCGGACATTCG 180  
DB 5121 CGTTCGTGCGGCTTTTAAAGATTTGTTTGTGTCGTGTCGTGTCGTGTCGTGTCGT 5180  
QY 181 GTGGCAGCCTCATCATCTCCCTTCTGCTGCGCAAGAGCTGTGGCTACTGTACTTC 240  
DB 5181 GTGTTACGTTATTAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5240  
QY 241 CGGCGCAGTGTGCGAGGTGTACTGGCGCTGACGTGCTCTTTCACCTTCGTCATC 300  
DB 5241 CGGCTACGTGTGCGAGGTGTATTTGGCGCTTCGAGCTGTTTGTATTTGTTATTC 5300  
QY 301 GTGCACTGTGGCCCATCAGCCTGTGACCGCTACCTGAGCGCGCGCTGAGTAC 360  
DB 5301 GTGTATTTGTGCGTTATTAATTTGTGATCGTTATTTGGGTGCTGATCCGGGTGGAGTAT 5360  
QY 361 AACTCCAAAGCGACCCCGCCGATCATGATCATCTCCATGCTGATGCTCATGCTCC 420  
DB 5361 AATTATTAAGCGTATTTGCGCTGATTAAGTATTAATTTTATTTGTGTGTTATTCGTC 5420  
QY 421 GCGGTATCTGCTGCGCCCTCATCTACAGGCGACAGGCGCCCGACCGCGCGG 480  
DB 5421 GTGCTATTTTGTGTGCTTTTATTTATTAAGGCGATTAAGGTTTTTATGTCGCGGG 5480  
QY 481 CGGCCCCAGTGCAGCTCAACAGAGGCGCTGTACATCTGCGCTTCAGATCGATCT 540
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Db      5481 CGTTTTAGTAAATTAAATTAGAGGTTGGTAATTTTGGTTTAAATGATCGATT 5540
QY      541 TTCTTGCTCTCTGCTCATCATGATCTCTGCTACCTGGCATCTACATGATCGCAAA 600
Db      5541 TTTTGTCTTTTGTGTTTATTAATGATTTTGTATTTAGTGATTAATTTGATCGTTAA 5600
QY      601 CGAGCAACCGCAGAGGTCCAGGCGCCAGGGGCGCTGGGAGGGTGATGCTCAAGCAG 660
Db      5601 CGTAGTATGCTAGAGGTTTAAAGGGTTAAAGGGGCTTGGGTAAGGGTGAAGTTAAAG 5660
QY      661 CCCCGACCCGACCATGCTGGGGGCTTTGGCTCAGCCAACTGCGAGCCCTGCTGTG 720
Db      5661 TTTCGATTCGATTAATGATGAGGTTGGGTTTGTATTAATTTGATTTGATTTGTC 5720
QY      721 GCTTCTGCGAGAGGTCAACGAGACACTCGAAGTCCACTGGGAGAGAGAGGGGGAG 780
Db      5721 GTTTTCTTGAAGAGTTAACGATATTCGAAAGTTTATTTGGGAGAGAGAGGGGGAG 5780
QY      781 ACCCTGAAGATCTGGGAGCCCGGCTTGGCCACCCAGTTGGGCTGCCCTTCCCACTCA 840
Db      5781 ATTTTGAAGATATTTGGGATTCGGGTTTGTATTTAGTTGGGTTGTTTAAATTTA 5840
QY      841 GCGCAGGCGCAAGAGAGGGGTTTGTGGGCGCATCTCCAGAGATGAAGCTGAAGAGAG 900
Db      5841 GGTAGGAGTTAAAGAGGGGTTTGTGGGCTATTTTAAAGATGAAGTTGAAGAGAGAG 5900
QY      901 GAGAGAGAGAGAGAGAGTGAACCCAGGCACTGCGAGTCTCCGGCTCAGCTTGC 960
Db      5901 GAGAGAGAGAGAGAGAGTGAATTTGAAATTTAGTAGTATGTTTGGTTTAAATTTGT 5960
QY      961 AGCCCCCGCTGCGACGACCCAGGCGCTCCCGG 994
Db      5961 AGTTTTCGTTGATGATGATTAAGGTTTTCGGG 5994

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RESULT 15

AAI99931 ID AAI99931 standard; DNA; 1383 BP.

AC AAI99931;

DT 18-FEB-2002 (first entry)

XX Human alpha-2CAR encoding DNA.

XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;

XX polymorphic site; allelic variant; cardiovascular disease;

XX central nervous system disease; adenylyl cyclase; MAP kinase activity;

XX phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.

OS Homo sapiens.

XX Key location/Qualifiers

XX CDS 1..1386

XX FT /tag= a

XX FT /product= "alpha-2CAR"

XX FT /note= "sequence includes a 12 nucleotide polymorphic

XX FT site at nucleotides 961-972 absent in the

XX FT alpha-2CAR variant (AAI99933)"

XX WO200179561-A2.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-US12575.

XX 17-APR-2000; 2000US-0551744.

XX 10-AUG-2000; 2000US-0636259.

XX 19-OCT-2000; 2000US-0692077.

XX (LIGGETT S B.

XX (SMALL) K M.

XX Liggett SB, Small KM;
 PI WPI, 2001-611728/70.
 DR P-PSDB; AAM52124.
 DR
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 XX
 PS Example 15; Page 157; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 or (II)
 CC or a site comprising (A) (999GCG999CG) or (B) (999GCG999CG) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC remoxolamine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlating to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2CAR, the
 CC sequence includes a 12 nucleotide polymorphic site at nucleotides
 CC 961-972, absent in the alpha-2CAR variant (AAI99933).
 CC
 XX
 SO Sequence 1383 BP; 164 A; 482 C; 500 G; 237 T; 0 other;

Query Match 34.2%; Score 459.4; DB 23; Length 1383;
 Best Local Similarity 63.2%; Pred. No. 2.1e-82;
 Matches 831; Conservative 0; Mismatches 406; Indels 78; Gaps 5;

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QY      13 GACCCCTACTCCGTGACGAGGCGGCGCATAGCGGCGGCGCATCTTCTCATTTCTC 72
Db      130 GGCAGTACTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 189
QY      73 TTACACATCTTGGGCAACGCTGTCATCTGCGCTGTGTTACACAGCGCTGTCGCGC 132
Db      190 TTACCGGTGTGGGCAACGCTGTCATCTGCGCTGTGTTACACAGCGGCGGCGGCGGCG 249
QY      133 GCGCCCTAAGAACTGTTCTCTGTCGTGTCGTGCGGCGGCGGCGGCGGCGGCGGCGGCG 192
Db      250 GCGCACAAGAACTCTTCTCTGTCGTGTCGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 309
QY      193 ATCATCCCTTTCTGCTGCGCAACAGCTGCTGCGCTACTGTACTTTCGCGGCGGCGGCG 252
Db      310 GTATGCGCTTCTCTGTCGTGCGCAACAGCTACTGCGCTACTGCGGCGGCGGCGGCGG 369
QY      253 TGGAGGTGTAACCTGCGCTGCAAGCTGCTTCTGCACTCTGCTGCACTCTGCGGCGGCG 312
Db      370 TGGCGGTGTAACCTGCGCTGCAAGCTGCTTCTGCACTCTGCTGCACTCTGCGGCGGCG 429
QY      313 GCGATAGCGCTGCAACGCGCTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 372
Db      430 GCGATAGCGCTGCAACGCGCTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 489
QY      373 ACCCGCGCGCATCATAGTGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432
Db      490 ACACCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 549
QY      433 CTGCGCGCGCTCATCTCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 492

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Db 550 TTCCCGCCGCTGCT---CGCTTACCGCCAGCCCGCCGCTTACCCGCACTGC 606
Qy 493 AAGCTCAACGAGAGGCTGGTACATCTGGACCTCAGATCGGATCTTTGTCTCT 552
Db 607 GGCTCAACGAGAGCTGGTACATCTGTCTCTCTGATCGGCTCTTTCGCGCC 666
Qy 553 TGCCTCATCATGATCTTGTCTACCTGCGCATCTTACCTGATTCGCAACGCGAACCGC 612
Db 667 TGCCTCATCATGAGGCTGTCTAGCGCGCATCTTACCGATGGCCAGCGTCGCACGCGC 726
Qy 613 AGAGTCCCAAGGCGCAAGGGGGGCTGGGCAAGGTGATCCAGCAGCCCGACCCGAC 672
Db 727 A---CGCTCAGCGAAGAACCGCCCGGTGGCCCGCGAGGTGCTCCGACTACCGAA 783
Qy 673 CATGTGGGCTTTGGCTCAGCCAACTGCGACCCCTGGCTCTGTGGCTTCTGCGAGA 732
Db 784 AACGGGCTGGGCGGCGCGAGGC-----GA 809
Qy 733 GAGGTCAACGAGACCTCGAAGTCCATGGGAGAGAGAGAGAGAGAGAGAGAGAGAT 792
Db 810 GGGAGAGAGGGGCACTGCGGCGCCCGCGCGGCGAGCGTGAAGCCGGA----- 856
Qy 793 ACTGGGACCCGGGCTTGGCCACCCAGTTGGGCTGCTCCCACTCAGGCGAGGCGAG 852
Db 857 ---CGAGACAGGCGAGCGCGAGAGGCGGCGCGCGGCGCGGCGCGGCGGCGG 912
Qy 853 AAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAGTGAAGAGAGAGAGAGAGAGAG 912
Db 913 CGGCGGCGAGCGGCGGAGAGGGGGGCGCGGCGGTGAGAGAGAGAGAGAGAGAGAG 972
Qy 913 GAAGAGTGTGAACCCCGAGAGTGCAGTGTCTCCGGCTCAGCTTGCAGCCCGCGCTG 972
Db 973 GGGGCGGCTGATGTGGGGGGCGCTGACCGCTCCAGGTCTCCGGGGCCCGGTGGCGCTC 1032
Qy 973 CAGCAGCCACAGGAGCTCCGAGGTGCGGCACTTACGTGAGCGAGGTCTTGGGAGG 1032
Db 1033 TCGCGGCGCAGCTCGCGCTCCGTGAGTTCCTTCTGCGCGCGCGCGCGCGAGC 1092
Qy 1033 GGGGTGGGTCTATAGTGGGCACTGTGGCTGCGAGGCGCAGCTGACCCGAGAGAG 1092
Db 1093 AGCGT-----GTGCGCGCGAGAGGTGGCCAGGCGCGCGAGAGAG 1131
Qy 1093 CGCTTCACTTCGTCGTGGCTGTGTGATTTGGGCTTGTGCTGTGCTTCCCTTC 1152
Db 1132 CGCTTCACTTTTGTGCTGTGTGTATGGGCGGTTCGTGCTGTGTGCTTCCCTTC 1191
Qy 1153 TTCTTCACTTACAGCTGGGCGGCTGTCGCGAGCAGTGAAGTGTGCCCATGGGCTC 1212
Db 1192 TTCTTCACTTACAGCGCTGTAGGCGATCTGCGGAGGCGTGCAGAGTGGCCGGCGGCTC 1251
Qy 1213 TTCAAGTTCCTTCTTGGATGGGCTACTGCAACAGCTCACTGAAACCTGTTATCTACAC 1272
Db 1252 TTCAAGTTCCTTCTTGGATGGGCTACTGCAACAGCTCACTGAAACCTGTTATCTACAC 1311
Qy 1273 ATCTTCAACAGAGACTTCCCGGCTTCCGAGAGATCTGTGCGGCGCGGTGA 1327
Db 1312 GTCTTCAACAGAGATTTCCGCGCATCTTCAAGCAATCTTCCGAGAGAGAG 1366

Search completed: February 7, 2004, 20:50:59
Job time : 400.682 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 20:26:52 ; Search time 89.2013 Seconds
(without alignments)
6650.337 Million cell updates/sec

Title: US-09-692-077D-2

Perfect score: 1344
Sequence: 1 atggaccaccagaccacca.....ggaccacagcgcctgcgta 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB. seq.*
2: /cgn2_6/prodata/2/ina/5B COMB. seq.*
3: /cgn2_6/prodata/2/ina/5A COMB. seq.*
4: /cgn2_6/prodata/2/ina/6B COMB. seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB. seq.*
6: /cgn2_6/prodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321.8	98.3	2072	4 US-09-016-434-1181	Sequence 1181, Ap
2	445	33.1	1382	4 US-09-016-434-1256	Sequence 1256, Ap
3	432.6	32.2	3604	4 US-09-016-434-1180	Sequence 1180, Ap
4	184.8	13.8	3335	1 US-07-676-174A-1	Sequence 1, Appl
5	163.4	12.2	3335	1 US-08-194-338-1	Sequence 1, Appl
6	158.6	11.8	921	1 US-08-722-001-17	Sequence 17, Appl
7	158.6	11.8	1567	1 US-08-722-001-24	Sequence 24, Appl
8	157	11.7	1738	1 US-08-334-698-3	Sequence 3, Appl
9	157	11.7	1738	1 US-08-228-932-3	Sequence 3, Appl
10	157	11.7	1738	1 US-08-468-939-3	Sequence 3, Appl
11	157	11.7	1738	2 US-08-406-855A-3	Sequence 3, Appl
12	157	11.7	1738	2 US-08-722-001-13	Sequence 3, Appl
13	157	11.7	1738	2 US-08-244-354-3	Sequence 3, Appl
14	157	11.7	1738	4 US-09-206-899-3	Sequence 3, Appl
15	157	11.7	1738	4 US-09-444-783-3	Sequence 3, Appl
16	157	11.7	1738	4 US-09-688-415-3	Sequence 3, Appl
17	157	11.7	1738	4 US-09-016-434-1402	Sequence 1402, Ap
18	157	11.7	1738	5 PCT-US95-04203-3	Sequence 3, Appl
19	149.6	11.1	1776	1 US-08-722-001-13	Sequence 13, Appl
20	149.6	11.1	1776	1 US-08-722-001-29	Sequence 29, Appl
21	149.6	11.1	2002	4 US-09-016-434-1172	Sequence 1172, Ap
22	149.6	11.1	2140	1 US-08-334-698-1	Sequence 1, Appl
23	149.6	11.1	2140	1 US-08-228-932-1	Sequence 1, Appl
24	149.6	11.1	2140	1 US-08-468-939-1	Sequence 1, Appl
25	149.6	11.1	2140	2 US-08-406-855A-1	Sequence 1, Appl
26	149.6	11.1	2140	2 US-08-722-190-1	Sequence 1, Appl
27	149.6	11.1	2140	3 US-08-244-354-1	Sequence 1, Appl

28	149.6	11.1	2140	3 US-09-206-899-1	Sequence 1, Appl
29	149.6	11.1	2140	4 US-09-444-783-1	Sequence 1, Appl
30	149.6	11.1	2140	4 US-09-688-415-1	Sequence 1, Appl
31	149.6	11.1	2140	5 PCT-US95-04203-1	Sequence 1, Appl
32	139.8	10.4	1601	1 US-08-722-001-7	Sequence 7, Appl
33	139.8	10.4	1997	1 US-08-722-001-27	Sequence 27, Appl
34	139.8	10.4	2004	1 US-08-722-001-11	Sequence 11, Appl
35	138.4	10.3	1930	4 US-09-016-434-1171	Sequence 1171, Ap
36	138.4	10.3	2463	1 US-08-370-542-1	Sequence 1, Appl
37	138.4	10.3	2463	1 US-08-542-358-1	Sequence 1, Appl
38	138.4	10.3	2463	3 US-09-018-351-1	Sequence 1, Appl
39	138.2	10.3	1639	1 US-08-334-698-5	Sequence 5, Appl
40	138.2	10.3	1639	1 US-08-228-932-5	Sequence 5, Appl
41	138.2	10.3	1639	1 US-08-468-939-5	Sequence 5, Appl
42	138.2	10.3	1639	2 US-08-406-855A-5	Sequence 5, Appl
43	138.2	10.3	1639	2 US-08-722-190-5	Sequence 5, Appl
44	138.2	10.3	1639	3 US-08-244-354-5	Sequence 5, Appl
45	138.2	10.3	1639	3 US-09-206-899-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-016-434-1181
; Sequence 1181, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1480
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEO ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178197
; US-09-016-434-1181
Query Match 98.3%; Score 1321.8; DB 4; Length 2072;
Best Local Similarity 99.2%; Pred. No. 2.4e-253;

Oy	13	GACCCCTACTCCGTCAGAGCCACAGCGGCATAGAGGGGGGCATACCTTCTCTATCTGC	72
Db	132	GGCACGTACTGAGCGGGGCGCGGTGGCAGAGGCTGGCTGCCGTGGTGGGCTTCTCATCGTC	191
Oy	73	TTTACCATCTTCGCGACGCTTCGTGATACCTGAGCTGTGTGACAGCGCGCTCGCTGCGC	132
Db	192	TTTCAACCGTGGGGGACATGCTGTGGTGGATGCGCGTGGACCAAGCGGGGCGTGGCG	251
Oy	133	GCCCTCAAGAACCTGTCTCTGGTGTGCTGGCGCGCGCGACATCTGTGTGGCACGCTC	192
Db	252	GCGCCACGAACCTCTTCCTGGTGTGCGCTGGCGCTCGCGCGACATCTGTGTGGCCACGCTG	311
Oy	193	ATCATCCCTTCTCGCTGGCCACAGAGGTCGTGGGCTGTGCTGTGGTATTCGCGGACCGTGG	252
Db	312	GTCAATGCCCTTCTGTTGGGCGCAACGAGCTCATGGCTGTACTGTGGTACTTGAGGAGGTGGG	371
Oy	253	TGCGAGGTGTACTGGCGCTCGACCTGTGCTTCTGTGACCTGTGCATGTGTGACCTGTGGC	312
Db	372	TGCGGCGGTGTACTGGCGCTCGATGTGCTGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	431
Oy	313	GCCATCAGCCTTGAACCGGCTACTGGGCGCGTGAAGCGCGGCGCTGGAATCAACTCAAGCGC	372
Db	432	GCCATCAGCCTTGAACCGGCTACTGGTGGGTGAAGCAGAGCGCGGTGAATCAACTCAAGCGC	491
Oy	373	ACCCGCGCGCGCATTAAGTGATCATCTCTACTGTGTGGCTCATGTGCGCGGTATCTTCG	432
Db	492	ACACCACCGCGCGGTCAAGGCCACATCTGTGGCGCGTGTGGCTCATCTCGGCGGTATCTTCC	551
Oy	433	CTGCGCGCGCTCATTAAGGGGAGACAGAGGCGCCCGACCGCGCGGGCGGCCCGCAATGCG	492
Db	552	TTCCGCGCGGTGTCTCTGCTTACCGCGCAGCGCCGACGCGCGCGCTTACCGCGGTGCG	608
Oy	493	AAGCTCAACCAAGAGGCGCTGTGTACTCTCTGGCGCTTCAGACATCGAATCTTCTTTGGCTCT	552
Db	609	GCGCTCAACGAGACGAACTGTGTACATCTGTGTCTCTGTGCATGTGGCTCTTCTTGGCGGCC	668
Oy	553	TGCTCATCATGATCTTGTGTCTACTCTGCGGATCTACTGATGTGCCAAACGACGACACCGC	612
Db	669	TGCTCATCATGAGGCTGTGTCTACTCGCGGATCTACTCGAATGGCCAACTGTGCGCACGCGC	728
Oy	613	AGAGGTCCAGGGCCCAAGGGGGGCGTGGGCAAGGTGATGTCCAAAGACCCCGAACCCGAC	672
Db	729	A-----CGCTCAAGCGAAGAGCGCGCCCTCGTGGGCCCC	761
Oy	673	CATGATGGGGCTTTGGCGCTCAAGCCAAATGCGCAGCGCGCTGTGTGGCTTCTTGCAGA	732
Db	762	GACGTGTGCTTCCCGCATCTACGAAACCGGGCTGGCGCGCGGCGACAGGCGGACGAGAAC	821
Oy	733	GAGTCAACGAGCACTCGAAGTCCACTTGGGAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAT	792
Db	822	GAGGCACTGCGGCGCCCGCGCGGACGTTGGAGCGGAGCGAAGAGCAGGCGACGCGCGAG	881
Oy	793	ACTGGGACCGCGGAGCTTGGCACACCAAGTTGGGCTGCGCTTCCCACTCAGGCGCAGGGCCAG	852
Db	882	AGGCGGCGCGCGCGCGCGCGCGCTTGGCGGCGGCGCGCGCGCGCGAGCGCGCGCGCGAG	941
Oy	853	AAGGAGGGGTGTTTGTGGGGCATCTCCAAAGGATGAAGTGAAGAGAGAGAGAGAGAGAG	912
Db	942	GCGCGGGGCGGT-----GCGGAGCGGAGAGGGGCG	971
Oy	913	GAAGAGTGTGAACCCCAAGAGATGCGCAATGTCTCGGCGCTCAGACTTTCAGGCGCCCGCGTG	972
Db	972	GCTAGTGTGGGGGGCGGTACCGGCTTCCAGATCCCGGGGGCGCGGTGTGCGCTGTGCGCGC	1031
Oy	973	CAGCAGCCACAGGGCTCCCGGGTGTGGCACCTTACGTGGCGAGGTGCTCTGTGGCAGG	1032
Db	1032	GCCAGCTCGCGCTCGTGAAGTCTTCTGTGCGCGCGCGCGGGCGCGCAGCAGC---	1088
Oy	1033	GCGGTGGGTGCTATAGTGTGGGCAAGTGTGTGGGTGCAAGGGCGCAGCTTACCCGGAGAG	1093
Db	1089	-----GTGTGCGCGCGCAGAGGTGGCCCAAGCGCGCGCTCAAGAG	1124

Oy		1093	CGCTTACCTTCGAGCTGGCTGTGTATGAGCCATTGTTTGCTCTGCTGGTCCCCTC	1152
Dd		1125	CGCTTACCTTTGTGCTGTGGCTGTGTATGAGGTGTGCTGCTGTGTTCCCTTC	1184
Oy		1153	TTCTTCAGCTACAGCCTTGGGGCCCATCTGCCGGAAGA CTGCAAGGTGCCCATGGCTC	1212
Dd		1185	TTCTTCAGCTACAGCCTGTATGGGCATCTGCCGCGAGGACTGCGAGGTGCCGCGCCTC	1244
Oy		1213	TTCCAGTTCTTCTTGTGTATGGGTACTGTGCAACGCTCATCGAAC CCTGTATATAACC	1272
Dd		1245	TTCAAGTTCTTCTTGTGTATGGGTACTGTGCAACGCTCATCGAAC CCGGTATATTAACG	1304
Oy		1273	ATCTTCAACGAGACTTCCGCCGTGCCCTTCGCGAGATCTCTGTGCCGCCCTGTGA	1327
Dd		1305	GCTTTCACCAAGATTTCCGGCCGATCTCTTAAGACAATCTCTTCGACGAGAGA	1359
 RESULT 3 US-09-016-434-1180 ; Sequence 1180, Application US/09016434 ; Patent No. 650938 ; GENERAL INFORMATION: ; APPLICANT: Janice Au-Young ; APPLICANT: Jeffrey J. Seilhamer ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION ; NUMBER OF SEQUENCES: 1490 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC. ; STREET: 3174 PORTER DRIVE ; CITY: PALO ALTO ; STATE: CALIFORNIA ; COUNTRY: USA ; ZIP: 94304 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/016.434 ; FILING DATE: HERewith ; CLASSIFICATION: ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: ; FILING DATE: ; CLASSIFICATION: ; ATTORNEY/AGENT INFORMATION: ; NAME: Zeller, Karen J. ; REGISTRATION NUMBER: 37,071 ; REFERENCE/DOCKET NUMBER: PA-0002 US ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (650) 855-0555 ; TELEFAX: (650) 845-4166 ; INFORMATION FOR SEQ ID NO: 1180: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 3604 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; IMMEDIATE SOURCE: ; LIBRARY: GENBANK ; CLONE: g178195 ; US-09-016-434-1180				
Oy		32.2%	Score 432.6;	DB 4; Length 3604;
		Best Local Similarity	61.8%;	Pred. No. 3.1e-77;
		Matches 828; Conservative	0;	Mismatches 439; Indels 72; Gaps 6;
Oy		15	CCCTTACTCGGTGAGGCGCACAGGGCGCATAGCGCGGCGCATACCTTCTCATCTTCTT	74
Dd		2155	CCCTTACTCCCTGAGGTGAGCGCTGACGCTGCTGTGCTGTGCTGTGCGCGCTGCTCATGCT	2214

QY 75 TACATCTTCGGCAAGCCTCTGTGATCTCTGGCTGTGTAAACAAGCGCTCGCTGCGCG 134
 Db 2215 CACCGCTTTGGGCAACGTGCTGTGATCATATGCGCGGTTCACAGAGCGCGCGCTCAAGCG 227
 QY 135 CCGTCGAACCTGTGTTCTGTGATGTGCGTGGCGCGCGCGCAATCTGTGTGGCAACGGCTAT 194
 Db 2275 GCCCCAAAACCTCTTCTGTGTGTCTGTGGCCTCGCGCGCAATCTGTGTGGCAACGGCTGT 233
 QY 195 CATCCCTTTCCTGCTGGCGCAACGAGCTGTGGCTACTGGTACTTTCGGCGCAGCTGTGT 254
 Db 2335 CATCCCTTTCCTGCTGGCGCAACGAGCTGTGGCTACTGGTACTTTCGGCGCAGCTTGGTG 239
 QY 255 CGAGGTGTAACCTGGCGCTCGACGTGCTCTTCTGTGACCTGTCCATCTGTGACCTGTGGCG 314
 Db 2395 CGAGATCTACTGGCGGCTCGACGTGTCTTCTGACGTGTGTTCATGTGTGACCTGTGTGGCG 2454
 QY 315 CATAGCGCTGGACCGGCTACTGTGGCGGTGAGCCGCGCGCTGAGATCAACTCCAGCGAC 374
 Db 2455 CATCAGCTGGACCGGCTACTGTTCATCAACAAGGCGCATCTGAGTACCAACTGAAACGAC 2514
 QY 375 CCGCGCGCGCATCAAGTGCATCATCCCTCACTGTGTGGCTCATGTGCGCGCGCTCATTTGGCT 434
 Db 2515 GCCCGCGCGCATCAAGCGCATCATCAACCGGTGTGATCACTGTGGCGCGCTCATTTCTTT 2574
 QY 435 GCGCGCGCTCATCT-----ACAAGGCGCAACAAGGCGCGCGCGCGCGCGCGCGCGCGCG 485
 Db 2575 CCGCGCGCTCATCTCATTCAGAAAGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2634
 QY 486 CCAATGCMACTCAACACGAGGCGCTGTATCATCCGTGGCTTCAGACATCCGATTTTCTT 545
 Db 2635 GCGGTGAGATCAAGACCAAGAAAGTGAAGCTCATCTGTGTGCAATCGGCTCTTCTT 2694
 QY 546 TGTCTCTTGGCTCATCATGATCTCTGTCTTAACTGTGGCATTTAACTGTGCAAAACGAC 605
 Db 2695 CGCTCCCTGTCTCATGATCTGTGTTAACTGTGGCATTTAACTGTGCAAAACGCTCG 2754
 QY 606 CAACCGCAGAGGCTCCAGAGGCGCAAGGGGGGGCGCTGGCAGAGGTAAATGCCAAGACCCCG 665
 Db 2755 CACCGCGTGGCAACCA-----GCGCGGGGATCCGAAGCGGTGT 2795
 QY 666 ACCCGACATGTGTGGGCTTTGGCTCAGCCAAACTGACACCGCTGTGCTGTGGCTTC 725
 Db 2796 CCGCGCGCGCGGGGGGCAACGAGCCAGGCGCAACGGTCTG----- 2836
 QY 726 TGCAGAGAGTCAACGACACTGGAATCCACTGTGGGAAAGAGAGGGGAGACCC 785
 Db 2837 -----GGCCCCGAGCGCAGCGCGGCGCGGGGGGGCGAGAGGCGCAACCGCTGTCCAC 2889
 QY 786 TGAAGTACTGGGACCCGAGGCTTGGCCACCAGTTGGGCTGTGCTTCCAACTCAAGGCCA 845
 Db 2890 CCAGTCAACCGCGCGCTGTGGCGAGCCGAGCGGGCGCGCGCGCGCGCGACACGACGCTT 2949
 QY 846 GGGCAGAAAGAGGAGTGTGTGTGGGGGATCTCCAGAGATGAAGCTGAAGAGAGAGAGA 905
 Db 2950 GGAACCTGAGAGAGCTGTCTTCCG-ACACGCGCAGCGGCTCTCAGAGGCCCCCAAGAC 3008
 QY 906 GAGAGGAGAAAGTGTGAACCCACAGCAGTGCAGATGTCTCGGCGCTCAGCTTGAAGCGC 965
 Db 3009 CCGAGCGCGGTCCCCGGGGGCAAAAGCAAGGCCGAGCGAGACGAGTGAAGCCGGGCGCA 3068
 QY 966 CCGCCTGAGAGGCAACAAGGCTCCCGGGTGTGCTGCGACCTTACGTGTGCAAGTGTCTCT 1025
 Db 3069 GCTGTGCGCGCGGGGCGGGGGGAGACGGGGAATCGGGAACGCGGCTGCAAGGCGCGGGGA 3128
 QY 1026 GGGCAGAGGCGGTGGTGTCTAAGATGGGAGTGTGTGGCTCGAAGAGGGCGCAGCTGACCG 1085
 Db 3129 GGAACCGGTGGGGGTCTCCAAAGCGTGTGGCTGTGGCGCGCGCG-----GACGAACCG 3180
 QY 1086 GGAAGAACGCTTCACTTCTGTGCTGTGCTGTGTGATTTGTGCTCTGTGGTT 1145
 Db 3181 CGAAGACGCTTCACTTCTGTGCTGTGCTGTGTGATTCGAAGAGTTCGTGTGTGTGCTGTGTT 3240
 QY 1146 CCGCTTCTTCTTCAAGCTACAGCTGGGCGCATCTGTGCCGAAGACCTCAAGGTGCCCA 1205

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Db      3241 CCCCTTCTTTCTTAACCTAGACGCTCAGCGCCGTGG-----GTGCTCCGTGCACG 3291
QY      1206 TGGCCTCTTCACAGTTCTTCTTGATCGAGTACTACGCAACAGTCACTGAACCTCTTAT 1265
Db      3292 CACGCTCTTCAATTCTTCTTCTGTTGGTGGCTACTACAAACAGCTCTTAAACCCGGTAT 3351
QY      1266 CTACACCATTCTTCAACACAGAGACTTCCGCCGTGCTCCGAGAGATCTGTGCCGCCGTG 1325
Db      3352 CTACACCATCTTCAACACAGATTTCCGCCGCGCTTCAAGAAGATCTCTGTGCGGGGGA 3411
QY      1326 GACCCAAGCGCGCTGTGA 1344
Db      3412 CAGGAAGCGGATCTGTGA 3430

RESULT 4
US-07-676-174A-1
; Sequence 1, Application US/07676174A
; Patent No. 5344776
; GENERAL INFORMATION:
; APPLICANT: Vantor, J. Craig
; TITLE OF INVENTION: Octopamine receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,174A
; FILING DATE: 19910328
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)861-3000
; TELEFAX: (202)822-8944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3335 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 319..2121
US-07-676-174A-1

Query Match          13.8%   Score 184.8; DB 1; Length 3335;
Best Local Similarity 55.9%; Pred. No. 3.7e-28;
Matches 351; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

2 TGACAACACAGAACCCCTACTCGGTGACGCGCACAGCGCCCATGAGCGGCCCATCACT 61
Db      611 TGGGCTTCACACGTGGCTGTGCTCGAAGTGGAGGCCCTTCTACCGCCCTGATTTCTCG 670
QY      62 TTCCTATTCTTTAACATCTTGGCAACGCTGTGATCATCTCGCTGTGTGACACGCC 121
Db      671 TCATTATCGCTGACCATCATCGGAACAATCCGTGTGATTTGAGTGTTCACCTACA 730
QY      122 GCTCGTGCAGCGCCCTTCAGAACCTGTTCTGTGTGTGCTGCGCCCGCCGACATCTGG 181

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Db 731 AGCCGTCGCGATGTCAGAACTTTCATAGTTTCGTCGCGGTGCGCATCTCAAG 790
Qy 182 TGAGCAAGCTCATCATCCCTTTTCGTCGTCGCAAGAGCTGTGGGCTATGGTACTTC 241
Db 791 TGGCCCTTCTGTGTGTCCTCCCTTCAACGTCGTTACTGATCTGGGCGCTGGAGTTCC 850
Qy 242 GCGCAGTGTGTGCGAGTGTACCTGGCGCTCGACGTCCTTCTGCACTGCTCATCG 301
Db 851 GCATCCAGCTGTGCAAGCTGTGCTACCTGGGCGAGTGTGTGTGCTGACAGTCCATCC 910
Qy 302 TGCACTGTGTGCGCATGAGCTGTGAGCCGCTGACCTGAGCCGCTGAGTACA 361
Db 911 TGAACCTGTGTGCGCATGAGCTGTGAGCCGCTGACCTGAGCCGCTGAGTACA 970
Qy 362 ACTCCAGGCGACCGCGCGCGCATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 421
Db 971 CCAGAGAGGAGCGCTGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1030
Qy 422 CCGTCATCTGTCGCGCGCGCTGATCTGACAGGCGCGAGCGCGCGCGCGCGCG 481
Db 1031 TGCTGATTAAGTATGCTGCGCGCTGATGCTGAGAGCTGCGCGAGTTCAGAGCG 1090
Qy 482 GCGCCAGTGAAGCTCAACAGAGAGCGCTGTACATCTGCGCTGCGAGATCGATCTT 541
Db 1091 CCAAGCGCTGCGAGTGAAGCTGCGAGCGAGCTGATCTGCTGCGCTGCGCTGCT 1150
Qy 542 TCTTTGCTCTTGTGCTCATGATCTTGTCTTACCTGCGCATCTGATCTGCGCAAC 601
Db 1151 TCTTTATTCGCTGCGCGCTGATGAGTCTTACATGATCTTGTGCGCGCGCG 1210
Qy 602 GCAGCAACGCGAGAGTCCAGGCGCA 629
Db 1211 GCGCGCTTAAGGAGAGCGAGCGCA 1238

RESULT 5

US-08-194-338-1

Sequence 1, Application US/08194338

Patent No. 5474898

GENERAL INFORMATION:

APPLICANT: Venter, John C.

APPLICANT: Fraser, Claire M.

APPLICANT: McComb, William R.

TITLE OF INVENTION: OCTOPAMINE RECEPTOR

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESS: Knobel, Martens, Olson and Bear

STREET: 620 Newport Center Drive, Sixteenth Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/194,338

FILING DATE: 08-FEB-1994

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/676,174

FILING DATE: 28-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Israel, Ned A.

REGISTRATION NUMBER: 29,655

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 319..2124
US-08-194-338-1

Query Match 12.2%; Score 163.4; DB 1; Length 3335;
Best Local Similarity 55.8%; Pred. No. 6,4e-24;
Matches 351; Conservative 0; Mismatches 276; Indels 2; Gaps 2;

Qy 2 TGAGCAAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 61
Db 611 TGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 670
Qy 62 TCTCATCTCTTTACATCTTGGCAAGCTGTGCTGCTGCTGCTGCTGCTGCTG 121
Db 671 TCAATATCGTGTACCATCATGGAACATCTGTGATTTGAGTGTTCATCAAG 730
Qy 122 GCTGCTGCGCGCGCTGCAAGACTGCTGTGCTGCTGCTGCTGCTGCTGCTG 181
Db 731 AGCGCTGCGCATCTGTCAGAACTTCTTCAATTTGCTGCGGAGTCCGATCTCAG 790
Qy 182 TGGCAGGCTCATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
Db 791 TGGCCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
Qy 242 GGGCAGAGTGTGAGTGTACCTGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCT 301
Db 851 GCATCAAGCTGTGCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 910
Qy 302 TGCA-CCTGTGCGCATGAGCTGAGCGCTGAGCGCTGAGCGCGCTGAGTAC 360
Db 911 TGAACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969
Qy 361 AACTCAAGGAGCGCGCGCGCTGATCAAGTGTGCTGCTGCTGCTGCTGCTGCT 420
Db 970 GCGCAGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1029
Qy 421 GCGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 1030 CTGCTATTAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1089
Qy 481 GCGCCAGTGAAGCTCAACAGAGAGCGCTGTATCTGCTGCTGCTGCTGCTGCT 540
Db 1090 GCGAGCGCTGCGAGCTGAGCTGAGCGAGCGCTGATCTGCTGCTGCTGCTG 1149
Qy 541 TCTTTGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 1150 TCTTTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1209
Qy 601 CGAGCAAGCGCGAGGCTCCAGGCGCA 629
Db 1210 GCGCGCTTAAGGAGAGCGAGCGCA 1238

RESULT 6

US-08-722-001-17

Sequence 17, Application US/08722001

Patent No. 5760054

GENERAL INFORMATION:

APPLICANT: Thompson, Wayne J.

APPLICANT: Huff, Joel R.

APPLICANT: Nerenberg, Jennie B.

APPLICANT: Lee, Hee-Yoon

APPLICANT: Bell, Ian M.

TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Apollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-17

Query Match 11.8%; Score 158.6; DB 1; Length 921;
Best Local Similarity 57.0%; Pred. No. 4.8e-23;
Matches 312; Conservative 0; Mismatches 229; Indels 6; Gaps 1;

63 CCTATTCTCTTACCAATCTTGGCAAGCTCTGTGATCTCTGCTGTGACCAAGCG 122
170 CTTATCTCTTTGCAATCGGGCAACATCTGATCTTGTGTGCTGCAACCG 229
123 CTCGCTGCGCGCCCTGAGAACCTGTCGTGCTGCTGCGCGCGCGCAATCCGGT 182
230 GCACTGCGGACGCGCAACAACTACTTCACTGCACTGCGCATGCGCACTGCTGTT 289
183 GCGCAGCTATCATCTCTTTCTGCGCAAGAGCTGCTGCGCTACTGTAATCTCG 242
290 GAGCTTACCGCTCTGCTCTCTCAAGCGGCTGAGAGTCTGCGTACTGAGTGG 349
243 GCGCAGCTGAGGAGGTGATCTGAGCGCTGAGCGCTCTTGTGACCTGCGCATCT 302
350 GCGGATTTCTGTGACATCTGGGCAAGCTGAGATGCTCTGTGACAGCGTCAATCT 409
303 GCACTGTGCGCAATCACTGAGCGCTTACCTGAGCGCGCTGAGAGTAA 362
410 GACCTGTGCGCAATCACTGAGCGCTTACCTGAGCGCGCTGAGAGTAA 469
363 CTCGAGCGGACCGCGCGCGCAAGAGTCAATCTGATCTGTGCTGATCGCGCG 422
470 CAGCTGTGATCCGAGGAGAGGCAATCTTGGCTGCTCAAGTGTGAGTCTGTG 529
423 CGTATCTGCTGCGCGCGCTCAATCTTAAAGGCGCAAGGCGCGCGCGCGCGG 482
530 CGTATCTGATGAGGCTCTCTTGTGGTGAAGAGCGCGCAACCA-----CGATGA 583
483 CCCCCGTGAGAGCTTAACGAGAGCGCTGTAATCTGAGCTTCCAGCATGGAATCTT 542
584 CAGAGGTGCGGGGTACCGAAGAACCTTTATATGCTCTTCTCTCTGAGGCTCTT 643

543 CTTTGCTCTTGGCTTATCAATGATCTTGTCTACCGGCAATCTGATCCCAACG 602
644 CTACATCTCTTGGCGGCTATCTGATCAATGATCTGCGGCTATATATGAGCAAG 703
603 CAGCAAC 609
704 AACCACT 710

RESULT 7
US-08-722-001-24
Sequence 24, Application US/08722001
Patent No. 576054
GENERAL INFORMATION:
APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel R.
APPLICANT: Nerenberg, Jennie B.
APPLICANT: Lee, Hee-Yoon
APPLICANT: Bell, Ian M.
TITLE OF INVENTION: ALPHALIC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Apollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-24

Query Match 11.8%; Score 158.6; DB 1; Length 1567;
Best Local Similarity 57.0%; Pred. No. 5.1e-23;
Matches 312; Conservative 0; Mismatches 229; Indels 6; Gaps 1;

63 CCTATTCTCTTACCAATCTTGGCAAGCTCTGTGATCTCTGCTGTGACCAAGCG 122
170 CTTATCTCTTTGCAATCGGGCAACATCTGATCTTGTGTGCTGCAACCG 229
123 CTCGCTGCGCGCCCTGAGAACCTGTCGTGCTGCTGCGCGCGCGCAATCCGGT 182
230 GCACTGCGGACGCGCAACAACTACTTCACTGCACTGCGCATGCGCACTGCTGTT 289
183 GCGCAGCTATCATCTCTTTCTGCGCAAGAGCTGCTGCGCTACTGTAATCTCG 242

Db 290 GAGCTTCAACGCTCTGCTTCTCAAGGCGCTTACAGAGTCTCGCTACCTGGTCTGG 349
Qy 243 GCGCAGTGGGAGGAGTGTACTTGGGCTGAGAGTCTCTTCTGCACTCGTTCATCT 302
Db 350 GCGGATTTTGTGTACATCTGGGAGCGCTGGATGTCTTGTCTGCAAGGCTCATTT 409
Qy 303 GCACTGTGTGCGCATCAAGCTGACCGCTACTGCGGCGTGAAGCGCGCTGAGTCA 362
Db 410 GAGCTGTGTGCGCATCTCAATGATGCTACTGCGGCTGCTGCTGCTGCTGCTGCT 469
Qy 363 CTCGAGCGACCGCGCGCGCATCAAGTCAATCTTCACTGTGTGCTCATGCGCG 422
Db 470 CAGCTGTGTCAACCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 529
Qy 423 CGTATCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
Db 530 CGTATCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 583
Qy 483 CCGCCAGTGAAGCTCAACGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
Db 584 CAGGAGTGTGGGGGTACCGAAGACCTTCTATGCTTCTTCTCTCTGCTGCTGCTCTT 643
Qy 543 CTTTGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
Db 644 CTATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 703
Qy 603 CAGCAAC 609
Db 704 AACCAAC 710

RESULT 8

US-08-334-698-3

Sequence 3, Application US/08334698
Patent No. 5556753
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
City: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,698
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/952,798
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 376901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-334-698-3

Query Match 11.7%; Score 157; DB 1; Length 1738;
Best Local Similarity 56.9%; Pred. No. 1.1e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

Qy 63 CTTATCTCTTATCAATCTTGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122
Db 285 CTTATCTCTTATCAATCTTGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
Qy 123 CTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
Db 345 GCACTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
Qy 183 GCGCAGCTATATCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
Db 405 GAGCTTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
Qy 243 GCGCAGTGTGTGAGGTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
Db 465 GCGATCTTCTGTGACATCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
Qy 303 GCACTGTGCGCGCATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
Db 525 GAGCTGTGCGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
Qy 363 CTCGAGCGACCGCGCGCGCATCAAGTCAATCTTCACTGTGTGCTCATGCGCG 422
Db 585 CAGCTGTGTCAACCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
Qy 423 CGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
Db 645 CGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
Qy 483 CCGCCAGTGAAGCTCAACGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
Db 699 CAGGAGTGTGGGGGTACCGAAGACCTTCTATGCTTCTTCTCTGCTGCTGCTCTT 758
Qy 543 CTTTGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
Db 759 CTATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
Qy 603 CAGCAAC 609
Db 819 AACCAAC 825

RESULT 9

US-08-228-932-3

Sequence 3, Application US/08228932
Patent No. 5578611
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
Theresa A. Branchek, John M. Weitzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
City: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,932
FILING DATE: 13-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-228-932-3

Query Match 11.7%; Score 157; DB 1; Length 1738;
Best Local Similarity 56.9%; Pred. No. 1.1e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

63 CCTCATCTCTTTACCACTTTGGCAACGCTCTGCTCATCTGCTGTGTTGACCAACCG 122
123 CTGCTGCGGG 182
285 CTTTCATCTCTTTGGCAACGCTCTGCTCATCTGCTGTGTTGACCAACCG 344
123 CTGCTGCGGG 182
345 GCACCTGCGGAGCGGCAACCACTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 404
183 GGGCAGCCTGATCATCTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
405 GAGCTTACCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
243 GCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
465 GCGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
303 GCACCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
525 GAGCTTACCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
363 CTCGACGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 422
585 CAGCGTGTGACCGCGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 644
423 GGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
645 GGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
483 CCGCCAGTGAAGCTCAACAGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
699 CAGGAGATGCGGGGTACCGGAGAGCCCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 758
543 CTTTGCTCTTGTGCTCACTGATCTTGTCTTACCTGCGCATCTACCTGATGCGCAACG 602
759 CTACATCTCTGCGGGGTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
603 CAGCAAC 609

Db 819 AACACC 825

RESULT 10
US-08-468-939-3
Sequence 3, Application US/08468939
Patent No. 5714381
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-468-939-3

Query Match 11.7%; Score 157; DB 1; Length 1738;
Best Local Similarity 56.9%; Pred. No. 1.1e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

63 CCTCATCTCTTTACCACTTTGGCAACGCTCTGCTCATCTGCTGTGTTGACCAACCG 122
285 CTTTCATCTCTTTGGCAACGCTCTGCTCATCTGCTGTGTTGACCAACCG 344
123 CTGCTGCGGG 182
345 GCACCTGCGGAGCGGCAACCACTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
183 GCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
405 GAGCTTACCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
243 GCGCAGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
465 GCGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
303 GCACCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
525 GAGCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584

QY 363 CTCGACGCGACCCCGCGCCGATCAAGTCATCATCTGCTGCTCAATCCGCG 422
DB 585 CAGCGTGTGACCCGAGGAGGACATCTGGGCGCTCAGTGTCTGGTCTTGTTCAC 644
QY 423 CGTCATCTGCTGCGCGCCCTCATCTAACAGGCGACAGGCGCCCGCGCGCG 482
DB 645 CGTCATCTGCTGCGCGCTCTCTGCTGAGGAGGAGCGGACCCGAA-----CGATGA 698
QY 483 CCCCCGAGTGAAGTGAACGAGAGGCGTGTGATCTGCTGCTGCTGCTGCTGCT 542
DB 699 CAGAGTGTGGGGGTGACGAGAGACCTTCTATGCTCTTCTCTCTGCGCTCTCT 758
QY 543 CTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
DB 759 CTACATCTCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
QY 603 CAGCAAC 609
DB 819 AACCAAC 825

RESULT 11

US-08-406-855A-3
Sequence 3, Application US/08406855A
Patent No. 5861309
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08406855A
FILING DATE: 21-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION/DOCKET NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-406-855A-3

Query Match 11.7%; Score 157; DB 2; Length 1738;
Best Local Similarity 56.9%; Pred. No. 1,1e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

QY 63 CTTATCTCTTTTACCATCTTTCGCAACGCTGTGTCATCTGAGTGTGTAACGACCG 122
DB 285 CTTATCTCTTTTACCATCTTTCGCAACGCTGTGTCATCTGAGTGTGTAACGACCG 344
QY 123 CTCGCTGCGCGCCCTCAGAACTGTTCTGTGTGTGCTGTGCGCGCGCAATCTGT 182
DB 345 GCACTGCGGAGCCCAACCACTTCTGTAATGTAACCTGCGCATGCGCACTGCTGT 404
QY 183 GGCACGCTCATCTATCTCTTCTGCTGCGCAACGAGCTGTGAGTGTGTAATCTTCCG 242
DB 405 GAGCTTCACTGCTGCTGCTCTTCTGAGGAGCTGAGAGTGTGCTGCTACTGAGTGT 464
QY 243 GCGCAGTGTGTGAGAGTGTGATCTGAGCTGAGAGTGTGCTTCTGCACTGCTCATCT 302
DB 465 GCGGATCTTGTGTAATCTGAGGAGCGCGGAGTGTGCTGAGCAAGCTGCTCATCT 524
QY 303 GCACTGTGCGCATCAAGCTGAGCGCTGAGCGCGGTGAGCGCGCTGAGTGA 362
DB 525 GAGCTGTGCGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 584
QY 363 CTCGACGCGACCCCGCGCGCATCAAGTCATCATCTGCTGCTGCTGCTGCTGCT 422
DB 585 CAGCGTGTGACCCGAGGAGGACATCTGGCGCTGCTGCTGCTGCTGCTGCTGCT 644
QY 423 CGTCATCTGCTGCGCGCCCTCATCTAACAGGCGACAGGCGCCCGCGCGCGCG 482
DB 645 CGTCATCTGCTGCGCGCTCTCTTGGGTGAGAGGCGCGCACCCGAA-----CGATGA 698
QY 483 CCCCCGAGTGAAGTGAACGAGAGGCTGTGATCTGCTGCTGCTGCTGCTGCTGCT 542
DB 699 CAGAGTGTGGGGGTGACGAGAGACCTTCTATGCTCTTCTCTCTGCTGCGCTCT 758
QY 543 CTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
DB 759 CTACATCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
QY 603 CAGCAAC 609
DB 819 AACCAAC 825

RESULT 12

US-08-722-190-3
Sequence 3, Application US/08722190
Patent No. 5990128
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forray, George
APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08722190
FILING DATE: 4-APR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-722-190-3

Query Match 11.7% Score 157; DB 2; Length 1738;
Best Local Similarity 56.9%; Pred. No. 1,1e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

QY 63 CCTCATCTCTTTACATCTTGGCAACGCTGGTCACTGCTGTTGTTGACACCG 122
DB 285 CTTTCATCTCTTTGCAATGCGCAACATCTTATCTTGTCTGCGCTGCAACCG 344
QY 123 CTGCTGGCGGCCCTTCAAGACCTGTTCTGCTGCTGGCCGCGCAATCTGCT 182
DB 345 GCACCTGGAGAGCGCCCAACCACTTCAATGCAACCTGGCCATGGCGACCTGCT 404
QY 183 GGCACAGCTCATCTCTTCTGCTGCAACAGCTGGCTGCTGCTGCTGCTGCT 242
DB 405 GAGCTTACCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
QY 243 GCGCAGTGGTGGAGAGTGAATCTGCGCTGCACTGCTGCTGCTGCTGCTGCT 302
DB 465 GCGCAGTCTTGTGATGATGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
QY 303 GCACCTGCGCCATCAGCTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
DB 525 GAGCTTGGCGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
QY 363 CTCGAAGCGCACCGCGCGCGCATTAAGTCAATCTGCTGCTGCTGCTGCTGCT 422
DB 585 CACGCTGCTACCGCGAGAAAGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCT 644
QY 423 GGTATCTGCTGCGCCCTCATCTCAAGAGGAGCAAGGCGCCGCGCGCGCG 482
DB 645 GGTATCTCAATCGCGCTCTCTTGGGTGAAGAGCGCGCAACCA-----CGATGA 698
QY 483 CCCCAGTGCAGTCAACCAAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
DB 699 CAAAGAGTGGGGGTCAACCGAAGAACCTTCAATGCGCTCTCTCTCTGCGCTCT 758
QY 543 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
DB 759 CTATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
QY 603 CAGAAG 609
DB 819 AACCAAC 825

RESULT 13
US-08-244-354-3
Sequence 3, Application US/08244354
Patent No. 6015819
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP

STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,354
FILING DATE: April 1, 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-244-354-3

Query Match 11.7% Score 157; DB 3; Length 1738;
Best Local Similarity 56.9%; Pred. No. 1,1e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

QY 63 CCTCATCTCTTTACATCTTGGCAACGCTGGTCACTGCTGTTGTTGACACCG 122
DB 285 CTTTCATCTCTTTGCAATGCGCAACATCTTATCTTGTCTGCGCTGCAACCG 344
QY 123 CTGCTGGCGGCCCTTCAAGACCTGTTCTGCTGCTGGCCGCGCAATCTGCT 182
DB 345 GCACCTGGAGAGCGCCCAACCACTTCAATGCAACCTGGCCATGGCGACCTGCT 404
QY 183 GGCACAGCTCATCTCTTCTGCTGCAACAGCTGGCTGCTGCTGCTGCTGCTGCT 242
DB 405 GAGCTTGGCGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
QY 423 GGTATCTGCTGCGCCCTCATCTCAAGAGGAGCAAGGCGCCGCGCGCGCG 482
DB 645 GGTATCTCAATCGCGCTCTCTTGGGTGAAGAGCGCGCAACCA-----CGATGA 698
QY 483 CCCCAGTGCAGTCAACCAAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
DB 699 CAAAGAGTGGGGGTCAACCGAAGAACCTTCAATGCGCTCTCTCTCTGCGCTCT 758

QY 543 CTTGCTCTTGGCTCATCATGATCTTGTCTACCTGCGCATCTACCTGATCGCAACG 602
DB 759 CTACATCCCTCTGGCGGTCTATCTAGTACGATCGCGGTCTATATAGTGGCAAG 818
QY 603 CAGCAAC 609
DB 819 AACCAAC 825

RESULT 14

US-09-206-899-3
; Sequence 3, Application US/09206899
; Patent No. 6083705
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,899
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,855
; FILING DATE: 21-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1683
; OTHER INFORMATION:
; US-09-206-899-3

Query Match 11.7%; Score 157; DB 3; Length 1738;
Best Local Similarity 56.9%; Pred. No. 1,1e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

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DB 285 CTTTATCTCTTGGCGGTCTATCTAGTACGATCGCGGTCTATATAGTGGCAAG 344
QY 123 CTCGCTGGCGCGCCCTCAGAACCTGTTCTGTGTGCTGGCGCGCGCGGACATCTGTGT 182
DB 345 GCACTGTGGGAGCGCCGACCAACTTCACTTGTCAACCTGGCGCATGCGGACCTGTGT 404
QY 183 GGCACGCTCATCATCTCTTCTGCTGGCAAGAGCTGTGGGCTACTGTGATCTTGG 242

DB 405 GAGCTTACCGTCTGCGCCCTTCTCAGAGGCGCTTGAAGGTCTCGCTACTGGGTGG 464
QY 243 GCGACAGTGTGAGAGTGTACCTGCGGCTGACGCTCTTCTGTGACCTGTGCATGT 302
DB 465 GCGGATCTTCTGTGACATCTGGGACCGGTGATGTCTGTGTGACAGCGTCACTTCT 524
QY 303 GCACCTGTGCGCCATCAGCTGAGACCGTCACTGAGGCGGTGAGCGCGCTGAGTCA 362
DB 525 GAGCTGTGCGCATCTTCATGATGCTAATCGGGGTGGGCTACTCTGTGAGTATCC 584
QY 363 CTCGAAGCGCACCGCGCGCGCATCAAGTCAATCTCACTGTGTGTCTATCGCGCG 422
DB 585 CACGCTGTACCGCCGAGGAGGCGCATCTTGGCGCTGCTCAATGTCTGTGGTCTTGTCC 644
QY 423 CGTATCTGCTGCGCGCCCTCATCTACAAGGCGCAGAGGCGCCGACCGCGCGGG 482
DB 645 CTTATCTCATGCGGCTCTCTCTTGGGTGAAGAGCGGACCCAA-----CATGA 698
QY 483 CCCCCAGTCAAGCTCAACAGAGGCTGTATCATCTGAGCTTCCAGCATCGATCTTT 542
DB 699 CAAGAGTGGGGGTACCGAAGAACCTTCTATGCGCTTCTCTCTCTGCGCTCTT 758
QY 543 CTTGCTCTTGGCTCATCATGATCTTGTCTACTGCGCATCTACCTGATCGCAACG 602
DB 759 CTACATCCCTCTGGCGGTCTATCTAGTACGATCGCGGTCTATATAGTGGCAAG 818
QY 603 CAGCAAC 609
DB 819 AACCAAC 825

RESULT 15

US-09-444-783-3
; Sequence 3, Application US/09444783
; Patent No. 6420389
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, et al.
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,783
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TEXT:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: February 7, 2004, 20:38:27 ; Search time 512.783 Seconds
(without alignments)
9654.769 Million cell updates/sec

Title: US-09-692-077D-2
Perfect score: 1344
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1344	100.0	1344	US-10-001-073-2	Sequence 2, Appl1
2	1339.2	99.6	1344	US-09-825-923-1	Sequence 1, Appl1
3	1339.2	99.6	1344	US-10-077-870-1	Sequence 1, Appl1
4	1325	98.6	1353	US-10-001-073-1	Sequence 1, Appl1
5	1323.4	98.5	1353	US-09-825-923-3	Sequence 3, Appl1
6	1323.4	98.5	1353	US-10-077-870-3	Sequence 3, Appl1
7	1321.8	98.3	2072	US-10-305-720-1181	Sequence 1181, Ap
8	1321.8	98.3	2072	US-10-305-720-1181	Sequence 1181, Ap
9	617.6	46.0	6904	US-10-311-455-48	Sequence 48, Appl1
10	531.6	39.6	6904	US-10-311-455-47	Sequence 47, Appl1
11	464.2	34.5	1386	US-10-001-073-40	Sequence 40, Appl1
12	457.8	34.1	2826	US-10-225-567A-43	Sequence 43, Appl1
13	451.4	33.6	1374	US-10-001-073-42	Sequence 42, Appl1
14	446	33.2	1350	US-10-001-073-25	Sequence 25, Appl1
15	445.4	33.1	3653	US-10-225-567A-39	Sequence 39, Appl1

16	445	33.1	1382	US-10-305-720-1256	Sequence 1256, Ap
17	445	33.1	1382	US-10-101-510-754	Sequence 754, Appl
18	444.4	33.1	1350	US-10-001-073-24	Sequence 24, Appl
19	432.6	32.2	3604	US-10-305-720-1180	Sequence 1180, Ap
20	304.2	22.6	1758	US-10-101-510-450	Sequence 450, Appl
21	262.6	19.5	7353	US-10-311-455-46	Sequence 46, Appl
22	181.4	13.5	7353	US-10-311-455-45	Sequence 45, Appl
23	157	11.7	1738	US-10-305-720-1402	Sequence 1402, Ap
24	157	11.7	1738	US-10-185-991-3	Sequence 3, Appl1
25	157	11.7	1738	US-10-338-129-3	Sequence 3, Appl1
26	157	11.7	1738	US-10-338-667-3	Sequence 3, Appl1
27	157	11.7	1786	US-10-225-567A-35	Sequence 35, Appl
28	149.6	11.1	2002	US-10-305-720-1172	Sequence 1172, Ap
29	149.6	11.1	2130	US-10-225-567A-33	Sequence 33, Appl
30	149.6	11.1	2140	US-10-185-991-1	Sequence 1, Appl1
31	149.6	11.1	2140	US-10-238-129-1	Sequence 1, Appl1
32	149.6	11.1	2140	US-10-238-667-1	Sequence 1, Appl1
33	147.6	11.0	1896	US-10-270-333-83	Sequence 83, Appl
34	145.4	10.8	1704	US-10-270-333-125	Sequence 125, Appl
35	143.4	10.7	463	US-09-918-995-29557	Sequence 29557, A
36	142.6	10.6	2048	US-10-052-589-1	Sequence 1, Appl1
37	141	10.5	1548	US-10-054-616A-8	Sequence 8, Appl1
38	139.4	10.4	1548	US-10-054-616A-9	Sequence 9, Appl1
39	139.4	10.4	1548	US-10-054-616A-11	Sequence 11, Appl
40	138.4	10.3	1098	US-09-826-509-430	Sequence 430, Appl
41	138.4	10.3	1930	US-10-305-720-1171	Sequence 1171, Ap
42	138.4	10.3	1930	US-10-325-567A-7	Sequence 7, Appl1
43	138.2	10.3	1639	US-10-185-991-5	Sequence 5, Appl1
44	138.2	10.3	1639	US-10-238-129-5	Sequence 5, Appl1
45	138.2	10.3	1639	US-10-238-667-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-10-001-073-2
: Publication 2, Application US/10001073
: Identification No. US20030113725A1
: GENERAL INFORMATION:
: APPLICANT: Liggett, Stephen
: TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
: FILER REFERENCE: Small, Kirsten
: CURRENT APPLICATION NUMBER: US/10/001,073
: CURRENT FILING DATE: 2001-11-01
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 1344
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-001-073-2

Query Match	100.0%	Score 1344;	DB 15;	Length 1344;
Best Local Similarity	100.0%	Pred. No. 4.3e-11;		
Matches 1344;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAGCACCAAGAGACCCCTACTCCGTGCAGGCAACAGCGGCATAGAGCGGCCATCACC	60	
DB	1	ATGAGCACCAAGAGACCCCTACTCCGTGCAGGCAACAGCGGCATAGAGCGGCCATCACC	60	
QY	61	TTCTCATTTCTTTTACCATCTTTCGCAAGCGCTGTGATCTGCTGCTGTGTTACACAGC	120	
DB	61	TTCTCATTTCTTTTACCATCTTTCGCAAGCGCTGTGATCTGCTGCTGTGTTACACAGC	120	
QY	121	CGCTGCTGGCGCGCCCTCAAGACCTGTCCTGTGTCGCTGCGCGCGCGGCAATCTTG	180	
DB	121	CGCTGCTGGCGCGCCCTCAAGACCTGTCCTGTGTCGCTGCGCGCGCGGCAATCTTG	180	
QY	181	GTGGCCAGCTCATCATCTCTTCTCGCTGGCCCAAGAGCTGCTGGCTACTGTTACTTC	240	
DB	181	GTGGCCAGCTCATCATCTCTTCTCGCTGGCCCAAGAGCTGCTGGCTACTGTTACTTC	240	

QY	241	CGGGCAGCTGATGTCCAGAGGTGTAACCTTGCGCTGCAGCTGCTCTTCTGCACCTGCTCATT	3000
Db	241	CGGGCAGCTGATGTCCAGAGGTGTAACCTTGCGCTGCAGCTGCTCTTCTGCACCTGCTCATT	3000
QY	301	GTCGACCTGTGCGCGCATCAGCTTGAGCCGCTACTGGGCGGTGAGCGCGGCTGTGAGTAC	3600
Db	301	GTCGACCTGTGCGCGCATCAGCTTGAGCCGCTACTGGGCGGTGAGCGCGGCTGTGAGTAC	3600
QY	361	AACCTCAAGCGCACCCCGCGCGCATCAAGTGCAATCCTCACTGTGTGGCTATCGCC	4200
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QY	421	GCGGTCATCTCGGCGCGCGCGCGCTATCAAGAGGCGCACAGAGGCGCCCAAGCGCGCGG	4800
Db	421	GCGGTCATCTCGGCGCGCGCGCGCTATCAAGAGGCGCACAGAGGCGCCCAAGCGCGCGG	4800
QY	481	CGCGCCCAAGTGCAAGCTCAACAGAGAGCGCTGTGATCATCTGTGCTCTTCAGATCGAATCT	5400
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Db	961	AAGCCCCCGCTCAGTAGGCCACAGAGGCTCCCGGGGTCTGGGCCAACCCTAAGTGGCCAGGTG	10200
QY	1021	CTCTTGAGGAGGAGGCGGTGAGTCTATAGTGTGGGCGAGTGTGCGTGAAGAGGCGAGGTG	10800
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Db	1081	AACCGGAGAGAGCGCTTCACTTTCGTGTGCGCTGTGTGATTTAGGCGTTTGTGTGCTGCG	11400
QY	1141	TGGTTCCCGCTTCTTCTTCAAGCTACAGGCTTGGCGCGCATCTGCGCGAACACTGTGCAAGTGTG	12000
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QY	1201	CCCCATGAGCTCTTTCAGATTTCTTCTTGATCGGCTACTGCAACAGCTCACTGAACCT	12600
Db	1201	CCCCATGAGCTCTTTCAGATTTCTTCTTGATCGGCTACTGCAACAGCTCACTGAACCT	12600
QY	1261	GTATATCTACACATTTCAACAGAGCTTCCGCGGTGCTTTCGAGAGATCTGTGCGCG	13200
Db	1261	GTATATCTACACATTTCAACAGAGCTTCCGCGGTGCTTTCGAGAGATCTGTGCGCG	13200

QY	1321	CCGTGACCCAGACGGCCTGTGA	1344
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RESULT 2

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: Sequence 1 Application US/09825923
: Patent No. US20010016338A1
: GENERAL INFORMATION:
: APPLICANT: Snapir, Amir
: APPLICANT: Heinonen, Paula
: APPLICANT: Alhopuro, Pia
: APPLICANT: Karvonen, Matti
: APPLICANT: Koulou, Markku
: APPLICANT: Pesonen, Ulla-mari
: APPLICANT: Scheinin, Mika
: APPLICANT: Salonen, Jukka T
: APPLICANT: Tuominen, Tomi-Pekka
: APPLICANT: Iakka, Timo A
: APPLICANT: Myys"nen, Kristiina
: APPLICANT: Salonen, Riitta
: APPLICANT: Kauphanen, Jussi
: APPLICANT: Valkonen, Veli-Pekka
: TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
: FILE REFERENCE: Alpha-2B-AR variant
: CURRENT FILING DATE: 2001-04-05
: PRIOR APPLICATION NUMBER: 09/422,985
: PRIOR FILING DATE: 2000-05-25
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 1
: LENGTH: 1344
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1341)
: OTHER INFORMATION: Coding sequence for variant human
: OTHER INFORMATION: alpha-2B-adrenoceptor protein
: US-09-825-923-1

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Query Match	99.6%	Score 1339.2	DB 9	Length 1344
Best Local Similarity	99.8%	Pred. No. 6e-310		
Matches 1341; Conservative	0	Mismatches 3	Indels 0	Gaps 0

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QY	61	TTCTCATTTCTTTTACCATCTTGGCAACGCTGGTCATCTGGCGTGTGTTAACACAGC	120
Db	61	TTCTCATTTCTTTTACCATCTTGGCAACGCTGGTCATCTGGCGTGTGTTAACACAGC	120
QY	121	CGCTCGGTGCGCGCCCTCAGAACCTGTTCCTGTGTGTGCGTGGCGCGCGACATCCTG	180
Db	121	CGCTCGGTGCGCGCCCTCAGAACCTGTTCCTGTGTGTGCGTGGCGCGCGACATCCTG	180
QY	181	GTGGCCACGCTATATCTCTTTCGTGTGGCAACGAGCTGTGGGCTACTGTGATCTTC	240
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QY	301	GTGCACCTGTGGCCCATAGCCTGGACCGCTACTGGGCGGTGGAGCGCGCGCTGGAGTAC	360
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Db 481 GCG 540
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Qy 601 CGGAGCAACCGGAGAGGTCCCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 601 CGGAGCAACCGGAGAGGTCCCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Qy 661 CCCGAGCCGAGCATGTGGTGGGCTTTTGAGCTCAAGCCCAAGCTGCGCGCTGTGTG 720
Db 661 CCCGAGCCGAGCATGTGGTGGGCTTTTGAGCTCAAGCCCAAGCTGCGCGCTGTGTG 720
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Db 721 GCTTTCTGCGAGAGGTCAACGCACTCGAAGTCACTGGGAGAAAGAGAGAGAGAG 780
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Qy 841 GGCAGAGGCGAG 900
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Qy 901 GAG 960
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Qy 1021 CTCTGCGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1080
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Qy 1201 CCCGAGGCGCGCTTCTGAGTCTTCTGAGTGGGCGTCACTGCAAGTCACTGCAAGT 1260
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Db 1321 CCGTGAACCGAGAGCGGCTGTGA 1344

RESULT 3
US-10-077-870-1
; Sequence 1, Application US/10077870
; Publication No. US2003003470A1
; GENERAL INFORMATION:

; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

Query Match 99.6%; Score 1339.2; DB 15; Length 1344;
Best Local Similarity 99.8%; Pred. No. 66-310;
Matches 1341; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 ATGAGCACCAGAGACCCCTACTCCGTGACAGGCCAAGCGGCATAGCGCGGCATCAAC 60
Qy 61 TTCTCTATTTCTTTTACATCTTGGCAAGCTTGGTCACTCTGCTGTGTGACCAAGC 120
Db 61 TTCTCTATTTCTTTTACATCTTGGCAAGCTTGGTCACTCTGCTGTGTGACCAAGC 120
Qy 121 GCGTGTGCG 180
Db 121 GCGTGTGCG 180
Qy 181 GTGCGCAGGCTATCATCTCTTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 181 GTGCGCAGGCTATCATCTCTTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Qy 241 GCGGCGAGGTGTGCGAGGTGTACCTGCGCTGCAAGTCTCTTCTGCACTGTGCATC 300
Db 241 GCGGCGAGGTGTGCGAGGTGTACCTGCGCTGCAAGTCTCTTCTGCACTGTGCATC 300
Qy 301 GTGACCTGTGCGCATCACTGAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 301 GTGACCTGTGCGCATCACTGAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGG 360
Qy 361 AACTCCAGGCGACCCCGCGCGCATCAAGTCACTCTCACTGTGTGCTCATCGCC 420
Db 361 AACTCCAGGCGACCCCGCGCGCATCAAGTCACTCTCACTGTGTGCTCATCGCC 420
Qy 421 GCGGTATCTGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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Qy 661 CCCGAGCCGAGCATGTGGTGGGCTTTTGAGCTCAAGCCCAAGCTGCGCGCTGTGTG 720
Db 661 CCCGAGCCGAGCATGTGGTGGGCTTTTGAGCTCAAGCCCAAGCTGCGCGCTGTGTG 720
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Db 721 GCTTCTGCGAGAGAGTCAACGCACTCGAATGCCATGCGGAGAAAGAGAGGAG 780
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Db 781 ACCCTGAAAGTACTGGGACCCGGGCTTGGCCACCACTTGGGCTGCCCTTCCCACTCA 840
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Qy 901 GAGAGAGAGAGAGAGAGTGAACCCAGGAGTGGCAGTGTCTCGGCTCTCAGCTTGC 960
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Qy 961 AGCCCCCGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
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Qy 1261 GTTATCTACACCACT 1320
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Db 1321 CCGTGAACCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1344

RESULT 4
US-10-001-073-1
; Sequence 1, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-1

Query March 98.6%; Score 1325; DB 15; Length 1353;
Best Local Similarity 99.3%; Pred. No. 1.5e-306;
Matches 1344; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

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Qy 181 GTGGCCACGCTCATCT 240
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Qy 241 GCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
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Db 421 GCGGTATCTGCGTGGCGGCCCTCATCTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
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Db 601 CGAGAGACCGGAGAGGAGTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
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Qy 721 GCTTCTGCGAGAGAGTCAACGAGCACTCGAAGTCACTGGGAGAGAGAGAGGAGGAG 780
Db 721 GCTTCTGCGAGAGAGTCAACGAGCACTCGAAGTCACTGGGAGAGAGAGAGGAGGAG 780
Qy 781 ACCCTGAAGATCTGGAGCCCGGCTTGGCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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Qy 841 GGCAGAGGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 894
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Qy 901 GAAG 960
Db 901 GAAG 960
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Qy	1192	TGCAAGGAGCCCAATGGCTCTTCACAGTTCTTCTTGGAATGGCTACTGCAACAGCTCA	1251
Db	1201	TGCAAGGTGCCCAATGGCTCTTCCAGTTCTTCTTGGAATGGCTACTGCAACAGCTCA	1266
Qy	1252	CTGAACCCCTGTATCTACACCATCTTCAACAGGACTTCGCGCGTGCCTTCCGAGAGATC	1311
Db	1261	CTGAACCTGTATCTTACACCATCTTCAACAGGACTTCGCGCGTGCCTTCCGAGAGATC	1320
Qy	1312	CTGTGCGCGCCGTGGAACCCAGACGGCTGTGTGA	1344
Db	1321	CTGTGCGCGCCGTGGAACCCAGACGGCTGTGTGA	1353

RESULT 5

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/ Sequence 3, Application US/09825923
/ Patent No. US20010016338A1
/ GENERAL INFORMATION:
/ APPLICANT: Snaflr, Amir
/ APPLICANT: Heinonen, Paula
/ APPLICANT: Alhopuro, Pia
/ APPLICANT: Karvonen, Matti
/ APPLICANT: Koulou, Markku
/ APPLICANT: Pesonen, Ulla-mari
/ APPLICANT: Scheinin, Mika
/ APPLICANT: Salonen, Jukka T
/ APPLICANT: Tuomala, Tomi-Pekka
/ APPLICANT: Lakka, Timo A
/ APPLICANT: Nyysanen, Kristina
/ APPLICANT: Salonen, Riitta
/ APPLICANT: Kauppinen, Jussi
/ APPLICANT: Valkonen, Veli-Pekka
/ TITLE OF INVENTION: A DNA molecule encoding a
/ TITLE OF INVENTION: protein, and uses thereof
/ FILE REFERENCE: Alpha-2B-AR variant
/ CURRENT APPLICATION NUMBER: US/09/825,923
/ CURRENT FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 09/422,985
/ PRIOR FILING DATE: 2000-05-25
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 1353
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1350)
/ OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
/ OTHER INFORMATION: protein
/ US-09-825-923-3

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Query Match	98.5%	Score 1323.4;	DB 9;	Length 1353;
Best Local Similarity	99.3%	Pred. No. 3.5e-306;		
Matches 1343; Conservative	0;	Mismatches 1;	Indels 9;	Gaps 1.

[illegible][illegible]

Query Match	98.5%	Score 1323.4;	DB 15;	Length 1353;
Best Local Similarity	99.3%	Pred. No. 3.5e-306;		
Matches 1343;	Conservative	0. Mismatch 1		

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RESULT 7
US-10-305-720-1181

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/ Publication No. US20040010136a1
/ GENERAL INFORMATION:
/ APPLICANT: An-Young, Janice K.; Sellhammer, Jeffrey J.
/ TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
/ FILE REFERENCE: PA-0002-1 CON
/ CURRENT APPLICATION NUMBER: US/10/305,720
/ PRIOR FILING DATE: 2002-11-26
/ PRIOR APPLICATION NUMBER: 09/016,434
/ NUMBER OF SEQ ID NOS: 1490
/ SOFTWARE: PERL Program
/ SEQ ID NO 1181
/ LENGTH: 2072
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: GenBank ID No. US20040010136a1 g178197
US-10-305-720-1181

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Query Match 98.3%; Score 1321.8; DB 12; Length 2072;
Best Local Similarity 99.2%; Pred. No. 8.9e-306;
Matches 1342; Conservative 0; Mismatches 2; Indels 9; Gaps 1;

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DB 533 CGCTGCTGCGCGCCCTCAGAACCTGTTCTGTGTGCTGCGCGCGCGCATCTTG 592
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DB 713 GTGACACTGTGCGCATCAGCTGGAACGCTTACTGAGCGGTGAGCGCGCTGAGTAC 772
QY 361 AACTCCAGCGCACCCCGCGCGCATCAAGTGCATCTCTCACTGTGTGCTCATGCGC 420
DB 773 AACTCCAGCGCACCCCGCGCGCATCAAGTGCATCTCTCACTGTGTGCTCATGCGC 832
QY 421 GCGCTCATCTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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DB 893 CGCGCCGAGTCAAGCTCAACAGAGGCTGTATCATCTGCGCGCGCGCGCGCGCG 952
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DB 953 TTCTTTGCTCTTGTGCTCATATGATCTTGTCTCACTGCGCATCTACTGCGCAA 1012
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DB 1193 ACCCTTGAATTAATCTGGGACCCGCGCTTGGCAACCTGAGGCTGCGCTTCCACTCA 1252
QY 841 GGGCAGGGCCGAGAGAGAGGCTTTTGGGAGCTCTCAGAGAGTGAAGCTGAA----- 894
DB 1253 GGGCAGGGCCGAGAGAGAGGCTTTTGGGAGCTCTCAGAGAGTGAAGCTGAAAGAGAG 1312
QY 895 ---GAGAGAGAGAGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 951
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DB 1373 TCAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1432
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DB 1553 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1612
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DB 1613 TGAAGGTGCGGCAATGAGCTTCTGCAAGTCTTCTGATCGGCTACTGCAAGCTCA 1672
QY 1252 CTGAACCTGCTTATCTACCATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAG 1311
DB 1673 CTGAACCTGCTTATCTACCATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAG 1732
QY 1312 CTGTCGCGCGCGCGGAGACCGAGAGCGGCTGCTGTA 1344
DB 1733 CTGTCGCGCGCGGAGACCGAGAGCGGCTGCTGTA 1765
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RESULT 8

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US-10-225-567A-41
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTISENSE PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41
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Query Match 98.3%; Score 1321.8; DB 15; Length 3274;
Best Local Similarity 99.2%; Pred. No. 9.3e-306;
Matches 1342; Conservative 0; Mismatches 2; Indels 9; Gaps 1;

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QY 61 TTCCATCTCTTTTACCATCTTGGGCAACGCTGTCATCTGGGCTGTGTACAGC 120
DB 61 TTCCATCTCTTTTACCATCTTGGGCAACGCTGTCATCTGGGCTGTGTACAGC 120
QY 121 CGCTGCTGCGCGCCCTCAGAACCTGTTCTGTGTGCTGCGCGCGCGCATCTTG 180
DB 121 CGCTGCTGCGCGCCCTCAGAACCTGTTCTGTGTGCTGCGCGCGCGCATCTTG 180
QY 181 GTGGCAGCTCATATCTCTTTCTGCTGGCAACGAGCTGTGGGCTACTGTACTTC 240
DB 181 GTGGCAGCTCATATCTCTTTCTGCTGGCAACGAGCTGTGGGCTACTGTACTTC 240
QY 241 CGGGCAGCTGTGGGAGAGTATCTGCGCTGCAAGTGTCTTCTGCACTCTGTCATC 300
DB 241 CGGGCAGCTGTGGGAGAGTATCTGCGCTGCAAGTGTCTTCTGCACTCTGTCATC 300
QY 301 GTGACACTGTGCGCATCAGCTGGAACGCTTACTGAGCGGTGAGCGCGCTGAGTAC 360
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RESULT 9

US-10-311-455-48

Best Local Similarity	76.4%;	DB 13;	Length 6904;
Matches 758;		Pred. No. 1.1e-137;	

[illegible]

Db 1364 TTTCTTACTCTTACTCATCATTAATCTTATCTTACTAGCCATCTACTTAATGCGCAAA 1305
Qy CGCAGCAACCGCAGAGGTGCCAGGGGCGCTGGGAGAGGTGATGCCAAGCAG 660
Db 1304 CGCAGCAACCGCAGAGGTGCCAGGGGCGCTGGGAGAGGTGATGCCAAGCAG 1245
Qy 661 CCGGAGCCGACCATGTGGGGCTTTGGCTTCAGCCAACTGCCAGCCCTGCTGTG 720
Db 1244 CCGGAGCCGACCATGTGGGGCTTTGGCTTCAGCCAACTGCCAGCCCTGCTGTG 1185
Qy 721 GCTTCTGCGAGAGGTGAGGACATCTGAAATCTCACTGGGAGAGAGAGGGGAG 780
Db 1184 ACTTCTACCAAAATAATCAAGAACATCGAATCTCAATAAAAAA 1125
Qy 781 ACCCTGAAGATCTGGGAGCCGAGGCTTGGCACCAGTTGGGGCTGCCCACTCA 840
Db 1124 ACCCTGAAGATCTGGGAGCCGAGGCTTGGCACCAGTTGGGGCTGCCCACTCA 1065
Qy 841 GCGCAGGCGCAGAGAGAGGTGTTGGGCGATCTCCAGAGATGAGTGAAGAGAG 900
Db 1064 AACCAAAACCAAAAAAATTTATTAATCATCTCCAAAAATTAATCAAAAAA 1005
Qy 901 GAGAGAGAGAGAGAGTGTGAACCCAGGAGTGCAGTGTCTCGGCTCACTTGC 960
Db 1004 AAAAAAATAAAAAAATTAATAAATCCCAACAAATATCTCCGACTCACTTAC 945
Qy 961 AGCCCGCGCTGACAGGCGCAGGCGCTCCG 992
Db 944 AACCCCGCTGACAGGCGCAGGCGCTCCG 913

RESULT 10
US-10-311-455-47
; Sequence 47, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Methylation of Cytosine
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 47
; LENGTH: 6904
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 6084
; OTHER INFORMATION: n is a or g or c or t
US-10-311-455-47

Query Match 39.6%; Score 531.6; DB 13; Length 6904;
Best Local Similarity 70.9%; Pred. No. 3,5e-117;
Matches 705; Conservative 0; Mismatches 289; Indels 0; Gaps 0;

Qy 1 ATGACCAACCGCAGAGGTGCCAGGGGCGCTGGGAGAGGTGATGCCAAGCAG 60
Db 5001 ATGACCAACCGCAGAGGTGCCAGGGGCGCTGGGAGAGGTGATGCCAAGCAG 5060
Qy 61 TTCTCTACTCTTACTCATCATTAATCTTATCTTACTAGCCATCTACTTAATGCGCAAA 120

Db 5061 TTTTATATTTTATATATTTTGGTAAAGTTTGGTAAATTTGGTGTGTTGATAGT 5120
Qy 121 CGCTGCTGCGGCGCCCTCAGAACCTGTTCCGTGATGCTGCGCGCGCCGACATCTCG 180
Db 5121 CGCTGCTGCGGCGCCCTCAGAACCTGTTCCGTGATGCTGCGCGCGCCGACATCTCG 5180
Qy 181 GTGGCAAGCTCATATCCCTTCTCGTGGCAGAACAGAGCTGTGGGCTACTGTACTTC 240
Db 5181 GTGGCAAGCTCATATCCCTTCTCGTGGCAGAACAGAGCTGTGGGCTACTGTACTTC 5240
Qy 241 CCGGAGCCGACCATGTGGGGCTTTGGCTTCAGCCAACTGCCAGCCCTGCTGTG 300
Db 5241 CCGGAGCCGACCATGTGGGGCTTTGGCTTCAGCCAACTGCCAGCCCTGCTGTG 5300
Qy 301 GTGACCGTGGCGCATCTAGCCTGGAACGCTTACCTGAGGCGGAGCGCGCTGGAGTAC 360
Db 5301 GTGACCGTGGCGCATCTAGCCTGGAACGCTTACCTGAGGCGGAGCGCGCTGGAGTAC 5360
Qy 361 AACTCAAGCGCAGCCCGCGCGCATCAAGTGCATCTCACTGTGTGCTCATCGCC 420
Db 5361 AACTCAAGCGCAGCCCGCGCGCATCAAGTGCATCTCACTGTGTGCTCATCGCC 5420
Qy 421 GCGCTCATCTGCTGCGCGCCCTCATCTCAAGGCGCAGCGCCCGCGCGCG 480
Db 5421 GCGCTCATCTGCTGCGCGCCCTCATCTCAAGGCGCAGCGCCCGCGCGCG 5480
Qy 481 CGCCCCAGGCGCAGCTCAACAGAGGCGCTGATCTCCGCGCTCCAGATGGAATCT 540
Db 5481 CGCCCCAGGCGCAGCTCAACAGAGGCGCTGATCTCCGCGCTCCAGATGGAATCT 5540
Qy 541 TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTCACTGTGTGCTCATCGCC 600
Db 5541 TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTCACTGTGTGCTCATCGCC 5600
Qy 601 CGCAGCAACCGCAGAGGTGCCAGGGGCGCTGGGAGAGGTGATGCCAAGCAG 660
Db 5601 CGCAGCAACCGCAGAGGTGCCAGGGGCGCTGGGAGAGGTGATGCCAAGCAG 5660
Qy 661 CCGGAGCCGACCATGTGGGGCTTTGGGCTTCAGCCAACTGCCAGCCCTGCTGTG 720
Db 5661 CCGGAGCCGACCATGTGGGGCTTTGGGCTTCAGCCAACTGCCAGCCCTGCTGTG 5720
Qy 721 GCTTCTGCGAGAGGTGCCAGGACATCGAATCTGCGGAGAGAGAGAGAGAGAG 780
Db 5721 GCTTCTGCGAGAGGTGCCAGGACATCGAATCTGCGGAGAGAGAGAGAGAGAG 5780
Qy 781 ACCCTGAAGATCTGGGAGCCGAGGCTTGGCACCAGTTGGGCTGCCCACTCA 840
Db 5781 ACCCTGAAGATCTGGGAGCCGAGGCTTGGCACCAGTTGGGCTGCCCACTCA 5840
Qy 841 GCGCAGGCGCAGAGAGAGGTGTTGGGCGATCTCCAGAGATGAGTGAAGAGAG 900
Db 5841 GCGCAGGCGCAGAGAGAGGTGTTGGGCGATCTCCAGAGATGAGTGAAGAGAG 5900
Qy 901 GAGAGAGAGAGAGAGTGTGAACCCAGGAGTGCAGTGTCTCGGCGCTCACTTGC 960
Db 5901 GAGAGAGAGAGAGAGTGTGAACCCAGGAGTGCAGTGTCTCGGCGCTCACTTGC 5960
Qy 961 AGCCCGCGCTGACAGGCGCAGGCGCTCCG 994
Db 5961 AGCCCGCGCTGACAGGCGCAGGCGCTCCG 5994

RESULT 11
US-10-001-073-40
; Sequence 40, Application US/10001073
; Publication No. US2003013725A1
; GENERAL INFORMATION:
; APPLICANT: Ligelec, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCR
; CURRENT APPLICATION NUMBER: US/10/001.073

; CURRENT FILING DATE: 2001-11-01
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 40
 ; LENGTH: 1386
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-001-073-40

Query Match 34.5%; Score 464.2; DB 15; Length 1386;
 Best Local Similarity 62.9%; Pred. No. 3.6e-101;
 Matches 827; Conservative 0; Mismatches 413; Indels 75; Gaps 4;

13 GACCCCTACTCCGTCAGAGCCACAGCGGCTAGAGGCGGCACTACCTTCCATTTCTC 72
 130 GGCAGTACTCGGCGGCGGCGGTCAGAGGCTGCTCCGTTGGGCTTCTCATCTC 189
 73 TTACCATCTTCCGGAAGGCTCTGTCTATCTGCTGTGTGAACAGCCGCTGCTGCG 132
 190 TTCACTGCTGGGCAAGTGTGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 249
 133 GCGCTCAGAACTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 192
 250 GCGCAGACAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
 193 ATCATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 252
 310 GTATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 369
 253 TGCAGGTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
 370 TGCAGGTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429
 313 GGCATCAGCTGACCGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
 430 GGCATCAGCTGACCGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489
 373 ACCCGCGCGCGCATCAAGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432
 490 ACACACGCGCGGCTCAAGGCTCAAGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
 433 CTGCGCGCGCTCACTCAAGGCTCAAGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492
 550 TTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
 493 AAGCTCAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
 607 GGCCTCAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
 553 TGCCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
 667 TGCCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
 613 AGAGGTCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 672
 727 A-----CGCTCAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
 673 CATGTTGGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
 760 GACGTTGGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819
 733 GAGGTCAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792
 820 GGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 879
 793 ACTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 852
 880 AGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 921
 853 AAGGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 912
 922 CGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981

QY 913 GAAGATGTGAACCCAGAGAGTCCAGTGTCTTCGAGCTTCAAGTCCAGCCCGCTG 972
 DB 982 GCTGATGTGGGCGCTGACCGCTTCAAGGTCCTCCGCGGCGCGGCTGCTGCTGCTGCTG 1041
 QY 973 CAGCAGCCACAGAGGCTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1032
 DB 1042 GCGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1098
 QY 1033 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1092
 DB 1099 -----GTGTGCGCGCGCAAGGTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAG 1134
 QY 1093 CGCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1152
 DB 1135 CGCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
 QY 1153 TTCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1212
 DB 1195 TTCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
 QY 1213 TTCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
 DB 1255 TTCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314
 QY 1273 ATCTTCAACAGAGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1327
 DB 1315 GTCTTCAACAGAGATTTCCGCGCATCTCTTCAAGCAATCTTCTTCCAGAGAGA 1369

RESULT 12

US-10-225-567A-43
 ; Sequence 43, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lifespan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burner, Glenn P.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 43
 ; LENGTH: 2826
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-225-567A-43

Query Match 34.1%; Score 457.8; DB 15; Length 2826;
 Best Local Similarity 63.1%; Pred. No. 1.3e-99;
 Matches 830; Conservative 0; Mismatches 407; Indels 78; Gaps 5;

QY 13 GACCCCTACTCCGTCAGAGGCAAGGCGGCTAGAGGCGGCGCATACCTTCTCATTTCTC 72
 DB 1021 GGCAGTACTCGGCGGCGGCGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 QY 73 TTACCATCTTCCGGAAGGCTCTGTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 DB 1081 TTACCATCTTCCGGAAGGCTCTGTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
 QY 1133 GCGCTCAGAACTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1212
 DB 1141 GCGCTCAGAACTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
 QY 1193 ATCATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314
 DB 1201 GTATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1369
 QY 1253 TGCAGGTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1312

Dd		1261	TGCGGCCTGTACTTGCCCTCGAATGCTGTTTGTTCACCTGTGGATGTGTGATCTGTGT	1320
Oy		313	GCCATCAGCCTTGAAACCGCTACTGGCCCTGAAGCCGCCGCTTGAGATCAACTCAAGCGC	372
Dd		1321	GCCATCAGCCTTGAAACCGCTACTGGCTGGTGAACGACAGCCGCTGAGTACAACCTGAAGCGC	1380
Oy		373	AACCCGCGCCCATCAAGAATGATCATCTCTCACTGTGTGGCTCATTCGCCCGCTCATCTCG	432
Dd		1381	ACACCACCGCCGCTCAAGGCCAACCATGTGCTGCTGTGTGCTCATCTTCGGCGCTCATCTCC	1440
Oy		433	CTGCCGCCCTCATCTTAACAAGGACGACACAGGAGCCCCCACGCCGCGCGGCCGCCCAAGTGC	492
Dd		1441	TTCCCGCGCGTGTCT---CGCTCTACGCCACAGCCCACAGCGCGCCTTACCCTGAGTGC	1497
Oy		493	AAGCTCAACAGAGAGCCTGTGATCATCTGTGCCTTCACAGCATCGAATCTTTTGTGCTCT	552
Dd		1498	GGCCTCAACGACGAGACCTGTGATCATCTGTGCTCTGTGCATCGGCTCTTTGTGGCGCC	1557
Oy		553	TGCTCTATCATGATCTTGTGTCTACTCTGGCATCTACTGATTCGCCAACAACGACGACCGC	612
Dd		1558	TGCTCTATCATGAGGCTGTGTCTACCGCGCATCTAACCAATGTGGCCAAACGCTGACGCGGC	1617
Oy		613	AGAGTCCCAAGGAGCCCAAAGGGGGGCGTGGGACAGGTGATCCAAAGCAACCCGACCCGAC	672
Dd		1618	A--CGCTCAGCGAAGACGGCGCCCGCTGGGCCCGACGAGTGCCTCCCACTAACGAA	1674
Oy		673	CATGTGTGGGCTTTGGCTCTAGCCCAAACTGCCAGCCCTGTGTGTCTTGCCAGA	732
Dd		1675	AAACGGGCTGGGCGCGGCGGACAGG-----GA	1700
Oy		733	GAGGTCAACGACACTCGAAGTCCACTGGGAGAAAGAGAGGGGAGAACCTTGAAAGAT	792
Dd		1701	GCGCGAAACGGGACACTGCGCGCCCCCGCGCGACGCTGAGACCGGA-----	1747
Oy		793	ACTGGGAACCGGGGCTTGCCACCCCAAGTTGGGCTGCCCTTCCCACTCAGGCGACAGGCGAG	852
Dd		1748	----CGAAGCAGCCCAAGCCGCGCGAGAGGCGCGCGCGGCGCGGCGCTTGCGCGGGCGGG	1803
Oy		853	AAGGAGGAGTGTGTGTGGGCACTTTCACAGAGATGAAGCTGAAGAGAGAGAGAGAG	912
Dd		1804	CGCGCGGAGCGGGGCGGAGAGGGGGGCGCGGGCGGTGCGACGCGGACAGGGGGCGGGCGCG	1863
Oy		913	GAAAGATGTAAACCCACAGGACATGCTCAAGTGTCTCCGACTTCAAGCTTGACGCCCGCGCTG	972
Dd		1864	GGGCGGAGCTCAGTCGGGGGCGCTGACCGCTTCAGAGTCCCGGGGCGCGTGGCGGCTTC	1923
Oy		973	CAGCAGCCACAGGCTCCCCGGGTGTGGCCACCTTAGTGGGCAAGTCTCTTGAGCAGG	1032
Dd		1924	TGCGCGCGCAGCTCGCGCTCCGTCAGATTCTTCGTGTGCGCCCGCGCGCGGACGCGCAGC	1983
Oy		1033	GAGCGGAGTGTATAGTGTGGGCAATGATGTGGGCGTCAAGAGGCGCAGCTGACCCGGGAGAA	1092
Dd		1984	AGGCT-----GTGCGCGCGCAAGTGTGGCCACGAGCGCGGAGAA	2022
Oy		1093	CGCTTCACTTCTGTGCTGTGTGTGATTAAGCGCTTTTGTGCTCTGTGTGTTCCCTTC	1152
Dd		2023	CGCTTCACTTGT	2082
Oy		1153	TTCTTCACTTACGCTGTGGGGCCATCTGCGGAAAGCATGTCAGAGTGTGCCCATGAGCTTC	1212
Dd		2083	TTCTTCACTTACAGCTCTTACGGGATCTGCGCGGAGGCTTCCAGAGTGTCCCGGCGGCTTC	2142
Oy		1213	TTCCAGTCTTCTTGTGATGGGCTACAGCAACAGTCACTGAACCCGTATATCAAC	1272
Dd		2143	TTCAAGTCTTCTTGTGATGGGCTTACAGCAACAGTCACTGAACCCGTATATCAAC	2202
Oy		1273	ATCTTCAACCAAGACTTCCGCGCTGTCTTCCGAGAGATCTGTGCGCGCCCTGGA	1327
Dd		2203	GTCTTCAACCAAGATTTCCGGGCAATCTTCAAGCAATCTCTTCCAGCGAGGA	2257

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US-10-001-073-42
/ Sequence 42, Application US/10001073
/ Publication No. US2003011375A1
/ GENERAL INFORMATION:
/ APPLICANT: Liggett, Stephen
/ TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
/ FILE REFERENCE: 13073-PCT
/ CURRENT APPLICATION NUMBER: US/10/001,073
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SBO ID NO 42
/ LENGTH: 1374
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-001-073-42

Query Match      33.6%; Score 451.4; DB 15; Length 1374;
Best Local Similarity 62.5%; Pred. No. 46-98;
Matches 822; Conservative 0; Mismatches 406; Indels 87; Gaps 4

Db      13  GACCCCTACTCGTSCAGGCGCACACGCGCCAGAGCGCGCCATACCTTCTCATTTTC 72
      130  GGCACGTACTCGGCGGCGCGGTGCGAGGCTGCTGCTCCGTGCTTCTTCACTGTC 189
      73  TTTCACATCTTCGAGCAAGCTTCGTGATCTCTGAGTGTGTTGACCAAGCGGCTCGTGC 132
      190  TTCACTGATGAGGACAGTGTGATGATCGCGATGACCAAGCGCGGCGCTGCGC 249
      133  GCGCTCAAGAACTGTTCTGTGTGCTGCGCGCGCGCGCAATCTGTGAGCCAGCTC 192
      250  GGGCACAAGAACTCTTCTGTGTGCTGCGCGCTGCGCGCAATCTGTGAGCCAGCTG 309
      193  ATCACTCCCTTCTGCTGCGCGCAAGAGCTGCGGAGCTACTGTTACTTCGAGCGCAGT 252
      310  GTCACTGCTTCTCTGTGCGCACAGAGCTCATGCTCATGTGATCTTGAGGAGGTGTG 369
      253  TCGGAGGTGTAACCTGCGCTCGACGTTGCTTTCTGCACTCGTCCATCGTGCACCTG 312
      370  TCGCGGATGTAACCTGCGCTCGACGTTGCTTTTGCACCTGTCGATGATGATGATG 429
      313  GGCATCAGCTTGAGACCGCTACTGCGCGCTGAGCGCGCGCTGAGTCAACTCCAGCGC 372
      430  GGCATCAGCTTGAGACCGCTACTGCTGCTGAGCGAGCGCGCTGAGTCAACTCCAGCGC 489
      373  ACCCGCGCGCGATGAAGTGAATATCTCTGATGTTGGTCTCATCGCGCGCTCATCTG 432
      490  AATACAGCGCGGTGAAGGCAACATGCTGCGGTGATCTATCTGCGCGCTCATCTTC 549
      433  CTGCGCGCGCTCATCTAAGAGGACACAGAGGCGCCCAAGCGCGCGCGCGCCCAAGT 492
      550  TTCCCGCGCGTGTCTCTCTCTACCGGACGCGCGCGCGCGCGCTCAACCGGAGTGC 606
      493  AAGCTCAACAGAGGCGCTGTGATCTCTGCGCTGCAAGATGATCTTTCTTCTCTCT 552
      607  GGGCTCAACGAGACCTGTGATCTCTGCTCTCTCATGAGCTCTCTTCTTCCGCGCC 666
      553  TGGCTCATCATGATCTCTGTGATCTCTGCGGACATCTCATGTCGCAAGAGCAAGCG 612
      667  TGGCTCATCATGAGCTGTGATCTCTGCGGACATCTCATGTCGCAAGAGTGTGCAAGCG 726
      613  AGAGTCCAGAGGCGCAAGGAGGAGGCTGAGGAGGAGTCCAGACAGCGCGAGCCGAC 672
      727  A-----CGCTCAAGCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 759
      673  CATGTGAGGAGCTTTGGCTCAAGCCAACTGTCAGCGCTGTGAGCTTCTGCGCAGA 732
      760  GACGATGAGTCCCGACATCAAGAAAGCGGCTGAGCGCGCGCGCGCGCGAGCGAGAAC 819
      733  GAGGTCAACGACATCTGAGTTCATCTGAGGAGAGAGAGAGGAGGAGAGACCTCTGAAGT 792
      820  GGGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 879

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QY 793 ACTGGACCCGGGCGCTTGGCCACCAAGTGGGCTGCTCCCACTAGCGCAGGGCAG 852
 Db 880 AGCGGCGGCGCGCGCGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 939
 QY 853 AAGGAGGAGTGTGTGGGCGCATCTCCAGAGAGTGAAGAGTGAAGAGAGAGAGAGAG 912
 Db 940 GCGCGGCGCGCT-----GCGGACGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 969
 QY 913 GAAAGTGTGAACCCAGAGAGAGTGCAGAGTGTCTCGGCTCAGCTTGGAGAGCCCGCGCTG 972
 Db 970 GGTGAGTGGGAGCGCTGACCGCTCCAGAGTCCCGGAGCGCGAGCGCGCTTCTCGGCG 1029
 QY 973 CAGCAGCCACAGAGGCTCCCGGAGTGTGGCCACCCCTTCACTGAGGAGTGTCTCGGCGAG 1032
 Db 1030 GCGAGCTGCGCTCCGCTGAGATTCTTCTGTGCGCGCGCGCGCGCGCGCGCGCGAGAG 1086
 QY 1033 GCGGTGGGTGTATAGTGGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1092
 Db 1087 -----GTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAG 1122
 QY 1093 CGCTTACCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1152
 Db 1123 CGCTTACCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1182
 QY 1153 TTCTTCACTACAGAGCTGGGCGCGCATCTGCGGAGAGCATCTGAGAGTGGCCATGCGCTC 1212
 Db 1183 TTCTTCACTACAGAGCTGTAGAGCATCTGCGGAGAGCATCTGAGAGTGGCCATGCGCTC 1242
 QY 1213 TTCTTCACTTCTTGTGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1272
 Db 1243 TTCTTCACTTCTTGTGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1302
 QY 1273 ATCTTCAACAGAGATTCGCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1327
 Db 1303 GTCTTCAACAGAGATTCGCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1357

RESULT 14

US-10-001-073-25

Sequence 25: Application US/10001073

Publication No: US20030113725A1

GENERAL INFORMATION:

APPLICANT: Liggett, Stephen

APPLICANT: Small, Kirsten

TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms

FILE REFERENCE: 13073-PCT

CURRENT APPLICATION NUMBER: US/10/001,073

CURRENT FILING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 25

LENGTH: 1350

TYPE: DNA

ORGANISM: Homo sapiens

US-10-001-073-25

Query Match 33.2%; Score 446; DB 15; Length 1350;

Best Local Similarity 62.9%; Pred. No. 7,8e-97;

Matches 827; Conservative 0; Mismatches 415; Indels 72; Gaps 6;

QY 15 CCCCTACTCCGTCGAGCGACAGAGGCGCATAGCGCGCGCATCACTTCTCTACTTCTT 74
 Db 78 CCTTACTCCGTCGAGCGACCTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 137
 QY 75 TACCATCTTGGGCAAGCTCTGTGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 134
 Db 138 CACGCTTGGGCAAGCTGTGCTGTGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 197
 QY 135 CCCTCAGACCTGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 194
 Db 198 GCCCAAAACCTTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 257

QY 195 CATCCCTTCTGCTGGCGCAACAGACTGTGGGCTACTGTACTTCCGGCGACGTGTG 254
 Db 258 CATCCCTTCTGCTGGCGCAACAGACTCATGGGCTACTGTACTTCCGGCGACAGGCTGTG 317
 QY 255 CGAGTGTACCTGAGCGCTGAGCGCTGTCTTGTGACCTTCTTCATCTGCGACCTGTGCGC 314
 Db 318 CGAGTGTACCTGAGCGCTGAGCGCTGTCTTGTGACCTTCTTCATCTGCGACCTGTGCGC 377
 QY 315 CATGAGCTGTGACCTGAGCGCTGAGCGCTGTCTTGTGACCTTCTTCATCTGCGACCTGT 374
 Db 378 CATGAGCTGTGACCTGAGCGCTGAGCGCTGTCTTGTGACCTTCTTCATCTGCGACCTGT 437
 QY 375 CCGGCGCGCATCAAGTGCATCTCTCATCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 434
 Db 438 GCGGCGCGCATCAAGTGCATCTCTCATCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 497
 QY 435 GCGGCGCGCTCATCT-----ACAAGGCGCAAGAGGCGCGCGCGCGCGCGCGCGCGCG 485
 Db 498 CCGGCGCGCTCATCTCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557
 QY 486 CGAGTGCAGCTCAACAGAGAGCGCTGTGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 545
 Db 558 GCGTGTGAGATCAACAGAGAGTGTGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 617
 QY 546 TGCTCTTGTCTCATATATCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 605
 Db 618 GGTCTCTGCTCATATATCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 677
 QY 606 CAACCGGAGAGATCCAGAGGCGCAAGAGGCGCGCTGTGAGAGAGTGTGAGTCAAGAGCGCG 665
 Db 678 CACCGGCTGTGCTCATCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 737
 QY 666 ACCGAGCATGTGTGGGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 725
 Db 738 CGAGCGCAGGCGCGCAAGAGTGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 797
 QY 726 TGCAGAGAGGTCAACGAGCATCTGAAATCTCACTGCGGAGAGAGAGAGAGAGAGAGAG 785
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Db 1275 CTACACCATCTTCAACGACGATTTCCGCGCCCTTCAAGAAATCTCTGTG 1328

RESULT 15

US-10-225-567A-39

Sequence 39, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: Lifespan Biosciences

APPLICANT: Brown, Joseph P.

APPLICANT: Burner, Glenna C.

APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/257,144

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: PatentIn version 3.1

SEQ ID NO 39

LENGTH: 3653

TYPE: DNA

ORGANISM: Homo sapiens

US-10-225-567A-39

Query March 33.1%; Score 445.4; DB 15; Length 3653;

Best Local Similarity 62.9%; Pred. No. 1.2e-96;

Matches 84; Conservative 0; Mismatches 421; Indels 76; Gaps 7;

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1017 CACCGTGTGGGCAAGCGGCTGTGATCTCTGCTGTGTTGACAGCGGCGGCTCAAGGC 1076

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664 CGACCCGACCATGATGCGGCTTTGAGCTCAGCCAACTGCGAGCCCTGCTGTGCT 723

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2212 GACAG 2232

Search completed: February 8, 2004, 01:46:28

Job time: 523.283 secs

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		Homo sapiens, Similar to adrenergic, alpha-2A-, receptor, clone IMAGE:5266354, mRNA.

ACCESSION	BC035047	GI:23272892
VERSION	BC035047.1	
KEYWORDS	HTC.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2410)
Strausberg, R.
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
USA
Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

Email: cgabbs-remail.nih.gov
Tissue Procurement: Niklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiroaki Teshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>

contact: amadan@eystembiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at: <http://image.llnl.gov>
Series: IRAX Plate: 73 Row: 0 Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 1571669
This clone has the following problem: frame shifted.

FEATURES

SOURCE

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Best Local Similarity	62.9%;	Pred. No. 1.6e-77;		
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OY	135	CCCTCAGAACCTGTTCCTGTGTGTGGCTGGCGCGCGCGGACATCTCTGGGTGCAGCTCAT	194
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OY	195	CATCCCTTTCCTGTGTGGCAACGAGCTGTGGGCTACTGTGATCTTCGGCGCAGCTGTG	254
Db	471	CATCCCTTTCCTGTGTGGCAACGAGTCAATGGGCTTACTGTGATCTTCGGCAAGGCTGTG	530
OY	255	CGAGGTGACTGTGGCGCTGACGTGTCTTCTGCACTCTGTCACTGTGCACTGTGTGCG	314
Db	531	CGAGATCTTACTGTGGCGCTGACGTGTCTTCTGTGACGTGTGTCACTGTGTGCACTGTGTGCG	590
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Db	591	CATCAGCCTTGGACCGGCTTACTGTGTCACTCAACAGCGCATTCAGATACAACTTGAAGCGCAC	650
OY	375	CCCGGCGCGCATCAAGTGCATCATCTCTCATCTGTGTGCTCATTCGCGCGGCTCATCTCGCT	434
Db	651	GCGGCGCGCATCAAGGCGCATCATCACTCGTGTGGTCACTTCGCGCGCTCATCTCTT	710
OY	435	GCGGCGCGCTCATCT-----ACAAAGGCGACCAAGGCGCCCGACGCGCGGCGCGCC	485
Db	711	CCGCGCGGCTCATCTCATTCAGAGAAAGGCGGCGCGCGCGCGCGCGCGCGCGCGAGCC	770
OY	486	CCAAGTCAGAGCTCAACAGAGAGCGCTGTGATCATCTGTGCTTCAGAGCATCGATCTTCTT	545
Db	771	GCGCTGCGAGTCAACGACAGAAAGTGTAGTATCTGTGTGTCATCTCGCTCTCTTCTT	830
OY	546	TGCTCTTGTGCTCATCATGATCTTGTGTCACTGTGGCATCTCACTGATTCGCAACGACAG	605
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OY	664	CGACCCGACCATGTGTGGGCTTTTGGCTCAGCCAACTGCCAGCCCTGTGTCTTGTGTCT	723
Db	951	CGAGCGCAGGCCCAACGGTCTGTGGCGCCCGAGCGAGCGCGGCGCGCGGG-----GGGCGCA	1005
OY	724	TCTGCGAGAGGTCACAGCACTCGAAGTCCACTGTGGGAGAGAGAGAGGGGAGAC	783
Db	1006	GAGGCGCAACCGTGTGCCACCCACTCAACGCGCGCCCTGTGCGAGCCCGCGCGCGGG	1065
OY	784	CCTGAAGATACGTGGAACCCCGGCGCTTGTGCACCACTGTGTGGCTGTGCCATCTCAGGC	843
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Db	1126	C-----CTTCAAGGGCGCCCGCAGACCCGAGCGCG	1153
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Best Local Similarity	61.3%;	Pred. No. 4.4e-69;		
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Oy	75	TACCATCTTCGGCAACGCTCTGGTTCATCTGGCTGTGTGACCAACCGCTCGCTCGCGGC	134
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Oy	135	CCCTTCAGAACTGTCTCTGGTGTGCTGTGGCCGCGCCCGCAATCTGTGTGGCCACGCTCAT	194
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Oy	195	CATCCCTTTCTCGCTGGCCCAAGACTGTGGGCTACTGTGTGTACTTCCGGCCGACGTTGGT	254
Db	1130	CATTCCCTTTCTTTGGCCCAAGAGTTATGGGTTTACTGTGTACTTTGGTAAAGTGTGGTG	1188
Oy	255	CGAGTGTACTGTGGGCTCGACGTGTCTTCTGTGCACTCTGTCCATCGTGCACCTGTGGCC	314
Db	1190	TGAGTCTATTTTGGCTCTCGACGTGTCTTTTGGACGTGTCTCAATAGTGCACCTGTGGCC	1249
Oy	315	CATCAGCTTGGACCGCTACTGTGGCCGTGACCGCGCGCTGGAGTTCAACTCCAAAGCCGAC	374
Db	1250	CATCAGCTTTAACCGCTACTGTGTTCATACGAGAGCCATTCAGTTCAAACTTGAAGCCGAC	1309
Oy	375	CCCGGCGCCGATTCAAAGTGCATCATCTCTCACTGTGTGGGCTCATCGCGCGCTCATCTCGCT	434
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Db	1370	CCCCCGACTCATCTTCATAGAGAAAGAGGCGCTGGCGCGGGCGAGCAGCGCCGACGCC	1429
Oy	486	CCAGTGCAGCTCAACCAAGAGGCGCTGGTACATCTGTGGCTCTCCAGATTCGGATCTTTCTT	545
Db	1430	AAGCTGCAGATCAACGACAGAAAGTGTATGTCACTCTGTGTCATCTGGTTCTTCTTT	1489
Oy	546	TGCTCTCTTGCCTCATCATGATCTTGTGTACTCTGTGGCATCTTCACTGCATCGCCAAAGCAG	605
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Oy	606	CAACCGCAGAGTTCACGAGGCCAAGAGGGGAGCGCTGGGACGAGGTGATCCAAAGACCCCG	665
Db	1550	CACCCGCGTGCCTCCACGCGCCGCGGG-----TCCGAGCGCTGTTCGCGCGCGCCGCG	1603
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RESULT 5
AL544609

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ACCESSION	AL544609
VERSION	AL544609.2
	GI:31266452

KEYWORDS EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 1201)	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.	Full-length cDNA libraries and normalization

Unpublished
JOURNAL
COMMENT
On Feb 15, 2001 this sequence version replaced gi:12877089

Unpublished
JOURNAL
COMMENT
On Feb 15, 2001 this sequence version replaced gi:12877089

FEATURES

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sites of the PCMVSPORT e

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ORIGIN

Query Match	24.1%;	Score 324;	DB 9;	Length 1201;
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1201)
 L1, W.B., Gruber, C., Jesse, J., and Pojary, D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 13, 2001 this sequence version replaced gi:12793911.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5594.f For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DD007BC01Q1&cluster=5594.f. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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RESULT 7
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 LOCUS BO887729
 DEFINITION AGENCOURT_876435 NIH_MGC_129 Mus musculus cDNA clone IMAGE:631313

Accession	Version	KeyWords	Source	Organism	Reference	Authors	Title	Journal	Comment
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BO887729									
BO887729.1	GI:22279743								
EST.									
Mus musculus	(house mouse)								
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
1 (bases 1 to 988)									
NH-MGC http://mgc.nci.nih.gov/ .									
National Institutes of Health, Mammalian Gene Collection (MGC)									
Unpublished									
Contact: Robert Strausberg, Ph.D.									
Email: cgabs-remail.nih.gov									
Tissue Procurement: Susan L. Sullivan, PhD.									
cDNA Library Preparation: Reggen, Invitrogen Corp									
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)									
Clone sequencing by: Agencourt Bioscience Corporation									
Clone distribution: MGC clone distribution information can be									
found through the I.M.A.G.E. Consortium/LNLN at:									
http://Image.lnl.gov									
Plate: LAM13739	row: m	column: 06							
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2.2 kb. Constructed by: Primer: Oligo dt. Average insert size									
is a NH_MGC library."									
BASE COUNT	158 a	349 c	300 g	181 t					
ORIGIN									
Query Match	22.0%	Score 295.4	DB 13	Length 988					
Best Local Similarity	76.4%	Pred. No. 4.4e-48							
Matches 389	Conservative	0	Mismatches 116	Indels 4	Gaps 2				
106	GCTGTGTGACACGACCGCTCGCTGCGCGCCCTCAGAACTGTCTGTGCTGCTGCGC	165							
19	GCTGTGTGACACGACCGCGACGCTGCGCGCCCGCGAAGACTCTTCTGTGTCTGCGC	78							
166	GCCGC -CGACTCTGTGTGCGCGACGCTCATATCCCTTTCTGCGTGGCGACAGACT	224							
79	TCACCTACACACTCTGTGTGCGCGACACTGTATGCTCTTCTGCGCAATGAGCTCAT	138							
225	GGGCTACGTGACTCTCGCGCGCGAGTGTGAGGTGACCTGGCGCTCGACGTGCTCTT	284							
139	GGCTACGTGACTCTCGCGCGAGTGTGAGGTGATACCTGGCGACTGAGAGTCTCTT	198							
285	CTGACACTCTGCTCATCTGTGCACTGTGCGCATGACCTGAGCGCTACTGAGCGGTAG	344							
199	CTGACACTCTGCTCATCTGTGCACTGTGCGCATGATGCTGAGCGCTACTGAGCGGTAG	258							
345	CCGCGCGCTGAGTAACTCAAGCGGACCGCGCGCGCATCAAGTGCATCTCTCAG	404							
259	GCAAGCGGTAAAGTAACTCAAGCGGACCGCGCGGTCTCAAGGCACTATGTTGCGC	318							
405	TGTGTGCTATCGCGCGCGCTCATCTGTGCGCGCGCGCTCATCAAGGCGGACGAGG	464							
319	GTGTGTGCTATCTCGCGCTGCTATCTCTTCCCGCTCTGCTCT--CGTTCAACGCGG	375							

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	436	CTCCTGATAGGCTCCTTTGGGCGCTGCTCATATGGGCGCTGCTATGGCGCAT	495									
0y	585	CTACCTATGCGCAACGACGACGCA 613										
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RESULT 8												
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DEFINITION	BB643669	691 bp mRNA linear EST 26-OCT-2001										
ACCESSION	BB643669	RIKEN full-length enriched, adult male corpora										
VERSION	BB643669	quadrigenina Mus musculus cDNA clone B230352011 5', mRNA sequence.										
KEYWORDS	BB643669											
SOURCE	BB643669.1	GI:16478370										
ORGANISM	EST.											
REFERENCE	Mus musculus (house mouse)											
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 691)											
TITLE	Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Iizawa, T., Itoh, K., Kawaji, J., Kohno, H., Kouda, K., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasakawa, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.											
JOURNAL	RIKEN Mouse ESTs (Arakawa, T., et al. 2001)											
COMMENT	Unpublished											
	Contact: Yoshihide Hayashizaki											
	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute											
	The Institute of Physical and Chemical Research (RIKEN)											
	1-7-22 Shuho-cho, Tsukuba, Ibaraki, Japan 305-3858, Japan											
	Tel: 81-45-503-9222											
	Fax: 81-45-503-9216											
	Email: genome-res@gs.c.riken.go.jp,											
	URL: http://genome.gsc.riken.go.jp/											
	Carninci, P., Shibata, K., Hayashizaki, Y., Sugahara, Y., Itoh, K., Watanabe, K., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.											
	'M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.											
	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)											
	wagii, K., Fujimake, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watanabe, K., Okazaki, Y., Ishikawa, T., Oikawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.											
	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1751-1771 (2000)											
	Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.											
	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)											
	Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.											
	Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)											
	Please visit our web site (http://genome.gsc.riken.go.jp) for further details.											
	e mouse tissues.											
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quadrigemina"
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAAGATCCAAAGCTCTTTTTTTTTTTTTTVN 3', cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTTCGGATTATTAATTAATACCCCCCCCCC
3', cDNA was cleaved with XhoI and BamHI. Vector: a
modified Bluescript KS(+) after bulk excision from Lambda
PLC I."

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Best Local Similarity	70.8%	Pred. No. 9.1e-45		
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RESULT 9	AK046211/c	LOCUS	AK046211	2736 bp	mRNA	linear	HTC 05-DEC-2002
DEFINITION			Mus musculus adult male corpora quadrigenima cDNA, RIKEN full-length enriched library, clone:B20352011 product:unknown EST.				

ACCESSION	AK046211
VERSION	AK046211.1
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1
TITLE	Carninci, P. and Hayashizaki, Y.
JOURNAL	High-efficiency full-length cDNA cloning
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)
PubMed	99279253
REFERENCE	10349636
AUTHORS	2
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
JOURNAL	Itchih, M., Konno, H., Okasaki, Y., Muramatsu, M. and Hayashizaki, Y.
MEDLINE	Normalization and subtraction of cap-trapper-selected cDNAs to
PubMed	prepare full-length cDNA libraries for rapid discovery of new genes
REFERENCE	Genome Res. 10 (10), 1617-1630 (2000)
AUTHORS	3
TITLE	Shibata, K., Itchih, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.
JOURNAL	
MEDLINE	
PubMed	11042159
REFERENCE	
AUTHORS	

[illegible]

Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, T.,
 Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamamaki, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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 Knehl, P., Lewis, S., Matano, Y., Mikaido, I., Pezole, G.,
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 Carminci, P., de Bonaldo, M.F., Brownstein, M.J., Bull, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D.,
 Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, D., Mombauts, P., Nordone, P.,
 Rung, B., Schingwald, M., Rodriguez, R., Sakamoto, N., Saeki, H.,
 Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
 Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,
 and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 11217851

REFERENCE
 5

THE FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of mouse genome transcriptome based on functional annotation
 of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE
 JOURNAL
 REFERENCE
 6 (bases 1 to 2736)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carminci, P.

Fukuda, S., Furuno, M., Hasegaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyata, S., Kuizihara, C., Matsumaya, T., Miyazaki, K., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Salto, R., Saltoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE JOURNAL

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

source

Location/Qualifiers

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Best Local Similarity 70.8%; Pred. No. 1.3e-44;
Matches 388; Conservative 0; Mismatches 151; Indels 9; Gaps 1;

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RESULT 10 LOCUS DEFINITION

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AGENCOURT 10671423 NCI CGAP Zemb3 Danio rerio cDNA clone
IMAGE:6801483 5', mRNA sequence.

ACCESSION VERSION KEYWORDS

CA477609
CA477609.1 GI:24933961
EST.

SOURCE

Danio rerio (zebrafish)

ORGANISM

Burkholderia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.

REFERENCE

NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Chi-Bin Chen
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
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Location/Qualifiers

FEATURES

source

Location/Qualifiers

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OY		256	GAGGTGTAACCTGAGCGCTCGAAGTGTCTTCTTGCACTCTTCATCATGTGCACTGTGGCC	315
Db		546	GCGTTTAACTGGGCGCTGGAATGTGTCTGTTCGTTCGACGTCCTTCATCTGTCACCTGTGGCC	605
OY		316	ATCAGCTTGACCGCTACTGTGGCCGTGAGCCGCGCGCTGAGATACTCCAAAGCGAAC	375
Db		606	ATCAGCTTGACAGAGTACTGTGTCTGTCTGATCACCAAACGGGTGGCTVCAACTGAAACGACG	665
OY		376	CCGGGCGGCATCAAGTGCATCATCTCTCACTGTGGCTCATCGCGCGCTCATCTCGCTG	435
Db		666	CCGAGGCGGCATCAAGTGCATCATCTCTCACTGTGGCTCATCGCGCGCTCATCTCGCTG	725
OY		436	CCGCCCCCTCATC	447
Db		726	CCTCCGCTCATC	737
RESULT 11	BZ138792/c			
LOCUS	CH230-256D20..TV CHORI-230 Segment 2 Rattus norvegicus genomic clone	677 bp	DNA	linear GSS 11-OCT-2002
DEFINITION	CH230-256D20, genomic survey sequence.			
ACCESSION	BZ138792			
VERSION	BZ138792.1 GI:23779739			
KEYWORDS	GSS.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 677) Zhao,S., Shetty,J., Shatsman,S., Tsengaye,G., Geer,K., Shvartsbeyn, A., Gebregziorgis,B., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M. Jong P and Fraser C.M. Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished Other GSSes: CH230-256D20.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pjejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or eting_informtion.htm). BAC end plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Size: 256 row: D column: 20 Seq primer: T7 Clase: BAC ends.			
FEATURES	source			
	Location/Qualifiers			
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	/db_xref="taxon:10116"			
	/clone="CH230-256D20"			
	/sex="Female"			
	/cell_type="Brain"			
	/clone_1ib="CHORI-230 Segment 2"			
	/notes=Vector: pTABBAC1.3; Site 1: MboI; Site 2: MboI;			
	CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by			
	Pieter de Jong"			
BAGE COUNT	139 a 200 c 220 g 118 t			
ORIGIN				

	Query Match	19.5%	Score 262.6;	DB 28;	Length 677;	
	Best Local Similarity	74.4%	Pred. No. 1,2e-41;			
	Matches	331;	Conservative	0;	Mismatches 114;	Indels 0; Gaps 0;
OY	23	CCGTGACAGGCACAGCGGCCATAGCGGGCCCATTCATTCTTCAATTCCTTTAACATCT	82			
Db	502	CCCTGACAGTGAGCCTGACCTGCTGTGCTGCTGAGCTGCTGCTCATCTGCTTCAACCGTGT	443			
OY	83	TGGGAACGCTCTGTGTATCTTGCTGTGTGTGACACACCCCTGCTGCGGCCCTCAGA	142			
Db	442	TTGGCAACGTGCTGTGTATTATGCAATGTTCACACACCGCGCGCTCAAAAGCCCCACA	383			
OY	143	ACCCTGTCCGTGTGCTGAGCGCGCCGACATCTCTGTGSCACACCTCATTCCTT	202			
Db	382	ACCCTTCTGTGAGTCTCTGACTCTACGAGCATCTGTGTGCCACGCTGTATTCCTC	323			
OY	203	TCTGCTGAGCAACGACCTGCTGGCTACTGTGTAATTCGGCGCACGTGTGACAGTGT	262			
Db	322	TTTTCTTTGGCAACGAGGTTATGGGCTTACGTGTAATTTGTAAGTGTGTGACAGATCT	263			
OY	263	ACCTGSGCTGTGACGTGCTCTTTGCACTCTGTGCATCTGTGCACCTGTGTGCGCCATACCC	322			
Db	262	ACTTGGCCCTTCAAGTGTCTTTTTCACAGTGTCCATAAGTCTCTGTGCGCCATACCC	203			
OY	323	TGACACCCCTACTGGCGCGGTGAGCGCGCGCTGAGTACAACTCCAAAGGACACCCGCGCC	382			
Db	202	TTGACCGTACTGTGTTCATACGACGAGCCATCTGATACACTGAAGGACACGCGCGAGC	143			
OY	383	GCATCAAGTCATCATCTCTCATCTGTGTGCTCATCTGCCCGCATCTCGCTCCGCGCC	442			
Db	142	GCATTCMAAGGCATCTATGTCACTGTGTGGGTCACTCTGGCGGTATCTCTCCCGCAC	83			
OY	443	TCATCTACMAAGGCGACCGAGGCCCC	467			
Db	82	TCATCTCATAGAGAGAGAGGCGCC	58			
RESULT 12	CNSO3BOW	896 bp	DNA	linear	GSS 01-SEP-2000	
LOCUS	Tetradon nigroviridis genome survey sequence PUC-Ori end of clone					
DEFINITION	012P03 of library G from Tetradon nigroviridis, genomic survey					
ACCESSION	AL236849					
VERSION	AL236849.1					
KEYWORDS	GSS: genome survey sequence.					
SOURCE	Tetradon nigroviridis					
ORGANISM	Tetradon nigroviridis					
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;					
	Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;					
	Tetraodontidae; Tetraodontidae; Tetrapoda.					
TITLE	1 Roest Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,					
JOURNAL	Bernot,A., Fiammes,C., Winck,P., Broctier,F., Quetier,F.,					
MEDLINE	Saurin,W., Bernot,A., Bouneau,L., Billaule,A., Quetier,F.,					
PUBMED	Fiammes,C., Fischer,C., Bouneau,L., Billaule,A., Quetier,F.,					
REFERENCE	Characterization and repeat analysis of the compact genome of the					
AUTHORS	freshwater pufferfish tetradon nigroviridis					
	Genome Res. 10 (7), 939-949 (2000)					
	3 (bases 1 to 896)					
	Genoscope.					
	Direct Submission					

JOURNAL

This sequence is a single read and was generated as part of a large-scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
SOURCE

Bouice

BASE COUNT	ORIGIN
163 a	276 c
295 g	157 t
5 others	

	a	c	g	t	others
BASE COUNT ORIGIN	163	276	295	157	5

Query Match	16.6%;	Score 223.2;	DB 29;	Length 896;
Best Local Similarity	73.8%;	Pred. No. 7.1e-34;		
Matches 282; Conservative	1;	Mismatches 99;	Indels 0;	Gaps 0;

Qy	9	CCGAGAACCCCTACTCCGTCGACAGGCCACAGCGGCCTATGCGGGGCGATACCTTCCCTCAT	68
Db	488	CTCGAAGCGCTACTCTTTAGGGGACACCGCGCGCATCGCGGCTCGTCAAGCTTCCAT	547
Qy	69	TCTCTTTACCATCTTTCGGCAGACGCTCTGTGTCATCTCTGCTGTGTGACCAAGCCGCTGCT	128
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Qy	129	GCGCGCCCTCAAGACCTGTTCTCTGTGTGTGTGGCGCGCGCAATCCTGTGTGCGAC	188
Db	608	CAGAGGCGCGCAAGAACCTTTCCTGTGTGTCTCTGCGCACCGCGGACATCTCTGTGTGCGAC	667
Qy	189	GCTCATCATCCCTTTCGTGCTGAGCCAGAGCTGTGTGGTCACTGTGATCTTCCGGCGCAC	248
Db	668	CTGTGTGATGCCCTTCTCTCCGTGCAAGACGATGATGGGCTTACTGTATTTCCGCAAGAT	727
Qy	249	GTGTGTGCGAGTGTATCTGTGCGCTCGACGTGTCTTCTGTGACCTCTGTGCATCTGTGCACT	308
Db	728	CTGTGTGCGGGATTTTATCTGTGCTCTGTGATGTTTATTTCTGTGACCTCTGTGTGATCT	787
Qy	309	GTGTGCGCATCAGCTGTGACCGCTACTGTGGCGGTGAGCCGCGCGCTGTGATCAATCTCAA	368
Db	788	GTGTGCGCAATTAAGCTTGTGACCGCTACTGTGTCTGTCAAGCGAGCGGTTCAGTACAACTGAA	847
Qy	369	GCGCAACCCGCGCGCGATCAAG	390
Db	848	GAGGACCTCTCAAGCGGTAAAG	869

RESULT 13
BU468891

1000

LOCUS	736 bp	mRNA	linear	EST 30-NOV-2002
DEFINITION	6033655259p1	CSEQRBN21	Gallus gallus	CDNA clone CHEST263e16 5', mRNA sequence.

ACCESSION	BU468891	
VERSION	BU468891.1	GI:25962468
KEYWORDS	EST.	
SOURCE	Gallus gallus	(chicken)
ORGANISM	Gallus gallus	

Eukaryota; Metazoa; Chordata; Craniota; Euteleostomi;
Archosauaria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 736)

AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.
Bond, W.T., Tickle, C., Brown, W.P.A., Wilson, S.A. and Hubbard, S.I.

TITLE A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE 22335534
DIAMED 13445303

PUBMED	12445392
COMMENT	CONTACT:

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Tel: 01612008930
Fax: 01612260400

Fax: 0161 2360405
Email: Simon.Huth@btinternet.com

Location/Qualifiers

FEATURES
Source

Source

```

BASE COUNT
ORIGIN
150 a      214 c      192 g      180 t
      reannealing hybridization was used. "
      compatible sites of a custom modified MCS of the
      pBluescript (KS+) vector. The library was normalized in 2
      rounds using conditions adapted from Soares et al., PNAS
      (1996): 91: 9228-9232 and Bonaldo et al., Genome Research 6
      (1996): 791, except that a significantly longer

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Query Match	16.6%	Score 222.8;	DB 13;	Length 736;
Best Local Similarity	71.8%;	Pred. No. 8.1e-34;		
Matches 306;	Conservative	0;	Mismatches 117;	Indels 3;
				Gaps 1;

Oy 188 GCGTCAATCCCTTCTCGCGGCCAACAGACTGCTGGGGCTAAGTAATTCGCGGCA 247
 Db 4 CTCTGGTAAAGCTTCTCCTTGGCCAAAGACTGATGAATCACTGGTACTTTGGCAAG 63

[illegible]

RESULT 14

CD552619 570 bp mRNA linear EST 11-JUN-2003
LOCUS B0346C06-5 NIA Mouse E9.5 Whole Embryo cDNA Library (long) Mus
DEFINITION musculus cDNA clone NIA:B0346C06 IMAGE:30433469 5', mRNA sequence.
ACCESSION CD552619
VERSION CD552619.1 GI:31600350
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 570)
Piao, Y., Ko, N.T., Lam, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE 21429098
PUBMED 11544199
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: B0346 row: C column: 06
Seq primer: M13 Reverse
High quality sequence stop: 570
POLYANo.
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/dev_stage="whole embryo including extraembryonic tissues
at 9.5-days postcoitum"
/lab_host="DH10B"
/clone_1ib="NIA Mouse E9.5 Whole Embryo cDNA Library (long
)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 16 embryos at 9.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer (Invitrogen:
5'-GACAGTCTTCTAGATCGGAGCGCCCTTTTCTTTTCTTTT-3')
from 1 ug of total RNA, treated with T4 DNA polymerase,
and purified by ethanol-precipitation. The cDNAs were
ligated to lome-linker L1-SalI, purified by
phenol/chloroform, and separated from free linkers by
centrifugation 100. Then, the cDNAs were amplified by
long-range high fidelity PCR using Ex Taq polymerase
(Takara) with a primer SalI-S. The products were purified
by phenol/chloroform and centrifugation 100. The cDNAs were
digested with SalI and NotI enzymes and cloned into
SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E.
coli host was transformed with the ligation mixture by the
standard chemical method. The average insert size is about
3.0kb. The library was constructed by Julian Piao."

BASE COUNT 93 a 186 c 165 g 126 t
ORIGIN
Query Match 16.2%; Score 218.4; DB 14; Length 570;
Best Local Similarity 87.0%; Pred. No. 5.6e-33;
Matches 240; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
1 ATGAGCACACAGACCCCTACTCCGTGACAGCCACAGCGCCATAGCGGCGCATCAC 60
295 ATGCTCCACAGAGACCCCTACTCCGTGACAGCCACAGCGCCCATCGCGGCATAC 354
61 TTCTCATCTCTTTTACCATCTTCCGGAAGCGCTGGTATCTGCTGTGTGACAG 120
355 TTCTCATCTCTCTTACCATCTTCCGGAAGCGCTGGTATCTGCTGTGTGACAG 414
121 CGCTCGTGGCGCGCCCTCAAGAACCTTCTTGTGTGTGTGTGTGTGTGTGTGT 180
415 CGCTCTCTCCGTGACACACAAACCTTCTTGTGTGTGTGTGTGTGTGTGTGT 474
181 GTGGCAGCGCTATCATCTCTTCTTCTGCGCCCAAGAGCTGCTGCTGCTGCT 240
475 GTGGCTACTCTTATCATCTCTTCTTCTGCGCCCAAGAGCTGCTGCTGCTGCT 534
241 CGGCGCAGCTGTGTGTGAGGTGATCTGCGCTGAC 276
535 TGGCGTGTGTGTGTGAGGTGATCTGCGCTGAC 570
RESULT 15
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LOCUS Chicken alpha2 adrenergic receptor gene fragment probably subtype
DEFINITION a, genomic survey sequence.
ACCESSION AL606540
VERSION AL606540.1 GI:15591915
KEYWORDS GSS; Alpha2 adrenergic receptor gene.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 855)
Hunter, C. and Elgar, G.
Alpha2 adrenergic receptor gene
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 855)
REFERENCE Hunter, C.
Direct Submission
Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hmp.mrc.ac.uk
FEATURES
source
1..855
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/db_xref="taxon:9031"
Location/Qualifiers
BASE COUNT 201 a 248 c 245 g 161 t
ORIGIN
Query Match 16.2%; Score 218.4; DB 29; Length 855;
Best Local Similarity 74.1%; Pred. No. 6.2e-33;
Matches 292; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
224 TGGGCTACTGTAATCTTCCGCGGACAGTGTGAGTGAATCTTGAAGCTGCTCT 283
2 TGGGTTATTTGACTCTCGCAAAAGTCTGTGAGATCTAGCTGAGCGTGTCTGT 61
284 TCTGACCTCTGTCATCTGTGACCTGTGCGCATCAGCTTGAGACCTGACTGCGG 343
62 TCTGACCTCTGTCATCTGTGACCTGTGCGCATCAGCTTGAGACCTGACTGCGG 121
344 GCGGCGCGTGTGAGTGAATCTTCAAGGACCGCGCGCGCATCAAGTGCATCTCT 403
122 CACAGCCATTCAGTGAACCTCAAGCGACCCCGCGCGCATCAAGTGCATCTCT 181
404 CGTGTGCTCATTCGCGCGCGCTCATCTGCTGCGCGCGCTCATCTCAAGGCGAC 463
182 TGTCTGTGATCATCTGCGCGCGCTCATCTGCGCGCGCTCATCTCAAGGCGAC 241
464 GCCCCAGCGG-----CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 517

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Db      242 GTGGGACAGCAGGTGGACCAAGTGGGGGCGAGATGCAAGATCAATGACGAGAAGTGTACA 301
OY      518 TCCTGGCCTCCAGCATGGATCTTTCTTTGCTCTGCTGCTGCTCATGATCCTTGTCTPAC 577
Db      302 TCATCTGCTCGAGCATGGCTCTCTTCTTCACCCCGTGGCTCATCAAGATCCTGGTCTAG 361
OY      578 TGGCATCTTACCTGATGCGCCAAACGACGAAACCG 611
Db      362 TGGCATCTTATCAGATAGCCAAAGAGGCGAACCAAG 395
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Job time : 3118.08 sec8

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February, 6, 2004, 18:18:11 / Search time 37.6254 Seconds
(without alignments)
1898.370 Million cell updates/sec

Title: US-09-692-077D-7

Perfect score: 450
Sequence: 1 MDHQDPYSVQATAIAAAIT.....QDFRRAFRILCRPWTQTAW 450

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size: 20

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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4: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT.*
5: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT.*
6: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT.*
7: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT.*
8: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT.*
9: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT.*
10: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT.*
11: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT.*
12: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT.*
13: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT.*
14: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT.*
15: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT.*
16: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT.*
17: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT.*
18: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT.*
19: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT.*
20: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT.*
21: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT.*
22: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.*
23: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.*
24: /SIDSI1/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450	100.0	450	22	AAAM52117 Human alpha-2BAR t
2	450	100.0	450	22	AAE00990 Human alpha2B-adre
3	450	100.0	450	23	AAE26634 Human alpha-2B-adr
4	361	80.2	450	24	ABP81780 Human alpha-2B-adr
5	306	68.0	447	22	AAAM52118 Human alpha-2BAR t
6	306	68.0	447	22	AAE00989 Human alpha2B-adre
7	306	68.0	447	23	AAE26633 Human alpha-2B-adr
8	234	52.0	487	12	AAAI4149 Human alpha 2 beta
9	234	52.0	487	18	AAAI1804 Human alpha-2b adr

10	120	26.7	330	15	AAI48699	G-protein coupled
11	120	26.7	330	17	AAI02671	G-protein coupled
12	29	6.4	29	23	ABU67205	G-protein coupled
13	29	6.4	29	24	ABP53986	Human alpha 2B adr
14	26	5.8	457	22	AAAM52126	Human alpha-2CAR v
15	26	5.8	458	15	AAI54834	Human derived adre
16	26	5.8	461	22	AAAM52124	Human alpha-2CAR p
17	26	5.8	461	24	ABP81781	Human alpha 2c-adr
18	25	5.6	330	15	AAI48700	G-protein coupled
19	25	5.6	330	17	AAI02672	G-protein coupled
20	25	5.6	450	22	AAAM52122	Human alpha-2BAR p
21	25	5.6	450	25	AAAM52123	Human alpha-2BAR v
22	25	5.6	450	24	ABP81779	Human alpha 2A-adr
23	23	5.1	24	19	AAI39955	Peptide effecting
24	23	5.1	26	19	AAI39948	Peptide effecting
25	23	5.1	99	15	AAI50781	G-protein coupled
26	23	5.1	99	17	AAI02983	G-protein coupled
27	21	4.7	330	15	AAI48698	G-protein coupled
28	21	4.7	330	17	AAI02670	G-protein coupled
29	21	4.7	334	15	AAI48701	G-protein coupled
30	21	4.7	334	17	AAI02673	G-protein coupled
31	20	4.4	307	22	AAI08334	Human alpha 2 adre
32	20	4.4	307	24	ABG73538	Human alpha2-adren

ALIGNMENTS

RESULT 1
AAM52117 standard; Protein; 450 AA.
XX
AC AAM52117;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 167..399
FT /note= "featured in figure 2"
FT Domain 170..193
FT /label= "transmembrane_domain"
FT Region 301..303
FT /label= "polymorphic_site"
FT /note= "Polymorphic site absent in the variant protein (AAM52118)"
FT Region 310..312
FT /label= "polymorphic_site"
FT Domain 373..396
FT /label= "transmembrane_domain"
XX
XX MO200179561-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001MO-US12575.
XX
XX 17-APR-2000; 2000US-0551744.
XX 10-AUG-2000; 2000US-0636259.
XX 19-OCT-2000; 2000US-0652077.
XX
XX (LIGG/) LIGGETT S B.
XX (SMAL/) SMALL K M.
XX
XX LIGgett SB, Small KM;

XX WPI; 2001-611728/70.
DR N-PSDB; AAI99905.

PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -

XX Claim 20; Page 146-147; 163pp; English.

XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX alpha2A or alpha2C or fragment or complement of; and
XX (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX or a site comprising (A) (999ggcgggcg) or (B) (999ggcgctgg) at
XX positions 961-972 of (III). The method may be used for genotyping an
XX alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX whether an individual is at increased risk of developing a disease
XX associated with alpha2B, alpha2A or alpha2, comprising detecting a
XX polymorphic site which correlate to disease selected from cardiovascular
XX disease, central nervous system disease and combinations of these. In
XX addition, the technique may be used to predict an individual's response
XX to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
XX norepinephrine, clonidine, oxybutazoline, guanabenz, UK14304, BHT933 and
XX combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
XX these) by detecting the polymorphic site and correlating the site to a
XX predetermined response (where the response is correlated to adenylyl
XX cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX levels). The present sequence is that of the third intracellular loop of
XX the human alpha-2BAR protein, the sequence includes 3 amino acid
XX polymorphic site at residues 301-303 (EEB), absent in the alpha-2BAR
XX variant protein (AAM52118).

XX Sequence 450 AA;

Query Match 100.0%; Score 450; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MDHODPSVOATTAIAAATFTLFTIFGNALVILAVTSLSRAPQNLFIYSIAADIL 60
DB 1 MDHODPSVOATTAIAAATFTLFTIFGNALVILAVTSLSRAPQNLFIYSIAADIL 60
QY 61 VATTIIPESLANELGYYWFRRTWCYVLAIDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
DB 61 VATTIIPESLANELGYYWFRRTWCYVLAIDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQOPORGRPOCKNOEAMYLIASTGS 180
DB 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQOPORGRPOCKNOEAMYLIASTGS 180
QY 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQOPORGRPOCKNOEAMYLIASTGS 180
DB 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQOPORGRPOCKNOEAMYLIASTGS 180
QY 161 FPAPCLIMILVYIRLYLAKSNRGRPAKGGPGQSGSKOPRPHDGGALASATLPALASY 240
DB 161 FPAPCLIMILVYIRLYLAKSNRGRPAKGGPGQSGSKOPRPHDGGALASATLPALASY 240
QY 161 FPAPCLIMILVYIRLYLAKSNRGRPAKGGPGQSGSKOPRPHDGGALASATLPALASY 240
DB 161 FPAPCLIMILVYIRLYLAKSNRGRPAKGGPGQSGSKOPRPHDGGALASATLPALASY 240
QY 241 ASAREVNHSKSTGEKEGETPEPTGTALPPSMAALPNSGQOQKGVCASEDPAEEB 300
DB 241 ASAREVNHSKSTGEKEGETPEPTGTALPPSMAALPNSGQOQKGVCASEDPAEEB 300
QY 241 ASAREVNHSKSTGEKEGETPEPTGTALPPSMAALPNSGQOQKGVCASEDPAEEB 300
DB 241 ASAREVNHSKSTGEKEGETPEPTGTALPPSMAALPNSGQOQKGVCASEDPAEEB 300
QY 301 EEEEEECECPQAVPVPSPASACSPPLQOPQGSRVLTATLRGQVLTGRGVATGGQWRRR 360
DB 301 EEEEEECECPQAVPVPSPASACSPPLQOPQGSRVLTATLRGQVLTGRGVATGGQWRRR 360
QY 301 EEEEEECECPQAVPVPSPASACSPPLQOPQGSRVLTATLRGQVLTGRGVATGGQWRRR 360
DB 301 EEEEEECECPQAVPVPSPASACSPPLQOPQGSRVLTATLRGQVLTGRGVATGGQWRRR 360
QY 361 AQLTRKRTFTVLAVVGVFLCMFPFFESYSICALCPKCKVPHGLPFFFWIGCNSS 420
DB 361 AQLTRKRTFTVLAVVGVFLCMFPFFESYSICALCPKCKVPHGLPFFFWIGCNSS 420
QY 361 AQLTRKRTFTVLAVVGVFLCMFPFFESYSICALCPKCKVPHGLPFFFWIGCNSS 420
DB 361 AQLTRKRTFTVLAVVGVFLCMFPFFESYSICALCPKCKVPHGLPFFFWIGCNSS 420
QY 421 LNPVITYITFNODRRAFRRLICRPWTQTAM 450
DB 421 LNPVITYITFNODRRAFRRLICRPWTQTAM 450

```

DB 421 LNPVITYITFNODRRAFRRLICRPWTQTAM 450

RESULT 2

AAE00990
ID AAE00990 standard; Protein; 450 AA.

XX AAE00990;

DT 04-JUL-2001 (first entry)

XX Human alpha2B-adrenoceptor (alpha2B-AR) protein.

XX Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
XX glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
XX norepinephrine; epinephrine; therapy; vascular contraction;
XX coronary artery; coronary heart disease; CHD; chronic angina pectoris;
XX acute myocardial infarction; AMI; Prinzmetal's variant.

OS Homo sapiens.

XX Key Location/Qualifiers
XX Region 298..309
XX /note="Glutamic acid repeat"

XX MO200129082-AL.

XX 26-APR-2001.

XX 20-OCT-2000; 2000MO-FI00913.

XX 22-OCT-1999; 99US-0422985.

XX (JUVVA-) JUVANTTA PHARMA LTD OY.

XX Snapiir A, Heimonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
XX Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyyssönen K;
XX Salonen R, Kaunonen J, Valkonen J;

DR WPI; 2001-300318/31.

DB N-PSDB; AAD04762.

XX New DNA molecule encoding variant specific adrenoceptor protein with
XX deletion of specific amino acids located in the third intracellular
XX loop of the polypeptide, for treating vascular contraction of coronary
XX arteries

XX Disclosure; Page 29-31; 37pp; English.

XX The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) protein.
XX Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of
XX 12 glutamates, in an acidic stretch of 18 amino acids (amino acids
XX 294-311), located in the third intracellular loop of the receptor
XX polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR
XX mediate many of the physiological effects of the catecholamines,
XX norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is
XX useful for treating a mammal suffering from vascular contraction of
XX coronary arteries and a disease involving vascular contraction of
XX coronary arteries which is clinically expressed as coronary heart disease
XX (CHD), unstable chronic angina pectoris which is clinically expressed as
XX Prinzmetal's variant form or acute myocardial infarction (AMI).
XX Alpha2B-AR gene is used in gene therapy.

XX Sequence 450 AA;

Query Match 100.0%; Score 450; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MDHODPSVOATTAIAAATFTLFTIFGNALVILAVTSLSRAPQNLFIYSIAADIL 60
DB 1 MDHODPSVOATTAIAAATFTLFTIFGNALVILAVTSLSRAPQNLFIYSIAADIL 60

```

QY 61 VATTIIPPSLANELLGWYFRRTWCEVYALADVICTSSIVHLCAISLDRYMAVSRALEY 120
 DB 61 VATTIIPPSLANELLGWYFRRTWCEVYALADVICTSSIVHLCAISLDRYMAVSRALEY 120
 QY 121 NSKRTPRRIKICITLTWMLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMYIIASSIGS 180
 DB 121 NSKRTPRRIKICITLTWMLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMYIIASSIGS 180
 QY 181 FFAPCLIMILVYLRITLAKSNRRGPRAKGPQGSSEKOPRPHGALASAKLPALASV 240
 DB 181 FFAPCLIMILVYLRITLAKSNRRGPRAKGPQGSSEKOPRPHGALASAKLPALASV 240
 QY 241 ASAREVNGHSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDAEAE 300
 DB 241 ASAREVNGHSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDAEAE 300
 QY 301 EEEEBEECECPQAVPVSPASACSPPLQOPGSRVLTALRGVLTGRVGAIGQWMRRR 360
 DB 301 EEEEBEECECPQAVPVSPASACSPPLQOPGSRVLTALRGVLTGRVGAIGQWMRRR 360
 QY 361 AQLTRKRFTEVLAIVGVFLCWFPPFFSYSLGALCPKHCKVPHGLFQFFFWIGYCNS 420
 DB 361 AQLTRKRFTEVLAIVGVFLCWFPPFFSYSLGALCPKHCKVPHGLFQFFFWIGYCNS 420
 QY 421 LNPVIYITIFNODFRAPFRILCRPWTQTAW 450
 DB 421 LNPVIYITIFNODFRAPFRILCRPWTQTAW 450

RESULT 3
 AAE26634
 ID AAE26634 standard; Protein; 450 AA.

XX AAE26634;
 XX 13-DEC-2002 (first entry)
 DT
 XX
 DE Human alpha-2B-adrenoceptor protein.
 XX
 KW Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
 KW hypertension; hypotensive.
 XX
 OS Homo sapiens.
 XX
 PN MO200266617-A1.
 PD
 XX 29-AUG-2002.
 PF
 XX 13-FEB-2002; 2002WO-FI00113.
 PR
 XX 20-FEB-2001; 2001FI-0000323.
 PA
 XX (JURI-) JURILAB LTD OY.
 PI
 XX Salonen J;
 DR WPI; 2002-667063/71.
 DR N-PSDB; AAD26634.
 XX

PT Detecting a risk of hypertension and targeting treatment in a subject
 PT by determining the pattern of alleles encoding a variant
 PT alpha-2-adrenoceptor -
 XX
 PS Disclosure; Page 30-31; 35pp; English.

XX The invention relates to a method for detecting a risk of hypertension
 CC by determining the pattern of alleles encoding a variant alpha-2B-
 CC adrenoceptor (AR) protein. The methods and compositions of the invention
 CC are useful for detecting risks and targeting treatment for hypertension.
 CC The kit is also useful for selecting for clinical drug trials testing
 CC the antihypertensive effect of compounds. The present sequence is human
 CC alpha-2B-adrenoceptor protein.
 XX

SEQ Sequence 450 AA;
 Query Match 100.0%; Score 450; DB 23; Length 450;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHDPYSVQATAIAAATITLFTIFGNALVTLAVTSRLAPQNLFLVSLAADIL 60
 DB 1 MDHDPYSVQATAIAAATITLFTIFGNALVTLAVTSRLAPQNLFLVSLAADIL 60
 QY 61 VATTIIPPSLANELLGWYFRRTWCEVYALADVICTSSIVHLCAISLDRYMAVSRALEY 120
 DB 61 VATTIIPPSLANELLGWYFRRTWCEVYALADVICTSSIVHLCAISLDRYMAVSRALEY 120
 QY 121 NSKRTPRRIKICITLTWMLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMYIIASSIGS 180
 DB 121 NSKRTPRRIKICITLTWMLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMYIIASSIGS 180
 QY 181 FFAPCLIMILVYLRITLAKSNRRGPRAKGPQGSSEKOPRPHGALASAKLPALASV 240
 DB 181 FFAPCLIMILVYLRITLAKSNRRGPRAKGPQGSSEKOPRPHGALASAKLPALASV 240
 QY 241 ASAREVNGHSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDAEAE 300
 DB 241 ASAREVNGHSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDAEAE 300
 QY 301 EEEEBEECECPQAVPVSPASACSPPLQOPGSRVLTALRGVLTGRVGAIGQWMRRR 360
 DB 301 EEEEBEECECPQAVPVSPASACSPPLQOPGSRVLTALRGVLTGRVGAIGQWMRRR 360
 QY 361 AQLTRKRFTEVLAIVGVFLCWFPPFFSYSLGALCPKHCKVPHGLFQFFFWIGYCNS 420
 DB 361 AQLTRKRFTEVLAIVGVFLCWFPPFFSYSLGALCPKHCKVPHGLFQFFFWIGYCNS 420
 QY 421 LNPVIYITIFNODFRAPFRILCRPWTQTAW 450
 DB 421 LNPVIYITIFNODFRAPFRILCRPWTQTAW 450

RESULT 4
 ABBP1780
 ID ABBP1780 standard; Protein; 450 AA.

XX ABBP1780;
 XX 04-MAR-2003 (first entry)
 DT
 XX
 DE Human alpha 2b-adrenoceptor protein SEQ ID NO:42.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 PN MO200261087-A2.
 PD
 XX 08-AUG-2002.
 PF
 XX 19-DEC-2001; 2001WO-US50107.
 PR
 XX 19-DEC-2000; 2000US-257144P.
 PA
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.

PI Burmer GC, Roush CL, Brown JB;
 XX WPI; 2003-046718/04.
 DR N-PSDB; AB242624.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 XX cancer or autoimmune diseases
 PS Disclosure; Fig 1, 523pp; English.

CC The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide of a particular
 CC and (2) an isolated antibody having high specificity and high affinity
 CC in gene therapy. The antigenic peptides (I) can be used as GPCR modulators and
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful in detecting
 CC the presence or absence of corresponding GPCRs. The antigenic peptides for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related diseases, cell
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, host
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, memory
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242859 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

Sequence 450 AA:

Query Match 80.2%; Score 361; DB 24; Length 450;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDHDPYSVOATAIAAATLFTFGNALVITLRSRLAPQNLFLVSLAAADIL 60
 DB 1 MDHDPYSVOATAIAAATLFTFGNALVITLRSRLAPQNLFLVSLAAADIL 60
 QY 61 VATLIIPFSLANELLGYWYFRRTWCEVYALDVLCTSSIVHLCALISLDRYMAVSRALEY 120
 DB 61 VATLIIPFSLANELLGYWYFRRTWCEVYALDVLCTSSIVHLCALISLDRYMAVSRALEY 120
 QY 121 NSKRTFRRIKCIITLWVLAIVTSLPILYKDDGPPRRRPOCKLNOEAMVYIASISGS 180
 DB 121 NSKRTFRRIKCIITLWVLAIVTSLPILYKDDGPPRRRPOCKLNOEAMVYIASISGS 180
 QY 181 FPAFCIMLVYLRILYLAISNRGPRAKGPGQGSXKPRPDHGALASALPLASV 240
 DB 181 FPAFCIMLVYLRILYLAISNRGPRAKGPGQGSXKPRPDHGALASALPLASV 240
 QY 241 ASAREVNGSKSTGKEGETPEPDCTRALPPSAALPNSGQGXKGVCGASPEDEAEE 300
 DB 241 ASAREVNGSKSTGKEGETPEPDCTRALPPSAALPNSGQGXKGVCGASPEDEAEE 300
 QY 301 EEEEEECEPQAVPVSPASACSPPLQDPQGSRAVATLRGOVLGRGVGALGGQWRRR 360
 DB 301 EEEEEECEPQAVPVSPASACSPPLQDPQGSRAVATLRGOVLGRGVGALGGQWRRR 360
 QY 361 A 361
 DB 361 A 361

RESULT 5
 ID AAM52118 standard; Protein; 447 AA.
 XX AAM52118;
 AC AAM52118;
 XX 18-FBB-2002 (first entry)
 DT Human alpha-2BAR third intracellular loop variant.
 DE
 XX Human; genotyping: alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KM central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2BAR.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 170..193
 FT Region 307..309 /label= transmembrane_domain
 FT Domain /label= polymorphic_site
 FT 370..393 /label= transmembrane_domain
 FM WO200179561-A2.
 PD 25-OCT-2001.
 PF 17-Apr-2001; 2001WO-US12575.
 PR 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 PI Liggett SB, Small KM;
 XX WPI; 2001-611728/70.
 DR N-PSDB; AA199906.
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 PS Claim 20; Page 147-149; 163pp; English.
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I) - (III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IV)
 CC or a site comprising (A) (999GCG999CG) or (B) (999GCG999G) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, in
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR variant protein, the sequence is deleted for the 3

CC amino acid polymorphic site at residues 301-303 (EEE) of the wildtype
 CC protein (AAM52117).
 XX
 SO Sequence 447 AA;

Query Match 68.0%; Score 306; DB 22; Length 447;
 Best Local Similarity 100.0%; Pred. No. 1e-270;
 Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHODPYSVQATAIAAATFTLLFTFGNALVTLAVTSRLAPQNLFLVSLAADITL 60
 DB 1 MDHODPYSVQATAIAAATFTLLFTFGNALVTLAVTSRLAPQNLFLVSLAADITL 60
 QY 61 VATLIIPFSLANELLGWYFRRTWCEVYALADVLCFTSSIVHLCAISLDRYMAVSRALEY 120
 DB 61 VATLIIPFSLANELLGWYFRRTWCEVYALADVLCFTSSIVHLCAISLDRYMAVSRALEY 120
 QY 121 NSKRTPRRIKCIITLWVLIAAVISLPLIYKDGQPPGRGPPCKLQNEAMVYIIASSIGS 180
 DB 121 NSKRTPRRIKCIITLWVLIAAVISLPLIYKDGQPPGRGPPCKLQNEAMVYIIASSIGS 180
 QY 181 FFAFCLIMILVYLRIVYLIARSNRGRPAKGGPGQSGSKOPRPHGALASAKLPALASV 240
 DB 181 FFAFCLIMILVYLRIVYLIARSNRGRPAKGGPGQSGSKOPRPHGALASAKLPALASV 240
 QY 241 ASAREVNGHSKSTGEKEGETPEPTGTTRALPPSWAALPNSGQGEVCGASPEDAELEE 300
 DB 241 ASAREVNGHSKSTGEKEGETPEPTGTTRALPPSWAALPNSGQGEVCGASPEDAELEE 300
 QY 301 EEEEE 306
 DB 301 EEEEE 306

RESULT 6
 ID AAE00989 standard; Protein: 447 AA.
 XX AAE00989;

XX 04-JUL-2001 (first entry)
 XX Human alpha2B-adrenoceptor (alpha2B-AR) variant protein.
 XX

KM Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KM glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KM norepinephrine; epinephrine; therapy; vascular contraction; variant;
 KM coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KM acute myocardial infarction; AMI; Prinzmetal's variant.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 XX Region 298..306
 FT /note="Glutamic acid repeat"

XX W0200129082-A1.

XX 26-APR-2001.

XX 20-OCT-2000; 2000MO-FI00913.

XX 22-OCT-1999; 99US-0422985.

XX (JUVA-) JUVANTIA PHARMA LTD OY.

XX Snapit A, Heino P, Alhoniemi P, Karvonen M, Koulu M, Pesonen U,
 PI Scheinin M, Tuomola J, Tuomola T, Lakka TA, Myllynen K,
 PI Salonen R, Kallonen J, Vakkari V;

XX WPI; 2001-300318/31.
 XX N-PSDB; AAD04761.

PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries
 XX
 PS Claim 8; Page 26-27, 37pp; English.

CC The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) variant
 CC protein. Alpha2B-AR has a glutamic acid repeat element (amino acids
 CC 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino
 CC acids 294-311), located in the third intracellular loop of the receptor
 CC polypeptide. The variant is obtained by deletion of three glutamates from
 CC the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on
 CC chromosome 2. Alpha2-AR mediate many of the physiological effects of the
 CC catecholamines, norepinephrine and epinephrine. An antagonist of
 CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
 CC vascular contraction of coronary arteries and a disease involving
 CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
 CC clinically expressed as Prinzmetal's variant form or acute myocardial
 CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
 XX

SO Sequence 447 AA;

Query Match 68.0%; Score 306; DB 22; Length 447;
 Best Local Similarity 100.0%; Pred. No. 1e-270;
 Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHODPYSVQATAIAAATFTLLFTFGNALVTLAVTSRLAPQNLFLVSLAADITL 60
 DB 1 MDHODPYSVQATAIAAATFTLLFTFGNALVTLAVTSRLAPQNLFLVSLAADITL 60
 QY 61 VATLIIPFSLANELLGWYFRRTWCEVYALADVLCFTSSIVHLCAISLDRYMAVSRALEY 120
 DB 61 VATLIIPFSLANELLGWYFRRTWCEVYALADVLCFTSSIVHLCAISLDRYMAVSRALEY 120
 QY 121 NSKRTPRRIKCIITLWVLIAAVISLPLIYKDGQPPGRGPPCKLQNEAMVYIIASSIGS 180
 DB 121 NSKRTPRRIKCIITLWVLIAAVISLPLIYKDGQPPGRGPPCKLQNEAMVYIIASSIGS 180
 QY 181 FFAFCLIMILVYLRIVYLIARSNRGRPAKGGPGQSGSKOPRPHGALASAKLPALASV 240
 DB 181 FFAFCLIMILVYLRIVYLIARSNRGRPAKGGPGQSGSKOPRPHGALASAKLPALASV 240
 QY 241 ASAREVNGHSKSTGEKEGETPEPTGTTRALPPSWAALPNSGQGEVCGASPEDAELEE 300
 DB 241 ASAREVNGHSKSTGEKEGETPEPTGTTRALPPSWAALPNSGQGEVCGASPEDAELEE 300
 QY 301 EEEEE 306
 DB 301 EEEEE 306

RESULT 7
 ID AAE26633 standard; Protein: 447 AA.
 XX AAE26633;

XX 13-DEC-2002 (first entry)

XX Human alpha-2B-adrenoceptor variant.

KM Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
 KM hypertension; hypotensive; variant.
 XX

OS Homo sapiens.
 XX Synthetic.

XX W020026617-A1.

XX 29-AUG-2002.

PF 13-FEB-2002; 2002MO-F100113.
 XX 20-FEB-2001; 2001FI-0000323.
 PR (JURI-) JURILAB LTD OY.
 XX Salonen J;
 PI
 XX WPI; 2002-667063/71.
 DR N-PSDB; AAD44388.
 XX
 PT Detecting a risk of hypertension and targeting treatment in a subject
 PT by determining the pattern of alleles encoding a variant
 PT alpha-2-adrenoceptor
 PS
 PS Disclosure; Page 26-27; 35pp; English.
 XX
 CC The invention relates to a method for detecting a risk of hypertension
 CC by determining the pattern of alleles encoding a variant alpha-2-
 CC adrenoceptor (AR) protein. The methods and compositions of the invention
 CC are useful for detecting risks and targeting treatment for hypertension.
 CC The kit is also useful for selecting for clinical drug trials testing
 CC the antihypertensive effect of compounds. The present sequence is human
 CC alpha-2B-adrenoceptor variant.
 XX
 SQ Sequence 447 AA;

Query Match 68.0%; Score 306; DB 23; Length 447;
 Best Local Similarity 100.0%; Pred. No. 1e-270;
 Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MHOPDYSVQATTAIAAATLFTLFTFGNALVTIAVTSRSLAPQNFVLSLAADTL 60
 DB 1 MHOPDYSVQATTAIAAATLFTLFTFGNALVTIAVTSRSLAPQNFVLSLAADTL 60
 OY 61 VATTLLPSLANELLGWYFRRTWCYVYALDVLCTSSIVLCAISLDRYVAVERALEY 120
 DB 61 VATTLLPSLANELLGWYFRRTWCYVYALDVLCTSSIVLCAISLDRYVAVERALEY 120
 OY 121 NSKTPRRKICITLITWLIAAVISLPLIYKDGQOPGRPOCKLNOEAWYIIASSIGS 180
 DB 121 NSKTPRRKICITLITWLIAAVISLPLIYKDGQOPGRPOCKLNOEAWYIIASSIGS 180
 OY 181 FFAACILMITLVIRIYLIAKSNRGRPAKGGPGQESKOPRPHGALASAKLPALASV 240
 DB 181 FFAACILMITLVIRIYLIAKSNRGRPAKGGPGQESKOPRPHGALASAKLPALASV 240
 OY 241 ASAREVNGHSGKSTGEKEGETPEDTGTALPPSMALPNSGQKQKGVGASPEDAEER 300
 DB 241 ASAREVNGHSGKSTGEKEGETPEDTGTALPPSMALPNSGQKQKGVGASPEDAEER 300
 OY 301 EEEEE 306
 DB 301 EEEEE 306
 OY 301 EEEEE 306
 DB 301 EEEEE 306

RESULT 8
 AAR14149
 ID AAR14149 standard; Protein; 487 AA.
 AC AAR14149;
 XX
 DT 06-JAN-1992 (first entry)
 XX
 DE Human alpha 2 beta adrenergic receptor.
 XX
 KW Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta.
 XX
 OS Homo sapiens.
 XX
 EN US053337-A.
 XX
 PD 01-OCT-1991.

XX 30-OCT-1989; 89US-0428856.
 PF 30-OCT-1989; 89US-0428856.
 PR (NEUR-) NEUROGENETIC CORP.
 XX
 PA Weinshank RL, Hartig PR;
 PI
 XX WPI; 1991-310087/42.
 DR N-PSDB; AAQ14151.
 XX
 PT Isolated DNA encoding human adrenergic receptor - for detecting
 PT nucleic acids encoding alpha, 2-beta adrenergic receptor, for
 PT screening drugs.
 XX
 PS Disclosure; Fig 2; 15pp; English.
 XX
 CC Clone NGC-alpha2beta was isolated from a human spleen genomic
 CC library by screening with a fragment of the human 5-HT1A receptor
 CC gene. The gene was used to express recombinant receptor protein
 CC which can be used to produce antibodies for inhibition of receptor
 CC function.
 XX
 SQ Sequence 487 AA;

Query Match 52.0%; Score 234; DB 12; Length 487;
 Best Local Similarity 100.0%; Pred. No. 6.2e-205;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 128 RIKCITLITWLIAAVISLPLIYKDGQOPGRPOCKLNOEAWYIIASSIGSFFAPCII 187
 DB 165 RIKCITLITWLIAAVISLPLIYKDGQOPGRPOCKLNOEAWYIIASSIGSFFAPCII 187
 OY 188 MLVYLRIYLIYIAKSNRGRPAKGGPGQESKOPRPHGALASAKLPALASVANSREYN 224
 DB 225 MLVYLRIYLIYIAKSNRGRPAKGGPGQESKOPRPHGALASAKLPALASVANSREYN 224
 OY 248 GHSKSTGEKEGETPEDTGTALPPSMALPNSGQKQKGVGASPEDAEEREEEEEE 307
 DB 248 GHSKSTGEKEGETPEDTGTALPPSMALPNSGQKQKGVGASPEDAEEREEEEEE 307
 OY 308 EECPEQAVPSPASACSPPLQOPQSGSRVATLRGOVLLGRGVGAIGQWRRRA 361
 DB 345 EECPEQAVPSPASACSPPLQOPQSGSRVATLRGOVLLGRGVGAIGQWRRRA 361

RESULT 9
 AAM11804
 ID AAM11804 standard; Protein; 487 AA.
 AC AAM11804;
 XX
 DT 25-MAR-2003 (updated)
 DT 06-MAY-1997 (first entry)
 XX
 DE Human alpha-2b adrenergic receptor.
 XX
 KW Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
 KW epinephrine; signal transduction; neurotransmitter; ligand.
 XX
 OS Homo sapiens.
 XX
 EN US5595880-A.
 XX
 PD 21-JAN-1997.
 XX
 PF 22-OCT-1992; 92US-0965040.
 XX
 PR 30-OCT-1989; 89US-0428856.
 PR 30-MAY-1991; 91US-0707604.
 PR 22-OCT-1992; 92US-0965040.
 XX

PA (SYNA-) SYNAPTIC PHARM CORP.
 XX Hartig PR, Weinhank RL;
 XX WPI, 1997-107576/10.
 DR N-PSDB; AAT59499.
 XX
 XX Assay for alpha-2b adrenergic receptor ligands - using membranes of
 PT cells expressing recombinant receptor
 XX
 PS Disclosure; Fig 2A-E; 16pp; English.
 XX
 CC Human alpha-2b adrenergic receptor (AAW11804) is a member of the
 CC rhodopsin-like signal transducer family. Its amino acid sequence
 CC was deduced from a genomic DNA clone (AAT59499) obtd. from a human
 CC spleen DNA library. Vectors have been adapted to allow prodn. of
 CC alpha-2b adrenoreceptor in bacterial, yeast or mammalian cells;
 CC transfected Ltk- cells, designated L-NGC-alpha-2b, are deposited as
 CC ATCC CRL 10275. Membranes of transfected mammalian cells can used
 CC in novel methods to identify drugs which specifically interact
 CC with, and bind to, the alpha-2b adrenergic receptor.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 487 AA;
 SQ
 Query Match 52.0%; Score 234; DB 18; Length 487;
 Best Local Similarity 100.0%; Pred. No. 6,2e-205; Mismatches 0; Indels 0; Gaps 0;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 128 RIKCIIITLWLIAVLSPLPIYKDGQPPGRGRPOCKLNOEAWYIIASSIGSPAPCLI 187
 DB 165 RIKCIIITLWLIAVLSPLPIYKDGQPPGRGRPOCKLNOEAWYIIASSIGSPAPCLI 224
 QY 188 MIIYVLRITLIAXSNRGRPAKGGPGGSKQPPDHGALASAKLPALASVVSARVN 247
 DB 225 MIIYVLRITLIAXSNRGRPAKGGPGGSKQPPDHGALASAKLPALASVVSARVN 284
 QY 248 GHSKSTGKEGEGTPEDTGTALPPSWALPNSGGQGGVCGASPEDEAESEEEEEEE 307
 DB 285 GHSKSTGKEGEGTPEDTGTALPPSWALPNSGGQGGVCGASPEDEAESEEEEEEE 344
 QY 308 EECPEQAVPVSPASACSPPLQOPGSRVLTALRGVLTARGVGAIGGQWRRRA 361
 DB 345 EECPEQAVPVSPASACSPPLQOPGSRVLTALRGVLTARGVGAIGGQWRRRA 398
 RESULT 10
 AAR48699
 ID AAR48699 standard; Protein; 330 AA.
 XX
 AC AAR48699;
 XX
 DT 05-JUN-1996 (first entry)
 XX
 DE G-protein coupled human alpha-2 C2 adrenergic receptor protein.
 XX
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotic disorder; schizophrenia; dopamine; AMP; adenosine; thrombin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomagalovirus.
 XX
 OS Homo sapiens.
 XX
 FN WO9405695-A1.
 XX
 PD 17-MAR-1994.
 XX
 PF 09-SEP-1993; 93WO-US08528.
 XX
 PR 10-SEP-1992; 92US-0943236.
 XX
 PA (UNYV) UNIV NEW YORK STATE.

PI Murphy RB, Schuster DI;
 XX WPI, 1994-101120/12.
 DR
 XX
 XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 PT binding GPR ligands or modulating GPR binding
 PT
 PS Disclosure; Page 72-73; 160pp; English.
 XX
 CC Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagalovirus and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
 CC of polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 XX
 XX Sequence 330 AA;
 SQ
 Query Match 26.7%; Score 120; DB 15; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5.4e-101; Mismatches 0; Indels 0; Gaps 0;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 55 AAADIVATLIIIPSLANELIGVYFRTWCEVIALDVLFCTSSIVHLCAISIDRYAV 114
 DB 44 AAADIVATLIIIPSLANELIGVYFRTWCEVIALDVLFCTSSIVHLCAISIDRYAV 103
 QY 115 SRALEVNSKRTPRRIKCIITLWLIAVLSPLPIYKDGQPPGRGRPOCKLNOEAWYIL 174
 DB 104 SRALEVNSKRTPRRIKCIITLWLIAVLSPLPIYKDGQPPGRGRPOCKLNOEAWYIL 163
 RESULT 11
 AAM02671
 ID AAM02671 standard; peptide; 330 AA.
 XX
 AC AAM02671;
 XX
 DT 25-MAR-2003 (updated)
 DT 12-NOV-1996 (first entry)
 XX
 DE G-protein coupled human alpha-2 C2 adrenergic receptor.
 XX
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endocrine; bombesin; endocrine; rhodopsin;
 KW odorant; cytomagalovirus; serotoninergic.
 XX
 OS Homo sapiens.
 XX
 FN US5508384-A.
 XX
 PD 16-APR-1996.
 XX
 PF 09-SEP-1993; 93US-0118270.
 XX
 PR 09-SEP-1993; 93US-0118270.
 PR 10-SEP-1992; 92US-0943236.
 XX
 PA (UNYV) UNIV NEW YORK STATE.
 XX
 PI Murphy RB, Schuster DI;
 XX WPI, 1996-208785/21.
 DR
 XX
 PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrenia
 XX

PS	Disclosure;	Column 69-72; 184pp; English.
XX		
CC	Proteins AAM02657-W02720 represent a range of G-protein coupled receptor	
CC	(GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,	
CC	adenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,	
CC	odorant, cytochrome P450 and other GPR proteins. The receptor proteins	
CC	were used to design polypeptides, pref. based on the transmembrane	
CC	domain, for use in G-protein coupled receptor ligand binding assays.	
CC	The polypeptide fragments retain biological activity such as binding a	
CC	GPR ligand or modulating GPR ligand binding to a GPR (see	
CC	AAM02747-W02999 for examples of polypeptide fragments). The polypeptide	
CC	fragments can be used in compositions for treating subjects suffering	
CC	from a pathology related to a GPR abnormality e.g. a psychotic disorder	
CC	such as schizophrenia.	
CC	(Updated on 25-MAR-2003 to correct PF field.)	
XX		
XX	Sequence	330 AA;
QY	Query Match	26.7%; Score 120; DB 17; Length 330;
Db	Best Local Similarity	100.0%; Pred. No. 5.4e-10;
	Matches 120; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	55	AAADLVATLIIPESLANELGYWFRFRWCYVIALDVLFTSSIVHCAISLRYNAV 114
Db	44	AAADLVATLIIPESLANELGYWFRFRWCYVIALDVLFTSSIVHCAISLRYNAV 103
QY	115	SRALEYNKRTPRRRIKCIITLTVMLTAAVSLPPLTYKGQGPQPRGPCKLNQEAAYIL 174
Db	104	SRALEYNKRTPRRRIKCIITLTVMLTAAVSLPPLTYKGQGPQPRGPCKLNQEAAYIL 163
XX		
XX	RESULT 12	
XX	ABU67205	
ID	ABU67205	standard; peptide; 29 AA.
XX		
AC	ABU67205;	
DT	28-MAY-2003	(first entry)
XX		
DE	G-protein coupled receptor (GPCR) fragment #4.	
XX		
KW	Human; G-protein coupled receptor; receptor; GPCR; palmitoylation site;	
KW	phosphorylation cluster; arrestin; endosome; angina pectoris; rhinitis;	
KW	atherosclerosis; asthma; emphysema; inflammatory disease; glaucoma; pain;	
KW	rheumatoid arthritis; Obesity; Parkinson's disease; rat.	
XX		
OS	Homo sapiens.	
XX		
XX	US2002106739-A1.	
XX		
XX	08-AUG-2002.	
PD		
XX		
PF	05-NOV-2001; 2001US-0993844.	
XX		
PR	03-NOV-2000; 2000US-245772P.	
XX		
PR	08-JAN-2001; 2001US-260363P.	
XX		
PA	(OAKL/) OAKLEY R. H.	
PA	(BARA/) BARAK L. S.	
PA	(LAPO/) LAPORTE S. A.	
XX	(CARO/) CARON M. G.	
XX		
PI	Oakley RH, Barak LS, Laporte SA, Caron MG;	
XX		
XX	WPI; 2002-690758/74.	
XX		
PT	Modified G-protein coupled receptor useful for identifying an agonist,	
PT	inverse agonist or antagonist of the receptor, comprises a carboxyl	
PT	terminal having one or more clusters of phosphorylation -	
XX		
PS	Disclosure; Fig 2; 57pp; English.	
XX		
CC	The invention relates to a modified G-protein coupled receptor (GPCR)	

CC	comprising an NPXXY motif, and a carboxyl terminal tail which comprises a
CC	putative site of palmitoylation and clusters of phosphorylation, and a
CC	retained portion of a carboxyl terminal region of a GPCR portion fused to
CC	a portion of the carboxyl terminal from a second GPCR, that comprises
CC	phosphorylation clusters and a putative palmitoylation site 10-25 amino
CC	acid residues downstream of a second NPXXY motif. The modified GPCR is
CC	useful for screening compounds for GPCR activity which comprises
CC	providing a cell that expresses at least one modified GPCR, where the
CC	cell further comprises arrestin conjugated to a detectable molecule,
CC	exposing the cell to the compound, detecting the location of the arrestin
CC	within the cell, comparing the location of the arrestin within the cell
CC	in the presence of the compound to the location of the arrestin within
CC	the cell in the absence of the compound and correlating a difference
CC	between the location of arrestin within the cell in the presence of the
CC	compound and the presence of the location of the arrestin within the cell
CC	in the absence of the compound. Preferably, the arrestin is detected in
CC	endosomes. The GPCR and a nucleic acid encoding the modified GPCR are
CC	useful for preventing and/or treating a disease associated with GPCR in
CC	mammals, such as angina pectoris, atherosclerosis, asthma, emphysema,
CC	rheitis, inflammatory disease, rheumatoid arthritis, glaucoma, pain,
CC	obesity or Parkinson's disease, by modulating GPCR activity and affinity
CC	for arrestin. Sequences ABU67202-ABU67240 represent GPCR polypeptide
CC	fragments used in the scope of the invention.
CC	
SC	Sequence 29 AA:
Query Match	6.4%; Score 29; DB 23; Length 29;
Best Local Similarity	100.0%; Pred. No. 8, 5e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	422 NPVIYTIENODFRRARFRRIICREPTQTAW 450
D6	1 NPVIYTIENODFRRARFRRIICREPTQTAW 29
RESULT 13	
ID	ABP53986
ID	ABP53986 standard; peptide; 29 AA.
XX	
AC	ABP53986;
DT	10-JAN-2003 (first entry)
DE	Human alpha 2B adrenergic receptor class A GPCR.
KW	G-protein-coupled receptor; GPCR; detection; receptor; olfaction;
KV	photo-transduction; neurotransmission; vascular tone; cardiac output;
KX	digestion; pain; fluid electrolyte balance.
OS	Homo sapiens.
PN	WO200273199-A1.
PD	19-SEP-2002.
PR	13-MAR-2002; 2002MO-USO7434.
PR	13-MAR-2001; 2001US-275339P.
PA	(UYDU-) UNIV DUKE.
PI	Barak LS, Oakley RH;
WP	UPI; 2003-018747/OI.
Detecting G-protein-coupled receptor pathway activity comprises	
treating a cell having G-protein-coupled receptor activity with a test	
compound, obtaining a digital image of the cell and detecting position	
of conjugated proteins -	
Disclosure; Page 24; 42pp; English.	

CC The present invention describes a method for detecting G protein-coupled
CC receptor (GPCR) pathway activity. The method comprises: (1) providing at
CC least one cell expressing GPCR and conjugated proteins; (2) treating the
CC cell with a test compound; (3) obtaining a digital image of the cell by
CC detecting and measuring energy emitted from the detectable molecules; and
CC (4) detecting the localization of some of the conjugated proteins at one
CC of endocytic vesicles and endosomes. The method can be used for detecting
CC compounds that activate GPCR-activity in vivo and in vitro, where the
CC compound is useful for regulating various physiological functions
CC including photo-transduction, olfaction, neurotransmission, vascular
CC tone, cardiac output, digestion, pain and fluid electrolyte balance.
CC The present sequence represents a GPCR amino acid sequence which is given
CC in the exemplification of the present invention.
CC
SQ Sequence 29 AA:
Query Match 6.4%; Score 29; DB 24; Length 29;
Best Local Similarity 100.0%; Pred. No. 8.5e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 422 NPVTITTFNODFRRAFRRIICRPWTQTAM 450
Db 1 NPVTITTFNODFRRAFRRIICRPWTQTAM 29
RESULT 14
AAM52126
ID AAM52126 standard; Protein; 457 AA.
XX
AC AAM52126;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2CAR variant protein.
XX
XX Human alpha-2CAR variant protein.
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX polymorphic site; allelic variant; cardiovascular disease;
XX central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX phosphorylation; inositol phosphate; alpha-2CAR.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Domain 208..231
XX FT /label= transmembrane_domain
XX FT 379..402
XX FT /label= transmembrane_domain
XX PN MO200179561-A2.
XX
XX PD 25-OCT-2001.
XX
XX PF 17-APR-2001; 2001MO-US12575.
XX
XX PR 17-APR-2000; 2000US-0551744.
XX PR 10-AUG-2000; 2000US-0636259.
XX PR 19-OCT-2000; 2000US-0692077.
XX
XX PA (LIGG/) LIGGETT S B.
XX PA (SMAL/) SMALL K M.
XX
XX PI Liggett SB, Small KM;
XX
XX WPI; 2001-611728/70.
XX N-PSDB; AAI99933.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
XX disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
XX
XX Claim 78, Page 160-162; 163pp; English.
XX

CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (999gcg99gcg) or (B) (999gcg99gcg) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2CAR variant
CC protein, deleted for a 4 amino acid polymorphic site at residues 321-324
CC of the wildtype protein (AAM52124).
CC
SQ Sequence 457 AA:
Query Match 5.8%; Score 26; DB 22; Length 457;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 87 VYLADVLFCSTSVHLCATSLDRYW 112
Db 126 VYLADVLFCSTSVHLCATSLDRYW 151
RESULT 15
AAR54834
ID AAR54834 standard; Protein; 458 AA.
XX
AC AAR54834;
XX
DT 01-FEB-1995 (first entry)
XX
DE Human derived adreneline alpha 2CII receptor.
XX
XX adreneline receptor; alpha CII; screening; detection; pharmacology;
XX drugs.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Misc-difference 1
XX FT /note= "may or may not be present, but is only
XX FT present if amino acid residues 2-17 are
XX FT present"
XX FT Peptide 2..17
XX FT /label= N-terminal peptide
XX FT /note= "may or may not be present"
XX
XX PN JP06121686-A.
XX
XX PD 06-MAY-1994.
XX
XX PF 12-OCT-1992; 92JP-0272744.
XX
XX PR 12-OCT-1992; 92JP-0272744.
XX
XX PA (ASAH) ASAH KASEI KOGYO KK.
XX
XX WPI; 1994-185923/23.
XX N-PSDB; AAG64890.
XX

```

PT Adrenaline receptor gene encoding alpha 2CII receptor - for
PT screening drugs reactive to the alpha 2CII receptor
XX
XX Claim 1; Page 9-11; 13pp; Japanese.
XX
XX AA064890 encodes the amino acid sequence of a polypeptide
CC (AA064890) that constitutes human derived adrenaline alpha 2CII
CC receptor. The DNA can be used for the study of the pharmacological
CC importance of the gene expression in humans.
XX
XX
SQ Sequence 458 AA;
Query Match 5.8%; Score 26; DB 15; Length 458;
Beet Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 87 VYIALDVLFTSSIVHLCALISIDRYW 112
Db 126 VYIALDVLFTSSIVHLCALISIDRYW 151

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Search completed: February 6, 2004, 18:23:31
 Job time : 38.6254 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 6, 2004, 18:22:12 ; Search time 15.0502 Seconds
(without alignments)
1265.095 Million cell updates/sec

Title: US-09-692-077D-7
Perfect score: 450
Sequence: 1 MDHQDPYSVQATAIAAAT.....QDFRRAFRILCRPTQTAW 450

Scoring table: OLIGO
Gapop 60.0 , Gapect 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 20

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA: *
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	26.7	330	1 US-08-118-270-20	Sequence 20, Appl
2	120	26.7	330	5 PCT-US93-08528-20	Sequence 20, Appl
3	26	5.8	461	1 US-08-194-338-4	Sequence 4, Appl
4	25	5.6	27	2 US-08-103-170-17	Sequence 17, Appl
5	25	5.6	56	3 US-07-741-453A-46	Sequence 46, Appl
6	25	5.6	330	1 US-08-118-270-21	Sequence 21, Appl
7	25	5.6	330	5 PCT-US93-08528-21	Sequence 21, Appl
8	25	5.6	358	2 US-08-465-971B-4	Sequence 4, Appl
9	25	5.6	450	1 US-08-194-338-5	Sequence 5, Appl
10	25	5.6	450	1 US-08-196-989B-11	Sequence 11, Appl
11	25	5.6	450	1 US-08-444-734A-8	Sequence 8, Appl
12	25	5.6	450	1 US-08-760-936-11	Sequence 11, Appl
13	25	5.6	450	4 US-09-225-024-11	Sequence 11, Appl
14	23	5.1	99	5 US-08-118-270-332	Sequence 332, App
15	23	5.1	99	5 PCT-US93-08528-332	Sequence 332, App
16	21	4.7	330	1 US-08-118-270-19	Sequence 19, Appl
17	21	4.7	330	5 PCT-US93-08528-19	Sequence 19, Appl
18	21	4.7	334	1 US-08-118-270-22	Sequence 22, Appl
19	21	4.7	334	5 PCT-US93-08528-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1.
US-08-118-270-20
; Sequence 20, Application US/08118270

Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-20

Query Match 26.7%; Score 120; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 2 6e-91;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AAADIVATIIIPSLANELGYYFRRTWCEVYLAADVLTCTSSIVHLCAISIDRYWAV 114
DB 44 AAADIVATIIIPSLANELGYYFRRTWCEVYLAADVLTCTSSIVHLCAISIDRYWAV 103
QY 115 SRAEYNSKTRPRRIKICILITWILAAVISLPLIYKGDGQPPQRRGRPOCKLNGEANYIL 174
DB 104 SRAEYNSKTRPRRIKICILITWILAAVISLPLIYKGDGQPPQRRGRPOCKLNGEANYIL 163

RESULT 2
PCT-US93-08528-20
; Sequence 20, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-20

Query Match 26.7%; Score 120; DB 5; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.6e-91;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 AAADILVATLIPSLANELLGYWFRRTWCEVIALDVLCTSSIVHLCALSLDRYAV 114
44 AAADILVATLIPSLANELLGYWFRRTWCEVIALDVLCTSSIVHLCALSLDRYAV 103

QY 115 SRALEYSKRTPRKICILITVWLIANVISLPPLIKGDQGPQRGRQCQLNQEAWYL 174
104 SRALEYSKRTPRKICILITVWLIANVISLPPLIKGDQGPQRGRQCQLNQEAWYL 163

Db

RESULT 3
US-08-194-338-4
Sequence 4, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobb, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-194-338-4

Query Match 5.8%; Score 26; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 VYIALDVLCTSSIVHLCALSLDRYV 112
Db 126 VYIALDVLCTSSIVHLCALSLDRYV 151

RESULT 4
US-08-103-170-17
Sequence 17, Application US/08103170
Patent No. 5885824
GENERAL INFORMATION:
APPLICANT: Yamada, Tadataka
APPLICANT: Yamada, Ira
TITLE OF INVENTION: Recombinant Genomic Clones Encoding
TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, Methods for Production
TITLE OF INVENTION: Thereof, and Proteins Encoded Therefrom
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSER: OELON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/633,060
FILING DATE: 24-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-017-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-4500
TELEFAX: (703) 486-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-103-170-17

Query Match 5.6%; Score 25; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 7.5e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 VYALDVLCFTSSIVHLCALISIDRY 111
DB 3 VYALDVLCFTSSIVHLCALISIDRY 27

RESULT 5

US-07-741-453A-46
Sequence 46, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN DAREY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-741-453A-46
Query Match 5.6%; Score 25; DB 3; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLCFTSSIVHLCALISIDRY 112
DB 4 YLALDVLCFTSSIVHLCALISIDRY 28

RESULT 6
US-08-118-270-21
Sequence 21, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESSES:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-21

Query Match 5.6%; Score 25; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 6.6e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLCFTSSIVHLCALISIDRY 112
DB 74 YLALDVLCFTSSIVHLCALISIDRY 98

RESULT 7
PCT-US93-08528-21
Sequence 21, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-21

Query Match 5.6%; Score 25; DB 5; Length 330;
Best Local Similarity 100.0%; Pred. No. 6,6e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YIADVLFTCTSSIVHCAISLDRYW 112
DB 74 YIADVLFTCTSSIVHCAISLDRYW 98

RESULT 8
US-08-465-971B-4
Sequence 4, Application US/08465971B
Patent No. 5942414
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEP51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Giffillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mullins, J G
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PFI187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-465-971B-4

Query Match 5.6%; Score 25; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 7.1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YIADVLFTCTSSIVHCAISLDRYW 112
DB 112 YIADVLFTCTSSIVHCAISLDRYW 136

RESULT 9

US-08-194-338-5
Sequence 5, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-194-338-5

Query Match 5.6%; Score 25; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 8.7e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YIADVLFTCTSSIVHCAISLDRYW 112
DB 109 YIADVLFTCTSSIVHCAISLDRYW 133

RESULT 10
US-08-196-989B-11
Sequence 11, Application US/08196989B
Patent No. 5585476
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanichik & Saliwanichik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,9898
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-196-989B-11

Query Match 5.6%; Score 25; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 8.7e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 YLADVLFCTSSIVHLCALISLDRYW 112
DB 109 YLADVLFCTSSIVHLCALISLDRYW 133

RESULT 11
US-08-444-734A-8
Sequence 8, Application US/08444734A
Patent No. 5610282
GENERAL INFORMATION:
APPLICANT: Sibley, David R.
APPLICANT: Monama, Frederick J.
APPLICANT: Mahan, Lawrence C.
APPLICANT: McVittie, Louis D.
TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and
TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
NUMBER OF INVENTION: cell lines
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,734A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,917
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/548,714
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH065,001FW1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-444-734A-8

Query Match 5.6%; Score 25; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 8.7e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 YLADVLFCTSSIVHLCALISLDRYW 112
DB 109 YLADVLFCTSSIVHLCALISLDRYW 133

RESULT 12
US-08-760-936-11
Sequence 11, Application US/08760936
Patent No. 5856443
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936
FILING DATE: December 6, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-760-936-11

Query Match 5.6%; Score 25; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 8.7e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 YLADVLFCTSSIVHLCALISLDRYW 112
DB 109 YLADVLFCTSSIVHLCALISLDRYW 133

RESULT 13

US-09-225-024-11

Sequence 11, Application US/09225024

Patent No. 6518414

GENERAL INFORMATION:

APPLICANT: MacLennan, A. John

TITLE OF INVENTION: Molecular Cloning and Expression of

NUMBER OF INVENTION: G-Protein Coupled Receptors

CORRESPONDENCE ADDRESS:

ADDRESS: Saliwanhik, Lloyd & Saliwanhik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/225,024

FILING DATE: 04-JAN-1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/760,936

FILING DATE: 6-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/196,989

FILING DATE: 15-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Doran R.

REGISTRATION NUMBER: 38,261

REFERENCE/DOCKET NUMBER: MAC-100C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 450 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

US-09-225-024-11

Query Match

Best Local Similarity 5.6%; Score 25; DB 4; Length 450;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB

88 YLADVLFTSIVHCAISDRW 112

109 YLADVLFTSIVHCAISDRW 133

RESULT 14

US-08-118-270-332

Sequence 332, Application US/08118270

Patent No. 5508384

GENERAL INFORMATION:

APPLICANT: Murphy, Randall B.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

NUMBER OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

CORRESPONDENCE ADDRESS:

ADDRESS: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY-2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 332:

SEQUENCE CHARACTERISTICS:

LENGTH: 99 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-118-270-332

Query Match

Best Local Similarity 5.1%; Score 23; DB 1; Length 99;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB

12 TAAIAATFLIFITFGNALVI 34

1 TAAIAATFLIFITFGNALVI 23

RESULT 15

PCT-US93-08528-332

Sequence 332, Application PC/TUS9308528

GENERAL INFORMATION:

APPLICANT: New York University

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

NUMBER OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

CORRESPONDENCE ADDRESS:

ADDRESS: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY-2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 332:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-332

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Query Match 5.1%; Score 23; DB 5; Length 99;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 12 TAAIAAAITFLIFTFGNALVI 34
Db 1 TAAIAAAITFLIFTFGNALVI 23

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Job time : 15.0502 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2004, 18:23:37 ; Search time 29.5987 Seconds
(without alignments)
3183.320 Million cell updates/sec

Title: US-09-692-077D-7
Perfect score: 450
Sequence: 1 MDHODPYSVQATAIAAAIT.....QDFRRAPRILCPWTQTAW 450

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 801455 seqs, 209382283 residues

Word size : 20

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
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 - 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
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 - 17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450	100.0	450	9 US-09-825-923-4	Sequence 4, Appl1
2	450	100.0	450	15 US-10-077-870-4	Sequence 4, Appl1
3	450	100.0	450	15 US-10-001-073-7	Sequence 7, Appl1
4	361	80.2	450	15 US-10-225-567A-42	Sequence 42, Appl1
5	306	68.0	447	9 US-09-825-923-2	Sequence 2, Appl1
6	306	68.0	447	15 US-10-077-870-2	Sequence 2, Appl1
7	306	68.0	447	15 US-09-993-844-18	Sequence 8, Appl1
8	29	6.4	29	15 US-10-001-073-8	Sequence 18, Appl1
9	26	5.8	458	15 US-10-001-073-46	Sequence 46, Appl1
10	26	5.8	461	15 US-10-225-567A-44	Sequence 44, Appl1
11	26	5.8	462	15 US-10-001-073-44	Sequence 44, Appl1
12	25	5.6	450	15 US-10-001-073-26	Sequence 26, Appl1
13	25	5.6	450	15 US-10-001-073-27	Sequence 27, Appl1
14	25	5.6	450	15 US-10-225-567A-40	Sequence 40, Appl1
15	21	4.7	307	15 US-10-060-795B-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1				
US-09-825-923-4				
Sequence 4, Application US/09825923				
Patent No. US20010016338A1				
GENERAL INFORMATION:				
APPLICANT: Snapir, Amir				
APPLICANT: Heinonen, Paula				
APPLICANT: Alhopuro, Pia				
APPLICANT: Karvonen, Matti				
APPLICANT: Koulu, Markku				
APPLICANT: Pesonen, Ullamari				
APPLICANT: Seheinlin, Mika T				
APPLICANT: Salonen, Jukka T				
APPLICANT: Tuomainen, Tomi-Pekka				
APPLICANT: Lakka, Timo A				
APPLICANT: Nyysanen, Kristina				
APPLICANT: Salonen, Riitta				
APPLICANT: Kaunonen, Uusi				
APPLICANT: Valkonen, Veli-Pekka				
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor				
FILE REFERENCE: protein, and uses thereof				
CURRENT APPLICATION NUMBER: US/09/825,923				
CURRENT FILING DATE: 2001-04-05				
PRIOR APPLICATION NUMBER: 09/422,985				
PRIOR FILING DATE: 2000-05-25				
NUMBER OF SEQ ID NOS: 10				
SOFTWARE: PatentIn Ver. 2.1				
SEQ ID NO 4				
LENGTH: 450				
TYPE: PRT				
ORGANISM: Homo sapiens				
US-09-825-923-4				
Query Match				
Best Local Similarity 100.0%; Score 450; DB 9; Length 450;				
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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Db	1	MDHODPYSVQATAIAAAITFLITFGNALVTLAVTSRSRAPQNLFLVSLAADIL	60	
Qy	61	VATLIIPFSLANELAGYWRFRRTWCEVYLAADVLTCTSSIVHLCAISLDRYMAVSRALEY	120	
Db	61	VATLIIPFSLANELAGYWRFRRTWCEVYLAADVLTCTSSIVHLCAISLDRYMAVSRALEY	120	
Qy	121	NSKRTPRRIKIIITWVLAAVISLPLIYKGDGPQPRGRPOCKLNOEAWYIIASSIGS	180	
Db	121	NSKRTPRRIKIIITWVLAAVISLPLIYKGDGPQPRGRPOCKLNOEAWYIIASSIGS	180	
Qy	181	FPAPCLIMILVYLIYLIARSNRGRAGGPGQGSKQPRPDHGALASAKLPALASV	240	
Db	181	FPAPCLIMILVYLIYLIARSNRGRAGGPGQGSKQPRPDHGALASAKLPALASV	240	
Qy	241	ASAREVNGHSKSTGEKEGETPEDTGTALPPSWAALPNSGGQKEGVCGASPEDEABEE	300	
Db	241	ASAREVNGHSKSTGEKEGETPEDTGTALPPSWAALPNSGGQKEGVCGASPEDEABEE	300	
Qy	301	EEEEEEECBPQAVPVSASACSPPLQOPQGSRVLTALRGQVILGRGVALIGQWMRRR	360	
Db	301	EEEEEEECBPQAVPVSASACSPPLQOPQGSRVLTALRGQVILGRGVALIGQWMRRR	360	
Qy	361	AQLTRERKFFVLAIVGVVLCWPPFFSLSGALCPKXICKVPHGLFOFFFWIGYCNSS	420	
Db	361	AQLTRERKFFVLAIVGVVLCWPPFFSLSGALCPKXICKVPHGLFOFFFWIGYCNSS	420	
Qy	421	LNPIYTIIPNODFRARFRILCPWTQTAW	450	
Db	421	LNPIYTIIPNODFRARFRILCPWTQTAW	450	

Db 421 LNPVITYTFNDPFRARFRIICRPWTQTAW 450

RESULT 2

US-10-077-870-4
Sequence 4, Application US/10077870
Publication No. US20030003470A1
GENERAL INFORMATION:

APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077.870

PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 4
LENGTH: 450

TYPE: PRT
ORGANISM: Homo sapiens
US-10-077-870-4

Query Match
Best Local Similarity 100.0%; Score 450; DB 15; Length 450;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHODPYSVQATTAIAAATFTLFTFGNALVTIAVTSRSLRAPONTFLVSLAADTL 60
Db 1 MDHODPYSVQATTAIAAATFTLFTFGNALVTIAVTSRSLRAPONTFLVSLAADTL 60
QY 61 VATLIIPFSLANELLGWYFRRTWCVEYIALDVLFTCTSSIVHLCALSLDRYMAVSRALEY 120
Db 61 VATLIIPFSLANELLGWYFRRTWCVEYIALDVLFTCTSSIVHLCALSLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIILTWLAAVTSLEPPLTYKDGQGPGRPOCKLNOAMWYTIASSIGS 180
Db 121 NSKRTPRRIKCIILTWLAAVTSLEPPLTYKDGQGPGRPOCKLNOAMWYTIASSIGS 180
QY 121 NSKRTPRRIKCIILTWLAAVTSLEPPLTYKDGQGPGRPOCKLNOAMWYTIASSIGS 180
Db 121 NSKRTPRRIKCIILTWLAAVTSLEPPLTYKDGQGPGRPOCKLNOAMWYTIASSIGS 180
QY 181 FFAPCILMILVYRIYLAKRSNRGPRKGGPGGSGSKOPRBDHGALASAKLPALASV 240
Db 181 FFAPCILMILVYRIYLAKRSNRGPRKGGPGGSGSKOPRBDHGALASAKLPALASV 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSMALPNSGQGGQGVCGASPEDEAEE 300
Db 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSMALPNSGQGGQGVCGASPEDEAEE 300
QY 301 EEEEEECEPOAVPVSPASACSPPLQOPGSRVLAIRGQVLLGRGVGAIIGQWRRR 360
Db 301 EEEEEECEPOAVPVSPASACSPPLQOPGSRVLAIRGQVLLGRGVGAIIGQWRRR 360
QY 361 AQLTREKRTFVLAVIGVFLCWPFPFSSYSLGAIQKHKVHGFLFOFFWYIGYCNSS 420
Db 361 AQLTREKRTFVLAVIGVFLCWPFPFSSYSLGAIQKHKVHGFLFOFFWYIGYCNSS 420
QY 421 LNPVITYTFNDPFRARFRIICRPWTQTAW 450
Db 421 LNPVITYTFNDPFRARFRIICRPWTQTAW 450

RESULT 3

US-10-001-073-7
Sequence 7, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:

APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Small, Kirsten
FILE REFERENCE: 13073-PCR
CURRENT APPLICATION NUMBER: US/10/001.073

NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-073-7

Query Match
Best Local Similarity 100.0%; Score 450; DB 15; Length 450;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHODPYSVQATTAIAAATFTLFTFGNALVTIAVTSRSLRAPONTFLVSLAADTL 60
Db 1 MDHODPYSVQATTAIAAATFTLFTFGNALVTIAVTSRSLRAPONTFLVSLAADTL 60
QY 61 VATLIIPFSLANELLGWYFRRTWCVEYIALDVLFTCTSSIVHLCALSLDRYMAVSRALEY 120
Db 61 VATLIIPFSLANELLGWYFRRTWCVEYIALDVLFTCTSSIVHLCALSLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIILTWLAAVTSLEPPLTYKDGQGPGRPOCKLNOAMWYTIASSIGS 180
Db 121 NSKRTPRRIKCIILTWLAAVTSLEPPLTYKDGQGPGRPOCKLNOAMWYTIASSIGS 180
QY 181 FFAPCILMILVYRIYLAKRSNRGPRKGGPGGSGSKOPRBDHGALASAKLPALASV 240
Db 181 FFAPCILMILVYRIYLAKRSNRGPRKGGPGGSGSKOPRBDHGALASAKLPALASV 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSMALPNSGQGGQGVCGASPEDEAEE 300
Db 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSMALPNSGQGGQGVCGASPEDEAEE 300
QY 301 EEEEEECEPOAVPVSPASACSPPLQOPGSRVLAIRGQVLLGRGVGAIIGQWRRR 360
Db 301 EEEEEECEPOAVPVSPASACSPPLQOPGSRVLAIRGQVLLGRGVGAIIGQWRRR 360
QY 361 AQLTREKRTFVLAVIGVFLCWPFPFSSYSLGAIQKHKVHGFLFOFFWYIGYCNSS 420
Db 361 AQLTREKRTFVLAVIGVFLCWPFPFSSYSLGAIQKHKVHGFLFOFFWYIGYCNSS 420
QY 421 LNPVITYTFNDPFRARFRIICRPWTQTAW 450
Db 421 LNPVITYTFNDPFRARFRIICRPWTQTAW 450

RESULT 4

US-10-225-567A-42
Sequence 42, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:

APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225.567A

PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257.144
NUMBER OF SEQ ID NOS: 2292

SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 450

TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-42

Query Match
Best Local Similarity 80.2%; Score 361; DB 15; Length 450;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHODPYSVQATTAIAAATFTLFTFGNALVTIAVTSRSLRAPONTFLVSLAADTL 60
Db 1 MDHODPYSVQATTAIAAATFTLFTFGNALVTIAVTSRSLRAPONTFLVSLAADTL 60

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Qy 61 VATTIIPFSLANELLGWYFRRRTWCEVYALDVLCFTSSIVHLCAISLDRWAVSRALEY 120
Db 61 VATTIIPFSLANELLGWYFRRRTWCEVYALDVLCFTSSIVHLCAISLDRWAVSRALEY 120
Qy 121 NSKRTPRRIKCIITLTVWLIAAVISLPLIYKDGQPPGRGRPOCKLQOEAMVYIIASSIGS 180
Db 121 NSKRTPRRIKCIITLTVWLIAAVISLPLIYKDGQPPGRGRPOCKLQOEAMVYIIASSIGS 180
Qy 181 FFAPCLIMILVYLRIYLIARSNRRGPRAKGGPQGGSKOPRPHGALASAKI.PALASV 240
Db 181 FFAPCLIMILVYLRIYLIARSNRRGPRAKGGPQGGSKOPRPHGALASAKI.PALASV 240
Qy 241 ASAREVNGHSKSTGEKEGETPEDTGTRALPPSWAALPNSGQGGKEGVCGASPEDEABEE 300
Db 241 ASAREVNGHSKSTGEKEGETPEDTGTRALPPSWAALPNSGQGGKEGVCGASPEDEABEE 300
Qy 301 EEEEEEECEPPQAVPVSPASACSPPLQOQGSRVLTALRGQVLLGRGVGAIQGGQWRRR 360
Db 301 EEEEEEECEPPQAVPVSPASACSPPLQOQGSRVLTALRGQVLLGRGVGAIQGGQWRRR 360
Qy 361 A 361
Db 361 A 361

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RESULT 5

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US-09-825-923-2
; Sequence 2, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heimonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Marci
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Myyrynen, Kristina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kaunonen, Jussi
; APPLICANT: Valonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: protein, and uses thereof
; CURRENT APPLICATION NUMBER: US/09/825,923
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-2

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Query Match 68.0%; Score 306; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 4.3e-242;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MDHDPYSVQATAIAAATFLILFTIFGNALVILAVLTSRSLRAPONLFLVLSIAADIL 60
Db 1 MDHDPYSVQATAIAAATFLILFTIFGNALVILAVLTSRSLRAPONLFLVLSIAADIL 60
Qy 61 VATTIIPFSLANELLGWYFRRRTWCEVYALDVLCFTSSIVHLCAISLDRWAVSRALEY 120
Db 61 VATTIIPFSLANELLGWYFRRRTWCEVYALDVLCFTSSIVHLCAISLDRWAVSRALEY 120
Qy 121 NSKRTPRRIKCIITLTVWLIAAVISLPLIYKDGQPPGRGRPOCKLQOEAMVYIIASSIGS 180
Db 121 NSKRTPRRIKCIITLTVWLIAAVISLPLIYKDGQPPGRGRPOCKLQOEAMVYIIASSIGS 180

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Db 121 NSKRTPRRIKCIITLTVWLIAAVISLPLIYKDGQPPGRGRPOCKLQOEAMVYIIASSIGS 180
Qy 181 FFAPCLIMILVYLRIYLIARSNRRGPRAKGGPQGGSKOPRPHGALASAKI.PALASV 240
Db 181 FFAPCLIMILVYLRIYLIARSNRRGPRAKGGPQGGSKOPRPHGALASAKI.PALASV 240
Qy 241 ASAREVNGHSKSTGEKEGETPEDTGTRALPPSWAALPNSGQGGKEGVCGASPEDEABEE 300
Db 241 ASAREVNGHSKSTGEKEGETPEDTGTRALPPSWAALPNSGQGGKEGVCGASPEDEABEE 300
Qy 301 EEEEE 306
Db 301 EEEEE 306

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RESULT 6

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US-10-077-870-2
; Sequence 2, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent Ver. 3.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-2

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Query Match 68.0%; Score 306; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 4.3e-242;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MDHDPYSVQATAIAAATFLILFTIFGNALVILAVLTSRSLRAPONLFLVLSIAADIL 60
Db 1 MDHDPYSVQATAIAAATFLILFTIFGNALVILAVLTSRSLRAPONLFLVLSIAADIL 60
Qy 61 VATTIIPFSLANELLGWYFRRRTWCEVYALDVLCFTSSIVHLCAISLDRWAVSRALEY 120
Db 61 VATTIIPFSLANELLGWYFRRRTWCEVYALDVLCFTSSIVHLCAISLDRWAVSRALEY 120
Qy 121 NSKRTPRRIKCIITLTVWLIAAVISLPLIYKDGQPPGRGRPOCKLQOEAMVYIIASSIGS 180
Db 121 NSKRTPRRIKCIITLTVWLIAAVISLPLIYKDGQPPGRGRPOCKLQOEAMVYIIASSIGS 180
Qy 181 FFAPCLIMILVYLRIYLIARSNRRGPRAKGGPQGGSKOPRPHGALASAKI.PALASV 240
Db 181 FFAPCLIMILVYLRIYLIARSNRRGPRAKGGPQGGSKOPRPHGALASAKI.PALASV 240
Qy 241 ASAREVNGHSKSTGEKEGETPEDTGTRALPPSWAALPNSGQGGKEGVCGASPEDEABEE 300
Db 241 ASAREVNGHSKSTGEKEGETPEDTGTRALPPSWAALPNSGQGGKEGVCGASPEDEABEE 300
Qy 301 EEEEE 306
Db 301 EEEEE 306

```

RESULT 7

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US-10-001-073-8
; Sequence 8, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms

```

FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001.073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 447
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-073-8

Query Match 68.0%; Score 306; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 4,3e-242;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHDPYVQATPAIAAATFLILFTFGNALVTLAVTSGSLAPQNLPLVLSIAADIL 60
DB 1 MDHDPYVQATPAIAAATFLILFTFGNALVTLAVTSGSLAPQNLPLVLSIAADIL 60
QY 61 VATLIIPSLANELLGYVFRRTWCCEVYALDVLFCTSSIVHCAISLDRYMAVSRALEY 120
DB 61 VATLIIPSLANELLGYVFRRTWCCEVYALDVLFCTSSIVHCAISLDRYMAVSRALEY 120
QY 121 NSKRPRIKCIILTWLIAVVISLPLIKGQGPQGRPOCKNOEAMVTLASISGS 180
DB 121 NSKRPRIKCIILTWLIAVVISLPLIKGQGPQGRPOCKNOEAMVTLASISGS 180
QY 181 FFAPELIMILVLYLAIYLIARNSNRGRPRAGQGGESKQPRDHGALASAKLPALASV 240
DB 181 FFAPELIMILVLYLAIYLIARNSNRGRPRAGQGGESKQPRDHGALASAKLPALASV 240
QY 241 ASAREVNGHKSSTGEKEGETPEDTGRALPSSWALPNSGQCGEVCASPEDEAEE 300
DB 241 ASAREVNGHKSSTGEKEGETPEDTGRALPSSWALPNSGQCGEVCASPEDEAEE 300
QY 301 EEEEEE 306
DB 301 EEEEEE 306

RESULT 8
US-09-993-844-18
Sequence 18; Application US/09993844
Patent No. US20020106739A1
GENERAL INFORMATION:
APPLICANT: Oakley, Robert H.
APPLICANT: Barak, Lawrence S.
APPLICANT: Laporte, Stephanie A.
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Modified G-Protein Coupled Receptors
FILE REFERENCE: 033072-026
CURRENT APPLICATION NUMBER: US/09/993,844
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,772
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/260,363
PRIOR FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 29
TYPE: PRT
ORGANISM: Human
US-09-993-844-18

Query Match 6.4%; Score 29; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 NPVYITFNDFRRAPRIICRPMWTOTAW 450
DB 1 NPVYITFNDFRRAPRIICRPMWTOTAW 29

RESULT 9
US-10-001-073-46
Sequence 46; Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001.073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-073-46

Query Match 5.8%; Score 26; DB 15; Length 458;
Best Local Similarity 100.0%; Pred. No. 5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 VYALDVLFTSSIVHCAISLDRYW 112
DB 126 VYALDVLFTSSIVHCAISLDRYW 151

RESULT 10
US-10-225-567A-44
Sequence 44; Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-44

Query Match 5.8%; Score 26; DB 15; Length 461;
Best Local Similarity 100.0%; Pred. No. 5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 VYALDVLFTSSIVHCAISLDRYW 112
DB 126 VYALDVLFTSSIVHCAISLDRYW 151

RESULT 11
US-10-001-073-44
Sequence 44; Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001.073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44
LENGTH: 462
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-073-44

Query Match 5.8%; Score 26; DB 15; Length 462;
Best Local Similarity 100.0%; Pred. No. 5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 YLALDVLPCTSSIVHLCALISLDRYW 112
DB 126 YLALDVLPCTSSIVHLCALISLDRYW 151

RESULT 12
US-10-001-073-26
Sequence 26, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001.073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-073-26

Query Match 5.6%; Score 25; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 YLALDVLPCTSSIVHLCALISLDRYW 112
DB 109 YLALDVLPCTSSIVHLCALISLDRYW 133

RESULT 13
US-10-001-073-27
Sequence 27, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001.073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-073-27

Query Match 5.6%; Score 25; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 YLALDVLPCTSSIVHLCALISLDRYW 112
DB 109 YLALDVLPCTSSIVHLCALISLDRYW 133

RESULT 14

US-10-225-567A-40
Sequence 40, Application US/10225567A
Publication No. US20030113796A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225.567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-40

Query Match 5.6%; Score 25; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 YLALDVLPCTSSIVHLCALISLDRYW 112
DB 109 YLALDVLPCTSSIVHLCALISLDRYW 133

RESULT 15
US-10-060-795B-4
Sequence 4, Application US/10060795B
Publication No. US20030040022A1
GENERAL INFORMATION:
APPLICANT: Civeill, Olivier
APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Machida, Curtis A.
TITLE OF INVENTION: Dopamine Receptors and Genes
FILE REFERENCE: 90-1092-CCC
CURRENT APPLICATION NUMBER: US/10/060.795B
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 09/238977
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 08/474892
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/973588
PRIOR FILING DATE: 1992-11-09
PRIOR APPLICATION NUMBER: 07/438544
PRIOR FILING DATE: 1989-11-20
PRIOR APPLICATION NUMBER: 07/273373
PRIOR FILING DATE: 1988-11-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 307
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-795B-4

Query Match 4.7%; Score 21; DB 15; Length 307;
Best Local Similarity 100.0%; Pred. No. 4.5e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 YLALDVLPCTSSIVHLCALISL 108
DB 109 YLALDVLPCTSSIVHLCALISL 129

Search completed: February 6, 2004, 18:28:03
Job time : 30.5987 secs

Mon Feb 9 08:28:43 2004

us-09-692-077d-7.oligo.rapb

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 18:20:56 ; Search time 16.5552 Seconds

(without alignments)
2614.040 Million cell updates/sec

Title: US-09-692-077d-7

Sequence: 1 MDHODPYSVQATTAIAAAIT.....QDFRRAFRRLICRPTQTAW 450

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 20

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	80.2	450	2 A37223	alpha-2B-adrenergic
2	176	39.1	276	2 I53161	alpha-2-adrenergic
3	71	15.8	448	2 I51883	alpha-2B-adrenergic
4	71	15.8	455	2 S28221	alpha-2-C2 adrenergic
5	63	14.0	453	2 A35642	alpha-2B-adrenergic
6	26	5.8	458	2 A48392	alpha 2C4 adrenoce
7	26	5.8	458	2 A40392	alpha-2-adrenergic
8	26	5.8	458	2 A37869	alpha-2B-adrenergic
9	26	5.8	458	2 I49480	alpha-2C-adrenergic
10	26	5.8	461	2 A31237	alpha-2B-adrenergic
11	25	5.6	432	2 I50829	alpha-2-adrenocept
12	25	5.6	450	2 A38316	alpha-2-adrenocept
13	25	5.6	450	2 B40392	alpha-2-adrenergic
14	25	5.6	450	2 JH0190	alpha-2-adrenergic
15	25	5.6	450	2 A34169	alpha-2A-adrenergic
16	25	5.6	450	2 I49481	alpha-2 adrenergic

ALIGNMENTS

RESULT 1
A37223
alpha-2B-adrenergic receptor - human
N/Alternate names: alpha-2C2-adrenergic receptor
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 29-Oct-1999
C/Accession: A37223; I39407; S14308; A36158
R/Weinshank, R.L.; Zgonick, J.M.; Macchi, M.; Adam, N.; Lichtblau, H.; Branche, T.A.;

Mol. Pharmacol. 38, 681-688, 1990
A/Title: Cloning, expression, and pharmacological characterization of a human alpha-2B-ac
A/Reference number: A37223; MUID:91042469; PMID:2172775
A/Accession: A37223
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-450 <WEI>
R/Lomaney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, T.L.; Caron, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 5094-5098, 1990
A/Title: Expansion of the alpha-2-adrenergic receptor family: cloning and characterization
A/Reference number: I39407; MUID:90311349; PMID:2164221
A/Accession: I39407
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-450 <LOM>
A/Cross-references: GB:M34041; NID:g178197; PIDN:AA51666.1; PID:g178198
R/Chajlant, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept
A/Reference number: S14308; MUID:9192139; PMID:1849485
A/Accession: S14308
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 56-185 <CH>
A/Cross-references: GB:X59684; NID:g28635
A/Note: this translation is not annotated in GenBank entry H8ALPH218, release 111.0
R/Chang, A.C.; Ho, T.F.; Chang, N.C.
Biochem. Biophys. Res. Commun. 172, 817-823, 1990
A/Title: In vitro amplification by polymerase chain reaction of a partial gene encoding t
A/Reference number: A36158; MUID:91054503; PMID:2173582
A/Accession: A36158
A/Molecule type: DNA
A/Residues: 95-361, 'OL', 364-389 <CHA>
A/Cross-references: GB:M38742; NID:g177867; PIDN:AA62823.1; PID:g177868
C/Genetics:
A/Gene: GDB:ADRA2B; ADRA2L1; ADRA2L1; ADRA2RL1
A/Cross-references: GDB:120539; OMIM:104260
A/Map position: 2p13-2q13
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match	80.2%	Score 361	DB 2	Length 450
Best Local Similarity	100.0%	Pred. No. 0		
Matches 361	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 MDHODPYSVQATTAIAAAITFLITFGNALVILAVITRSRAPONTPLVSLAADIL	60		
DB	1 MDHODPYSVQATTAIAAAITFLITFGNALVILAVITRSRAPONTPLVSLAADIL	60		
QY	61 VATTIIPFSLANELIGWYFRRTMCEVYALADVLCFTSSIVHLCAISLDRYMAVSRLEY	120		
DB	61 VATTIIPFSLANELIGWYFRRTMCEVYALADVLCFTSSIVHLCAISLDRYMAVSRLEY	120		
QY	121 NSKRTPRIRKICITLTVWLAIVISLPLIYKDGQPPQRRPOCKLNQEMAYIILASSIGS	180		
DB	121 NSKRTPRIRKICITLTVWLAIVISLPLIYKDGQPPQRRPOCKLNQEMAYIILASSIGS	180		
QY	181 FPAAPCLIMILVYLRITYIAVRSNRRGPRAGKGPQGGSKPPRPDHGALASAKIPALASV	240		
DB	181 FPAAPCLIMILVYLRITYIAVRSNRRGPRAGKGPQGGSKPPRPDHGALASAKIPALASV	240		
QY	241 ASAREVNGSKSGKEGEPEDTGTALPPSMAALPNSGGQKQEGVCCASPDEAEE	300		
DB	241 ASAREVNGSKSGKEGEPEDTGTALPPSMAALPNSGGQKQEGVCCASPDEAEE	300		
QY	301 EEEEEECEPQAVPVSPASACSPLOPQGSRVLTATLGRGVLAGVGAIGQWRRR	360		
DB	301 EEEEEECEPQAVPVSPASACSPLOPQGSRVLTATLGRGVLAGVGAIGQWRRR	360		
QY	361 A 361			
DB	361 A 361			

RESULT 2

153161
 alpha-2-adrenergic receptor, isolets of langerhans - rat (fragment)
 C:Species: Rattus sp. (rat)
 C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 30-May-1997
 C:Accession: 153161
 R:Wang, S.Y.; Pilkey, D.T.
 Diabetes 43, 127-136, 1994
 A:Title: Identification in isolets of langerhans of a new rat alpha-2-adrenergic receptor
 A:Reference number: 153161; MUID:94085695; PMID:8262309
 A:Accession: 153161
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-276 <RES>
 A:Cross-references: GB:S67316; NID:9456949
 A:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 39.1%; Score 176; DB 2; Length 276;
 Best Local Similarity 100.0%; Pred. No. 5, 8e-163;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 CTSSIVHCAISLDRYAVSRALRYNSKRTPRRIKIIITWLIAAVISLPLIYKGDQ 155
 DB 1 CTSSIVHCAISLDRYAVSRALRYNSKRTPRRIKIIITWLIAAVISLPLIYKGDQ 60
 QY 156 PQRGRPOCKLNOEWYIIASSIGSFAPCLIMILYLRIRIYLIAKSNRGRGKGGQ 215
 DB 61 PQRGRPOCKLNOEWYIIASSIGSFAPCLIMILYLRIRIYLIAKSNRGRGKGGQ 120
 QY 216 GESKOPRPHGALASAKIPALASVANSARVNGSKSTGEKEGETPEDTGRALP 271
 DB 121 GESKOPRPHGALASAKIPALASVANSARVNGSKSTGEKEGETPEDTGRALP 176

RESULT 3

151883
 alpha-2B-adrenergic receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
 C:Accession: 151883
 R:de Josselin, M.; Cloix, J.F.; Pecquery, R.; Giudicelli, Y.; Dause, J.P.
 Am. J. Hypertens. 8, 177-182, 1995
 A:Title: Differential sodium regulation between salt-sensitive and salt-resistant Sabra
 A:Reference number: 151883; MUID:95275492; PMID:7735946
 A:Accession: 151883
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-448 <RES>
 A:Cross-references: EMBL:X74400; NID:9840862; PIDN:CA52411.1; PID:9940816
 A:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 15.8%; Score 71; DB 2; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1, 2e-60;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 WCEVYALDVLFCSTSIHLCALISLDRYAVSRALRYNSKRTPRRIKIIITWLIAAVI 143
 DB 84 WCEVYALDVLFCSTSIHLCALISLDRYAVSRALRYNSKRTPRRIKIIITWLIAAVI 143
 QY 144 SLPLIYKGDQ 154
 DB 144 SLPLIYKGDQ 154

RESULT 4

528221
 alpha-2-C2 adrenergic receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
 C:Accession: 528221; JH0693

R:Chen, W.M.; Chang, A.C.; Shie, B.J.; Chang, Y.H.; Chang, N.C.A.
 Biochim. Biophys. Acta 1171, 219-223, 1992
 A:Title: Molecular cloning and characterization of a mouse alpha(2)C2 adrenoceptor sub

A:Reference number: 528221; MUID:91129625; PMID:1336336
 A:Accession: 528221
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-455 <CHR>
 A:Cross-references: EMBL:M94583
 A:Note: the authors translated the codon CCA for residue 161 as Phe, ACT for residue 33
 Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992
 A:Title: Cloning and expression of the mouse homology of the human alpha2-C2 adrenergic
 A:Reference number: JH0693; MUID:92378586; PMID:1354956
 A:Accession: JH0693
 A:Molecule type: DNA
 A:Residues: 6-228, 231-455 <CHR>
 A:Cross-references: GB:L00979; NID:9191547; PIDN:AAA7131.1; PID:9191548
 A:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:18-43/Domain: transmembrane #status predicted <TM1>
 F:55-81/Domain: transmembrane #status predicted <TM2>
 F:90-115/Domain: transmembrane #status predicted <TM3>
 F:114-158/Domain: transmembrane #status predicted <TM4>
 F:173-199/Domain: transmembrane #status predicted <TM5>
 F:377-402/Domain: transmembrane #status predicted <TM6>
 F:410-435/Domain: transmembrane #status predicted <TM7>

Query Match 15.8%; Score 71; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1, 2e-60;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 WCEVYALDVLFCSTSIHLCALISLDRYAVSRALRYNSKRTPRRIKIIITWLIAAVI 143
 DB 89 WCEVYALDVLFCSTSIHLCALISLDRYAVSRALRYNSKRTPRRIKIIITWLIAAVI 148
 QY 144 SLPLIYKGDQ 154
 DB 149 SLPLIYKGDQ 159

RESULT 5

A35642
 alpha-2B-adrenergic receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
 C:Accession: A35642
 R:Zeng, D.; Harrison, J.K.; D'Angelo, D.D.; Barber, C.M.; Tucker, A.L.; Lu, Z.; Lynch, K
 Proc. Natl. Acad. Sci. U.S.A. 87, 3102-3106, 1990
 A:Title: Molecular characterization of a rat alpha-2B-adrenergic receptor.
 A:Reference number: A35642; MUID:90222177; PMID:2158103
 A:Accession: A35642
 A:Molecule type: mRNA
 A:Residues: 1-453 <ZEN>
 A:Cross-references: GB:M32061; NID:9202589; PIDN:AAA40635.1; PID:9202590
 A:Note: 169-Phe was also found
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 14.0%; Score 63; DB 2; Length 453;
 Best Local Similarity 100.0%; Pred. No. 7, 1e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AITFLILFTIFGNALVLAIVTSRSRLAPONLFLVSLAAADIVATLIIIPSLANELIGY 77
 DB 23 AITFLILFTIFGNALVLAIVTSRSRLAPONLFLVSLAAADIVATLIIIPSLANELIGY 82
 QY 78 WYF 80
 DB 83 WYF 85

RESULT 6

A48392
alpha 2C4 adrenoceptor subtype - mouse
N/Alternate names: alpha 2C4 isoceptor
C/Species: Mus musculus (house mouse)
C/Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C/Accession: A48392
R/Chang, Y.H.; Chang, N.C.; Chen, W.M.; Chang, A.C.
Biochem. Mol. Biol. Int. 29, 467-474, 1993
A/Title: Molecular characterization of a murine homologue of alpha 2C4 adrenoceptor sub
A/Reference number: A48392; MUID:93250567; PMID:8387367
A/Accession: A48392
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-458 <CH>
A/Cross-references: GB:M97516; NID:g191728; PIDN:AAA37183.1; PID:g191729
A/Experimental source: DBA/2, liver
A/Note: Sequence extracted from NCBI backbone (NCBIN:131475, NCBIIP:131476)
C/Keywords: G protein-coupled receptor

Query Match 5.8%; Score 26; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 VYIALDVLFCTSSIVHCAISLDRYM 112
Db 126 VYIALDVLFCTSSIVHCAISLDRYM 151

RESULT 7
A40392
alpha-2-adrenergic receptor (clone RG10) - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C/Accession: A40392
R/Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A/Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic rec
A/Reference number: A40392; MUID:91244823; PMID:1645350
A/Accession: A40392
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-458 <LAN>
A/Cross-references: GB:M62371; NID:g206612; PIDN:AAA42033.1; PID:g206613
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 5.8%; Score 26; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 VYIALDVLFCTSSIVHCAISLDRYM 112
Db 126 VYIALDVLFCTSSIVHCAISLDRYM 151

RESULT 8
A37869
alpha-2B-adrenergic receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C/Accession: A37869; S13023
R/Florjanczyk, C.S.; Handy, D.E.; Bresnahan, M.R.; Zannis, V.I.; Gavras, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 1019-1023, 1991
A/Title: Cloning and expression of a rat brain alpha-2B-adrenergic receptor.
A/Reference number: A37869; MUID:91126047; PMID:1704126
A/Accession: A37869
A/Molecule type: mRNA
A/Residues: 1-458 <FLO>
A/Cross-references: GB:M58316; NID:g202585; PIDN:AAA40634.1; PID:g202586
A/Note: The authors translated the codon ACC for residue 69 as Asn and GCG for residue 8
R/Volgt, M.M.; McCune, S.K.; Kanterman, R.Y.; Felder, C.C.
FEBS Lett. 278, 45-50, 1991

A/Title: The rat alpha(2)-C4 adrenergic receptor gene encodes a novel pharmacological su
A/Reference number: S13023; MUID:91130596; PMID:1704314
A/Accession: S13023
A/Molecule type: DNA
A/Residues: 1-39, 'G', 41-68, 'N', 70-154, 'E', 156-244, 'S', 246-458 <VOI>
A/Cross-references: GB:X57659; NID:g288044; PIDN:CAA40861.1; PID:g288045
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 5.8%; Score 26; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 VYIALDVLFCTSSIVHCAISLDRYM 112
Db 126 VYIALDVLFCTSSIVHCAISLDRYM 151

RESULT 9
149480
alpha-2 adrenergic receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C/Accession: 149480
R/Link, R.; Daunt, D.; Barsh, G.S.; Chruscinski, A.; Koblika, B.
Mol. Pharmacol. 42, 16-27, 1992
A/Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and id
in antagonist binding.
A/Reference number: 149480; MUID:92342131; PMID:1353249
A/Accession: 149480
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-458 <RES>
A/Cross-references: GB:M99376; NID:g191880; PIDN:AAA37212.1; PID:g191881
C/Superfamily: vertebrate rhodopsin
C/Keywords: neurotransmitter receptor

Query Match 5.8%; Score 26; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 VYIALDVLFCTSSIVHCAISLDRYM 112
Db 126 VYIALDVLFCTSSIVHCAISLDRYM 151

RESULT 10
A31237
alpha-2C-adrenergic receptor - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999
C/Accession: A31237; S14309; S14310
R/Regan, J.W.; Koblika, T.S.; Yang-Feng, T.L.; Caron, M.G.; Lefkowitz, R.J.; Koblika, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 6301-6305, 1988
A/Title: Cloning and expression of a human kidney cDNA for an alpha-2-adrenergic recepto
A/Reference number: A31237; MUID:88320430; PMID:2842764
A/Accession: A31237
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-461 <REG>
A/Cross-references: GB:U03853; NID:g178193; PIDN:AAA35513.1; PID:g178194
R/Chajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep
A/Reference number: S14308; MUID:91192139; PMID:1849485
A/Accession: S14309
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 95-223 <CH>
A/Accession: S14310
A/Molecule type: DNA
A/Residues: 95-223 <CH2>
C/Genetics:
A/Gene: GDB:ADRA2C; ADRA1L2; ADRA2L2; ADRA2RL2

A/Cross-references: GDB:120540; OMIM:104250
 A/Map position: 4p16.3-4p15
 A/Title: Vertebrate rhodopsin
 A/Superfamily: G protein-coupled receptor; transmembrane protein
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match
 Best Local Similarity 5.6%; Score 26; DB 2; Length 461;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 YLALDVLCFTSSIVHLCALISLDRYW 112
 DB 126 YLALDVLCFTSSIVHLCALISLDRYW 151

RESULT 11

150829
 alpha-2-adrenoceptor - cuckoo wrasse
 C/Species: Labrus ocellatus (cuckoo wrasse)
 C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
 C/Accession: 150829
 R/Svensson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom, N.; Ala-Uocila, S.; Scheinin,
 B.; J. Pharmacol. 110, 54-60, 1993
 A/Title: Cloning and expression of a fish alpha-2-adrenoceptor.
 A/Reference number: 150829; PMID:94035926; PMID:7693288
 A/Accession: 150829
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-432 <SV>
 A/Cross-references: EMBL:U07743; NID:9467287; PIDN:AAA17386.1; PID:9467288
 C/Superfamily: vertebrate rhodopsin

Query Match
 Best Local Similarity 5.6%; Score 25; DB 2; Length 432;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLCFTSSIVHLCALISLDRYW 112
 DB 108 YLALDVLCFTSSIVHLCALISLDRYW 132

RESULT 12

A38316
 alpha-2-adrenergic receptor - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
 C/Accession: A38316
 R/Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., E.J.; Limbird, L.E.
 J. Biol. Chem. 265, 17307-17317, 1990
 A/Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2-ad
 A/Reference number: A38316; PMID:9106167; PMID:2170371
 A/Accession: A38316
 A/Molecule type: DNA
 A/Residues: 1-450 <GV>
 A/Cross-references: GB:J05652; NID:9164303; PIDN:AAA30984.1; PID:9164304
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match
 Best Local Similarity 5.6%; Score 25; DB 2; Length 450;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLCFTSSIVHLCALISLDRYW 112
 DB 109 YLALDVLCFTSSIVHLCALISLDRYW 133

RESULT 13

B40392
 alpha-2-adrenergic receptor (clone R610) - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
 C/Accession: B40392
 R/Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.

J. Biol. Chem. 266, 10470-10478, 1991
 A/Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic
 A/Reference number: A40392; PMID:91244823; PMID:1645350
 A/Accession: B40392
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-450 <LAN>
 A/Cross-references: GB:M62372; NID:9206615; PIDN:AAA42034.1; PID:9206616
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match
 Best Local Similarity 5.6%; Score 25; DB 2; Length 450;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLCFTSSIVHLCALISLDRYW 112
 DB 109 YLALDVLCFTSSIVHLCALISLDRYW 133

RESULT 14

JH0190
 alpha-2-adrenergic receptor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
 C/Accession: JH0190
 R/Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.
 Mol. Cell. Biochem. 97, 161-172, 1990
 A/Title: Molecular cloning, sequencing and expression of an alpha-2-adrenergic receptor
 A/Reference number: JH0190; PMID:91125329; PMID:2177834
 A/Accession: JH0190
 A/Molecule type: mRNA
 A/Residues: 1-450 <CHA>
 A/Experimental source: brain
 C/Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It med
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein

F/71-96/Domain: hydrophobic <HDI>
 F/106-131/Domain: hydrophobic <HII>
 F/150-175/Domain: hydrophobic <HIV>
 F/193-218/Domain: hydrophobic <HIV>
 F/375-400/Domain: hydrophobic <HIV>
 F/405-430/Domain: hydrophobic <VII>

Query Match
 Best Local Similarity 5.6%; Score 25; DB 2; Length 450;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLCFTSSIVHLCALISLDRYW 112
 DB 109 YLALDVLCFTSSIVHLCALISLDRYW 133

RESULT 15

A34169
 alpha-2A-adrenergic receptor - human
 N/Alternate names: alpha-2C10-adrenergic receptor
 C/Species: Homo sapiens (man)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 29-Oct-1999
 C/Accession: A34169
 R/Fraser, C.M.; Arkava, S.; McCombie, W.R.; Venter, J.C.
 J. Biol. Chem. 264, 11754-11761, 1989
 A/Title: Cloning, sequence analysis, and permanent expression of a human alpha2-adreneg
 A/Reference number: A34169; PMID:89308571; PMID:2568356
 A/Accession: A34169
 A/Molecule type: DNA
 A/Residues: 1-450 <FRA>
 A/Cross-references: GB:M33533; NID:9178195; PIDN:AAA51665.1; PID:9178196
 R/Koblika, B.K.; Mateu, H.; Koblika, T.S.; Yang-Feng, T.L.; Francke, U.; Caron, M.G.; L
 Science 258, 650-656, 1987

A/Title: Cloning, sequencing, and expression of the gene coding for the human platelet a

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OM protein - protein search, using SW model

Run on: February 6, 2004, 18:19:31 ; Search time 10.0334 Seconds
(without alignments)
2109.148 Million cell updates/sec

Title: US-09-692-077D-7
Perfect score: 450
Sequence: 1 MDHQDPYSVQATAAIAAIT.....QDFRAFRILICRPWTQTAW 450

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 20

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	450	100.0	450	1 A2AB_HUMAN	P18089 homo sapien
2	184	40.9	391	1 A2AB_ERIEU	O19012 erinaceus e
3	109	24.2	388	1 A2AB_ORYAF	O19032 orycteropu
4	103	22.9	394	1 A2AB_RABIT	O77830 oryctolagu
5	100	22.2	384	1 A2AB_ELEMA	O19014 elephas max
6	96	21.3	389	1 A2AB_HORSE	O77721 equus cabal
7	81	18.0	390	1 A2AB_DUGDU	O77713 dugong dugo
8	75	16.7	448	1 A2AB_CAVPO	O60475 cavia porce
9	71	15.8	455	1 A2AB_MOUSE	P30545 mus musculu
10	63	14.0	382	1 A2AB_DIDMA	O77715 didelphis m
11	63	14.0	386	1 A2AB_AMBHO	O18935 amblyomus
12	63	14.0	387	1 A2AB_MACPR	O19023 macroscelid
13	63	14.0	453	1 A2AB_RAT	P19328 rattus norv
14	62	13.8	389	1 A2AB_PROHA	O19054 procavia ca
15	62	13.8	392	1 A2AB_BOVIN	O19091 talpa europ
16	62	13.8	397	1 A2AB_TALEU	O77722 echinops te
17	38	8.4	384	1 A2AB_ECHTE	O60476 cavia porce
18	26	5.8	455	1 A2AC_CAVPO	P20066 rattus norv
19	26	5.8	458	1 A2AC_MOUSE	P20066 rattus norv
20	26	5.8	458	1 A2AC_RAT	P18825 homo sapien
21	26	5.8	462	1 A2AC_HUMAN	P35405 didelphis m
22	26	5.8	469	1 A2AC_DIDMA	O91081 labrus ossi
23	25	5.6	432	1 A2AR_LABOS	P32251 carassius a
24	25	5.6	436	1 A2AR_CARAU	O60474 cavia porce
25	25	5.6	450	1 A2AA_HUMAN	P08913 homo sapien
26	25	5.6	450	1 A2AA_HUMAN	O01338 mus musculu
27	25	5.6	450	1 A2AA_MOUSE	P18871 sus scrofa
28	25	5.6	450	1 A2AA_PIG	P22908 rattus norv
29	25	5.6	450	1 A2AA_RAT	Q28838 bos taurus
30	25	5.6	452	1 A2AA_BOVIN	

ALIGNMENTS

RESULT 1
ID A2AB_HUMAN STANDARD; PRT: 450 AA.
AC P18089; Q9BZKO;
DT 01-NOV-1990 (Rel. 16, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Subtype C2).
GN ADBA2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90311349; PubMed=2164221;
RA Lomasney J.W., Lorenz W., Allen L.F., King K., Regan J.W.,
RA Yang-Feng T.L., Caron M.G., Lefkowitz R.J.;
RT "Expansion of the alpha 2-adrenergic receptor family: cloning and
RT characterization of a human alpha 2-adrenergic receptor subtype, the
RT gene for which is located on chromosome 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5094-5098(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042469; PubMed=2172775;
RA Weinstein R.L., Zgombick J.M., Macchi M., Adham N., Lichthblau H.,
RA Branchek T.A., Hartig P.R.;
RT "Cloning, expression, and pharmacological characterization of a human
RT alpha 2B-adrenergic receptor.";
RL Mol. Pharmacol. 38:681-688(1990).
[3]
RP SEQUENCE FROM N.A.
RA Cayla C., Schack S., Bouloumie A., Dovedjian J.C., Paris H.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A., AND VARIANT 301-GLU-GLU-303.
RX MEDLINE=21265012; PubMed=11056163;
RA Small K.M., Brown K.M., Forbes S.L., Liggett S.B.;
RT "Polymorphic deletion of three intracellular acidic residues of the
RT alpha 2B-adrenergic receptor decreases G protein-coupled receptor
RT kinase-mediated phosphorylation and desensitization.";
RL J. Biol. Chem. 276:4917-4922(2001).
[5]
RP SEQUENCE OF 95-389 FROM N.A.
RX MEDLINE=91054503; PubMed=2173582;
RA Chang A.C., Ho T.F., Chang N.-C.A.;
RT "In vitro amplification by polymerase chain reaction of a partial
RT gene encoding the third subtype of alpha-2 adrenergic receptor in
RT humans.";
RL Biochem. Biophys. Res. Commun. 172:817-823(1990).
-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
IS CLONIDINE > NORBEPHEDRINE > EPINEPHRINE > OXYMETAZOLINE >
DOPAMINE > P-TYRAMINE > PHENYLEPHRINE > SEROTONIN > P-SYNEPHRINE /
P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >
CHLOROPROMAZINE > PHENTOLAMINE > MANSERINE > SPIPERONE > PRAZOSIN
> ALPRENOLOL > PROPRANOLOL > PINDOLOL.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC or send an email to license@ebi.ac.uk).

DR EMBL: M34041; AAA51666.1; -
DR EMBL: M38742; AAA62823.1; -


```

FT SITE 163 163 SIMILARITY . IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 167 167 (BY SIMILARITY).
FT SITE 167 167 (BY SIMILARITY).
FT NON TER 391 391
FT SEQUENCE 391 AA; 42919 MW; F21FA2757B1EB1DA CRC64;
Query Match Bebt Local Similarity 100.0%; Score 184; DB 1; Length 391;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 19 ITFLILPFIENALVILAVLSRSRAQONFLVSLAADILVNTLIPSLANELLGYW 78
Db 6 ITFLILPFIENALVILAVLSRSRAQONFLVSLAADILVNTLIPSLANELLGYW 65
OY 79 YFRRTWCVEVYALDVLFTCTSSIVHLCAISLDRYMAVSALEYSKRTPRRIKCIITLTVML 138
Db 66 YFRRTWCVEVYALDVLFTCTSSIVHLCAISLDRYMAVSALEYSKRTPRRIKCIITLTVML 125
OY 139 IAAVITSLPPLIKYGQGPQGRPOCKLNQEAAMYTLASSIGSFAPACIMILIVYRIYLI 198
Db 126 IAAVITSLPPLIKYGQGPQGRPOCKLNQEAAMYTLASSIGSFAPACIMILIVYRIYLI 185
OY 199 AKRS 202
Db 186 AKRS 189
RESULT 3
A2AB_ORYAF STANDARD; PRT; 388 AA.
ID A2AB_ORYAF
AC O19032;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Oryctolopus afer (Aardvark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Tubulidentata; Orycteropodidae; Orycteropus.
OX NCBI_TaxID=9918;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97357151; Pubmed=9214502;
RA Springer M.S., Clevon G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
RA Amrine H.M., Stanhope M.J.;
RL "Endemic African mammals shake the phylogenetic tree.";
RL Nature 388:61-64 (1997).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; Y12522; CAA73122.2; ALT SEQ.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.
FT NON_TER 1 1
FT TRANSMEM 1 25 1 (POTENTIAL).

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Query Match	Best Local Similarity	Score 109; DB 1; Length 388;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
FT	DOMAIN	26 36
FT	TRANSSEM	37 62
FT	DOMAIN	63 72
FT	TRANSSEM	73 95
FT	DOMAIN	96 117
FT	TRANSSEM	118 140
FT	DOMAIN	141 156
FT	TRANSSEM	157 180
FT	DOMAIN	181 352
FT	TRANSSEM	353 376
FT	DOMAIN	377 385
FT	TRANSSEM	386 >388
FT	DISULFID	72 151
FT	DOMAIN	280 291
FT	SITE	79 79
FT	SITE	163 163
FT	SITE	167 167
FT	NON TER	388 388
FT	SEQUENCE	388 AA; 42429 MW; 1810DC67E838897 CRC64;
SO	SEQUENCE	388 AA; 42429 MW; 1810DC67E838897 CRC64;
Query Match	Best Local Similarity	Score 109; DB 1; Length 388;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	19 ITTFLITFTFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIPFSLANELLGYW 78	
DB	6 ITTFLITFTFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIPFSLANELLGYW 65	
QY	79 YFRRTWCENVYIALDVLTCTSSIVHCAISLDRIYAVNSRALEYNSKRTPR 127	
DB	66 YFRRTWCENVYIALDVLTCTSSIVHCAISLDRIYAVNSRALEYNSKRTPR 114	
RESULT 4		
A2AB_RABIT	STANDARD; PRT; 394 AA.	
ID	A2AB_RABIT	
AC	077830;	
DT	15-JUL-1999 (Rel. 38, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).	
GN	ADRA2B.	
OS	Oryctolagus cuniculus (Rabbit).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
OX	NCBI_TaxId=9986;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Stanhope M.J., Madsen O.J., Waddell V.G., Clevon G.C., de Jong W.W.,	
RA	Springer M.S., Madsen O.O.M.;	
RL	Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.	
CC	-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE ACTION OF G	
CC	INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G	
CC	PROTEINS.	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).	
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
CC	-----	
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CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; Y16189; CAA76115.1; -	
DR	EMBL; Y15946; CAA75889.2; -	
DR	HSSP; P29274; IMWH.	
DR	InterPro; IPR000276; GPCR_Rhodopsn.	
DR	PIfam; PF00001; 7tm_1; 1.	

DR Pfam; PF00001; 7cm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.
FT NON_TER 1 1
FT TRANSMEM 1 25
FT DOMAIN 26 36
FT TRANSMEM 37 62
FT DOMAIN 63 72
FT TRANSMEM 73 95
FT DOMAIN 96 117
FT TRANSMEM 118 140
FT DOMAIN 141 156
FT TRANSMEM 157 180
FT DOMAIN 181 348
FT TRANSMEM 349 372
FT DOMAIN 373 381
FT TRANSMEM 382 >384
FT DISULFID 72 151
FT DOMAIN 281 285
FT SITE 79 79
FT SITE 163 163
FT SITE 167 167
FT SITE 167 167
FT NON_TER 384 384
SQ SEQUENCE 384 AA; 41911 MM; CF41B5GCC355B94F CRC64;
Query Match 22.2%; Score 100; DB 1; Length 384;
Best Local Similarity 100.0%; Freq. No. 4,4e-71;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 19 ITPIILITIGNALVILAVLTSSRLAPONTLFVSLAADIIVATLIPFSLANELLGYW 78
DB 6 ITPIILITIGNALVILAVLTSSRLAPONTLFVSLAADIIVATLIPFSLANELLGYW 65
QY 79 YFRRTWCEVLIADVFCFTSSIVHCAISLDRYAVSRAL 118
DB 66 YFRRTWCEVLIADVFCFTSSIVHCAISLDRYAVSRAL 105
RESULT 6
A2AB HORSE
ID A2AB HORSE STANDARD; PRT; 389 AA.
AC 077721;
DT 15-OCT-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1] SEQUENCE FROM N.A.
RX MEDLINE=98334573; PubMed=967998;
RA Stanhope M.J., Madsen O.J., Madsen V.G., Clevon G.C., de Jong W.W.,
RT Springer M.S.;
RT "Highly congruent molecular support for a diverse superordinal clade
RT of endemic African mammals";
RL Mol. Phylogenet. Evol. 9:501-508(1998).
RN [2] REVISIONS.
RP Madsen O.J.;
RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: Y15945; CA75898.2; -.
DR HSPB: P29274; 1MMH.
DR InterPro: IPR00276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Multigene family.
FT NON_TER 1 1
FT TRANSMEM <1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 363 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 364 387 6 (POTENTIAL).
FT DOMAIN >389 72 151 EXTRACELLULAR (POTENTIAL).
FT DISULFID 72 151 BY SIMILARITY.
FT DOMAIN 281 302 POLY-GU.
FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
FT SITE 163 163 SIMILARITY).
FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 167 167 (BY SIMILARITY).
FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 167 167 (BY SIMILARITY).
FT NON_TER 389 389
FT SEQUENCE 389 AA; 42257 MW; 992179431679B0FD CRC64;
SQ
Query Match 21.3%; Score 96; DB 1; Length 389;
Best Local Similarity 100.0%; Pred. No. 6, 1e-68;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 ITFLIFLFTFGNALVILAVLTSLRSLAPONLFLVSLAADIIVTLIIIPSLANELLGYW 78
DB 6 ITFLIFLFTFGNALVILAVLTSLRSLAPONLFLVSLAADIIVTLIIIPSLANELLGYW 65
QY 79 YFRRTWCEVYLAADVLEFCTSSIVHLCALISDRYAV 114
DB 66 YFRRTWCEVYLAADVLEFCTSSIVHLCALISDRYAV 101
RESULT 7
A2AB_DUGDU STANDARD; PRT; 390 AA.
ID A2AB_DUGDU
AC 077713;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRB2B.
OS Dugong dugon (Dugong).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Sirenia; Dugongidae; Dugong.
OX NCBI_TaxID=29137;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanhope M.J., Maden O.O.M., Wadell V.G., Clevon G.C., de Jong W.W.,
RA Springer M.S., Maden O.O.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: Y15947; CA75900.2; -.
DR HSPB: P29274; 1MMH.
DR InterPro: IPR00276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Multigene family.
FT NON_TER 1 1
FT TRANSMEM <1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 354 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 355 378 6 (POTENTIAL).
FT DOMAIN >390 72 151 EXTRACELLULAR (POTENTIAL).
FT DISULFID 72 151 ASP/GLU-RICH (ACIDIC).
FT NON_TER 390 390 BY SIMILARITY.
FT SEQUENCE 390 AA; 42562 MW; 779F849267F9F314 CRC64;
SQ
Query Match 18.0%; Score 81; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 3, 5e-56;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 VATIILIPSLANELLGYWYRRRTWCEVYLAADVLEFCTSSIVHLCALISDRYAVSRLEY 120
DB 48 VATIILIPSLANELLGYWYRRRTWCEVYLAADVLEFCTSSIVHLCALISDRYAVSRLEY 107
QY 121 NSKRTPRIRKIIITWVLI 141
DB 108 NSKRTPRIRKIIITWVLI 128
RESULT 8
A2AB_CAVPO STANDARD; PRT; 448 AA.
ID A2AB_CAVPO
AC 060475;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
GN ADRB2B.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley;
RX MEDLINE=96152573; PubMed=8573196;
RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.,
RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
and alpha 2C adrenoceptor subtypes. Radioligand binding and


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FT CONFLICT 229 230 MISSING (IN REF. 2).
SQ SEQUENCE 455 AA; 50615 MW; A3954AD7E0E6263 CRC64;
Query Match 15.8%; Score 71; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 2,7e-48;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 WCEVYALADVLCFSSIVHLCAISLDRYAVSRALVSKPTPRKICILTWLIAAVI 143
DB 89 WCEVYALADVLCFSSIVHLCAISLDRYAVSRALVSKPTPRKICILTWLIAAVI 148
OY 144 SLPLIYKGDQ 154
DB 149 SLPLIYKGDQ 159

RESULT 10
A2AB DIDMA STANDARD; PRT; 382 AA.
ID A2AB DIDMA
AC 077715;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OC NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98334573; PubMed=9667998;
RA Stanhope M.J., Madsen O.J., Waddell V.G., Clevon G.C., de Jong W.W.,
RA Springer M.S.;
RT "Highly congruent molecular support for a diverse superordinal clade
RT of endemic African mammals.";
RL Mol. Phylogenet. Evol. 9:501-508 (1998).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; Y15943; CAA75896.1; -.
DR HSSP; P29274; IMWH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT TRANSSEM 1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 346 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 347 370 6 (POTENTIAL).
FT DOMAIN 371 379 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 380 >382 7 (POTENTIAL).

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FT DISULFID 72 151 BY SIMILARITY.
FT DOMAIN 271 283 ASP/GLU-RICH (ACIDIC).
FT NON TER 382
SQ SEQUENCE 382 AA; 41870 MW; EAF12DD44B2AA19 CRC64;
Query Match 14.0%; Score 63; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 4,4e-42;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 ITFLILFTIRGNALVILAVLSRSLRAPQNLFLVSLAADIIVTLTIFSLAEILGYW 78
DB 6 ITFLILFTIRGNALVILAVLSRSLRAPQNLFLVSLAADIIVTLTIFSLAEILGYW 65
OY 79 YFR 81
DB 66 YFR 68

RESULT 11
A2AB AMBHO STANDARD; PRT; 386 AA.
ID A2AB AMBHO
AC O18935;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Amblysomus hottentotus (Hottentot golden mole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Chrysochloridae; Amblysomus.
OC NCBI_TaxID=9391;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97357151; PubMed=9214502;
RA Springer M.S., Clevon G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
RA Amrine H.M., Stanhope M.J.;
RT "Endemic African mammals shake the phylogenetic tree.";
RL Nature 388:61-64 (1997).
RN [2]
RP REVISION TO 121.
RX Madsen O.J.;
RA Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; Y12526; CAA73126.2; -.
DR HSSP; P29274; IMWH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.
FT TRANSSEM 1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 118 140 4 (POTENTIAL).

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FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 157 180 5 (POTENTIAL).
FT TRANSMEM 181 350 CYTOSOLIC (POTENTIAL).
FT TRANSMEM 351 374 6 (POTENTIAL).
FT TRANSMEM 375 383 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 384 >386 7 (POTENTIAL).
FT DOMAIN 280 289 ASP/GLU-RICH (ACIDIC).
FT DISULFID 72 151 BY SIMILARITY.
FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
FT SITE 163 163 SIMILARITY).
FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 167 167 (BY SIMILARITY).
FT NON TER 386 386 IMPLICATED IN CATECHOL AGONIST BINDING
SQ SEQUENCE 386 AA; 42157 MW; EC11E0B7192D95E CRC64;

Query Match 14.0%; Score 63; DB 1; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.4e-42;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLIFITFGNALVILAVLTSRSLRAPONLFLVSLAADIIVATLIIIPSLANELLGYW 78
DB 6 ITFLIFITFGNALVILAVLTSRSLRAPONLFLVSLAADIIVATLIIIPSLANELLGYW 65

QY 79 YFR 81
DB 66 YFR 68

RESULT 12
A2AB_MACPR STANDARD; PRT; 387 AA.
AC 019025;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Macrocyclides proboscideus (Short-eared elephant shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Macroscelidae; Macroscelididae; Macroscelides.
OX NCBI_TaxId=29082;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97357151; PubMed=9214502;
RA Springer M.S., Clevon G.C., Madsen O.J., de Jong W.W., Maddell V.G.,
RA Amrine H.M., Stanhope M.J.;
RT "Endemic African mammals shake the phylogenetic tree.";
RL Nature 388:61-64(1997).
RN [2]
RP REVISIONS TO 148 AND 255.
RA Springer M.S., Clevon G.C., Madsen O., de Jong W.W., Maddell V.G.,
RA Amrine H.M., Stanhope M.J.;
RL Submitted (May-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; Y12524; CAAT3124.2; -.
DR HSSP; P29274; IMWH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECB_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECB_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.
FT NON TER 1 1
FT TRANSMEM <1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOSOLIC (POTENTIAL).
FT TRANSMEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
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FT TRANSMEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 157 180 5 (POTENTIAL).
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FT TRANSMEM 352 375 6 (POTENTIAL).
FT DOMAIN 376 384 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 385 >387 7 (POTENTIAL).
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FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
FT SITE 163 163 SIMILARITY).
FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 167 167 (BY SIMILARITY).
FT NON TER 387 387 IMPLICATED IN CATECHOL AGONIST BINDING
SQ SEQUENCE 387 AA; 42587 MW; B74AD5F0EE23BD5A CRC64;

Query Match 14.0%; Score 63; DB 1; Length 387;
Best Local Similarity 100.0%; Pred. No. 4.4e-42;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLIFITFGNALVILAVLTSRSLRAPONLFLVSLAADIIVATLIIIPSLANELLGYW 78
DB 6 ITFLIFITFGNALVILAVLTSRSLRAPONLFLVSLAADIIVATLIIIPSLANELLGYW 65

QY 79 YFR 81
DB 66 YFR 68

RESULT 13
A2AB_RAT STANDARD; PRT; 453 AA.
AC P19328; O63021;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
GN ADRA2B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=90222177; PubMed=2158103;
RA Zeng D., Harrison J.K., D'Angelo D.D., Barber C.M., Tucker A.L.,
RA Lu Z., Lynch K.R.;
RT "Molecular characterization of a rat alpha 2B-adrenergic receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3102-3106(1990).
RN [2]
RP SEQUENCE OF 6-453 FROM N.A.
RC STRAIN=Sabra; TISSUE=Kidney;
RX MEDLINE=95275492; PubMed=755946;
RA le Joseec M., Cloix J.F., Pecquery R., Giudicelli Y., Dausse J.P.;
RT "Differential sodium regulation between salt-sensitive and salt-
RT resistant Sabra rats is not due to any mutation in the renal alpha
RT 2B-adrenoceptor gene.";
RL Am. J. Hypertens. 8:177-182(1995).

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CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: M32061; AAA40635.1; -;
DR EMBL: X74400; CA52411.1; -;
DR PIR: A35642; A35642.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOPOSN.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.
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FT TRANSSEM 10535 10549
FT TRANSSEM 10550 10564
FT TRANSSEM 10565 10579
FT TRANSSEM 10580 10594
FT TRANSSEM 10595 10609
FT TRANSSEM 10610 10624
FT TRANSSEM 10625 10639
FT TRANSSEM 10640 10654
FT TRANSSEM 10655 10669
FT TRANSSEM 10670 10684
FT TRANSSEM 10685 10699
FT TRANSSEM 10700 10714
FT TRANSSEM 10715 10729
FT TRANSSEM 10730 10744
FT TRANSSEM 10745 10759
FT TRANSSEM 10760 10774
FT TRANSSEM 10775 10789
FT TRANSSEM 10790 10804
FT TRANSSEM 10805 10819
FT TRANSSEM 10820 10834
FT TRANSSEM 10835 10849
FT TRANSSEM 10850 10864
FT TRANSSEM 10865 10879
FT TRANSSEM 10880 10894
FT TRANSSEM 10895 10909
FT TRANSSEM 10910 10924
FT TRANSSEM 10925 10939
FT TRANSSEM 10940 10954
FT TRANSSEM 10955 10969
FT TRANSSEM 10970 10984
FT TRANSSEM 10985 10999
FT TRANSSEM 11000 11014
FT TRANSSEM 11015 11029
FT TRANSSEM 11030 11044
FT TRANSSEM 11045 11059
FT TRANSSEM 11060 11074
FT TRANSSEM 11075 11089
FT TRANSSEM 11090 11104
FT TRANSSEM 11105 11119
FT TRANSSEM 11120 11134
FT TRANSSEM 11135 11149
FT TRANSSEM 11150 11164
FT TRANSSEM 11165 11179
FT TRANSSEM 11180 11194
FT TRANSSEM 11195 11209
FT TRANSSEM 11210 11224
FT TRANSSEM 11225 11239
FT TRANSSEM 11240 11254
FT TRANSSEM 11255 11269
FT TRANSSEM 11270 11284
FT TRANSSEM 11285 11299
FT TRANSSEM 11300 11314
FT TRANSSEM 11315 11329
FT TRANSSEM 11330 11344
FT TRANSSEM 11345 11359
FT TRANSSEM 11360 11374
FT TRANSSEM 11375 11389
FT TRANSSEM 11390 11404
FT TRANSSEM 11405 11419
FT TRANSSEM 11415 11429
FT TRANSSEM 11430 11444
FT TRANSSEM 11445 11459
FT TRANSSEM 11460 11474
FT TRANSSEM 11475 11489
FT TRANSSEM 11490 11504
FT TRANSSEM 11505 11519
FT TRANSSEM 11520 11534
FT TRANSSEM 11535 11549
FT TRANSSEM 11550 11564
FT TRANSSEM 11565 11579
FT TRANSSEM 11580 11594
FT TRANSSEM 11595 11609
FT TRANSSEM 11610 11624
FT TRANSSEM 11625 11639
FT TRANSSEM 11640 11654
FT TRANSSEM 11655 11669
FT TRANSSEM 11670 11684
FT TRANSSEM 11685 11699
FT TRANSSEM 11700 11714
FT TRANSSEM 11715 11729
FT TRANSSEM 11730 11744
FT TRANSSEM 11745 11759
FT TRANSSEM 11760 11774
FT TRANSSEM 11775 11789
FT TRANSSEM 11790 11804
FT TRANSSEM 118

RESULT 15
A2AB_BOVIN STANDARD; PRT; 392 AA.
ID A2AB_BOVIN 077700;
AC 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenocceptor) (Fragment).
GN ADRA2B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9834573; PubMed=9667998;
RA Stanhope M.J., Madsen O.J., Waddell V.G., Clevon G.C., de Jong W.W.,
RA Springer M.S.;
RT "Highly congruent molecular support for a diverse superordinal clade
of endemic African mammals";
RL Mol. Phylogenet. Evol. 9:501-508(1998).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y15944; CAA75897.2; -.
DR HSSP: P29274; LMW.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; Tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_P1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family.
FT
FT TRANSMEM 1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 356 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 357 380 6 (POTENTIAL).
FT DOMAIN 381 >392 EXTRACELLULAR (POTENTIAL).
FT DISULFD 72 151 BY SIMILARITY.
FT DOMAIN 283 292 POLY-GLU.
FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
SIMILARITY).
FT SITE 163 163 IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).
FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).
FT NON_TER 392 392
SO SEQUENCE 392 AA; 42839 MW; 471596A7446475E0 CRC64;
Query Match 13.8%; Score 62; DB 1; Length 392;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 19 ITPLILFTFGNALVILAVLTSSRLRAPQNLFLVSLAADIIVATLLIPESLANELLGYW 78
Db 6 ITPLILFTFGNALVILAVLTSSRLRAPQNLFLVSLAADIIVATLLIPESLANELLGYW 65
Cy 79 YF 80
Db 66 YF 67

Search completed: February 6, 2004, 18:24:04
Job time: 11.0334 secs

Db 6 ITFTLFTFGNALVTLVLTSLRAPOMLFVLSLAADILVATLIPFSLANELLGW 65
 Qy 79 YFRRTWCCEVYALDVLTCTSSIVHLCALSLDRYVAVSRALEYNKTRPRKICILITW 138
 Db 66 YFRRTWCCEVYALDVLTCTSSIVHLCALSLDRYVAVSRALEYNKTRPRKICILITW 138
 Qy 139 IAAVLSPLIYKGGDGPGRPOCKNOEAMVYIASSISGFAPCLIMLVYRIYLI 198
 Db 126 IAAVLSPLIYKGGDGPGRPOCKNOEAMVYIASSISGFAPCLIMLVYRIYLI 198
 Qy 199 AKRSNRGPR 210
 Db 186 AKRSNRGPR 197

RESULT 2

AC 08HY8 PRELIMINARY; PRT; 451 AA.
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DE Alpha-28 adrenoreceptor. 23, last sequence update
 OS Tupia belangeri (Northern tree shrew)
 OC Mammalia; Eulazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eulazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN [1]_Taxid=37347;
 RP SEQUENCE FROM N.A.
 RT Heliconia U. van Kampen M., Isovich E., Fluegge G.;
 RT upregulation in the paraventricular nucleus; chronic stress; persistent
 DR EMBL; A115033; A0472436.1; BMBL; GenBank/DBJ databases.
 SQ SEQUENCE 451 AA; 50356 MW; 31724030113BC60 CRC64;
 Query Match
 Best Local Similarity 42.2%; Score 190; DB 6; Length 451;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ITFTLFTFGNALVTLVLTSLRAPOMLFVLSLAADILVATLIPFSLANELLGW 78
 Db 19 ITFTLFTFGNALVTLVLTSLRAPOMLFVLSLAADILVATLIPFSLANELLGW 78
 Qy 79 YFRRTWCCEVYALDVLTCTSSIVHLCALSLDRYVAVSRALEYNKTRPRKICILITW 138
 Db 79 YFRRTWCCEVYALDVLTCTSSIVHLCALSLDRYVAVSRALEYNKTRPRKICILITW 138
 Qy 139 IAAVLSPLIYKGGDGPGRPOCKNOEAMVYIASSISGFAPCLIMLVYRIYLI 198
 Db 139 IAAVLSPLIYKGGDGPGRPOCKNOEAMVYIASSISGFAPCLIMLVYRIYLI 198
 Qy 199 AKRSNRGPR 208
 Db 199 AKRSNRGPR 208

RESULT 3

AC 08GL17 PRELIMINARY; PRT; 387 AA.
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DE Alpha-28 adrenoreceptor. 16, last sequence update
 OS AAR2B adrenoreceptor 28 (Fragment)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eulazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN [1]_Taxid=9685; Carnivora; Fissipedia; Felidae; Felis.
 RP SEQUENCE FROM N.A.

RX MEDLINE=21082081; PubMed=11214318;
 RA Maden O., Scally M., Douay C., Kao D., Deery R., Adkins R.,
 RA Parvelli, Stanhope M., de Jong W., Springer M.,
 RT Mammals: adaptive radiations in two major clades of placental
 CC Neure 409:610-614 (2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
 DR EMBL; A251174; BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
 DR InterPro; IP0000276; GPCR_Rhodopsin.
 DR PROSITE; PS00237; GPCR_Rhodopsin.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 1; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON TER 1
 SQ SEQUENCE 387 AA; 42546 MW; 2C1CD5D4B3F8D9B CRC64;
 Query Match
 Best Local Similarity 40.9%; Score 184; DB 6; Length 387;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ITFTLFTFGNALVTLVLTSLRAPOMLFVLSLAADILVATLIPFSLANELLGW 78
 Db 19 ITFTLFTFGNALVTLVLTSLRAPOMLFVLSLAADILVATLIPFSLANELLGW 78
 Qy 79 YFRRTWCCEVYALDVLTCTSSIVHLCALSLDRYVAVSRALEYNKTRPRKICILITW 138
 Db 79 YFRRTWCCEVYALDVLTCTSSIVHLCALSLDRYVAVSRALEYNKTRPRKICILITW 138
 Qy 139 IAAVLSPLIYKGGDGPGRPOCKNOEAMVYIASSISGFAPCLIMLVYRIYLI 198
 Db 139 IAAVLSPLIYKGGDGPGRPOCKNOEAMVYIASSISGFAPCLIMLVYRIYLI 198
 Qy 199 AKRS 202
 Db 199 AKRS 202

RESULT 4

AC 08S095 PRELIMINARY; PRT; 389 AA.
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DE Alpha-28 adrenoreceptor. 21, last sequence update
 OS AAR2B adrenoreceptor 28 (Fragment)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eulazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN [1]_Taxid=48986;
 RP SEQUENCE FROM N.A.
 RA Teeling E.C., Madeen O., Van den Busche R.A., de Jong W.W.,
 RA Stanhope M.J., Springer M.S.,
 RT "Microbes M.J., Springer M.S.,
 RT in Old World parathyroid and the convergent evolution of a key innovation
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
 DR EMBL; A219805; CAD11972.1; -1- SIMILARITY BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
 DR InterPro; IP0000276; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON TER 1
 SQ SEQUENCE 389 AA; 42907 MW; C203401584C560EE CRC64;

Query Match 40.9%; Score 184; DB 6; Length 389;
 Best Local Similarity 100.0%; Pred. No. 2.3e-170;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLILFTFGNALVILAVLTSRLAPQNLFLVSLAADIIVATLIIIPSLANELIGYW 78
 DB 6 ITFLILFTFGNALVILAVLTSRLAPQNLFLVSLAADIIVATLIIIPSLANELIGYW 65
 QY 79 YFRTWCEVYLAADVLFCTSSIVHLCAISIDRYAVASRALEYNSKRTPRRIKCIITLTVWL 138
 DB 66 YFRTWCEVYLAADVLFCTSSIVHLCAISIDRYAVASRALEYNSKRTPRRIKCIITLTVWL 125
 QY 139 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYIILASSIGSFAPCLIMILVLRITLYI 198
 DB 126 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYIILASSIGSFAPCLIMILVLRITLYI 185
 QY 199 AKRS 202
 DB 186 AKRS 189

RESULT 5

Q8MIES PRELIMINARY; PRT; 391 AA.
 ID Q8MIES
 AC Q8MIES; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha 2B adrenergic receptor (Fragment).
 GN ADRA2B.
 OS Hyalomys auillus (short-tailed gymmure).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Hylomyinae; Hylomya.
 NCBI_TaxID=48897;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Madsen O., Williamsen D., Ursing B.M., Arnason U., de Jong W.W.;
 RT "Molecular evolution of the alpha 2B adrenergic receptor";
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ505819; CAD4320.1; -
 DR InterPro; IPR00276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KM Receptor.
 FT NON_TER 1 1
 FT NON_TER 391 391
 SQ SEQUENCE 391 AA; 43133 MW; EB55AAD36B8A9769 CRC64;

Query Match 40.9%; Score 184; DB 6; Length 391;
 Best Local Similarity 100.0%; Pred. No. 2.3e-170;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLILFTFGNALVILAVLTSRLAPQNLFLVSLAADIIVATLIIIPSLANELIGYW 78
 DB 6 ITFLILFTFGNALVILAVLTSRLAPQNLFLVSLAADIIVATLIIIPSLANELIGYW 65
 QY 79 YFRTWCEVYLAADVLFCTSSIVHLCAISIDRYAVASRALEYNSKRTPRRIKCIITLTVWL 138
 DB 66 YFRTWCEVYLAADVLFCTSSIVHLCAISIDRYAVASRALEYNSKRTPRRIKCIITLTVWL 125
 QY 139 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYIILASSIGSFAPCLIMILVLRITLYI 198
 DB 126 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYIILASSIGSFAPCLIMILVLRITLYI 185
 QY 199 AKRS 202
 DB 186 AKRS 189

RESULT 6

Q8MIDO PRELIMINARY; PRT; 399 AA.
 ID Q8MIDO
 AC Q8MIDO; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha 2B adrenergic receptor (Fragment).
 GN ADRA2B.
 OS Manis tetracycla (Long-tailed pangolin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Pholidota; Manidae; Manis.
 NCBI_TaxID=73815;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Madsen O., Williamsen D., Ursing B.M., Arnason U., de Jong W.W.;
 RT "Molecular evolution of the alpha 2B adrenergic receptor";
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ505820; CAD4321.1; -
 DR InterPro; IPR00276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KM Receptor.
 FT NON_TER 1 1
 FT NON_TER 399 399
 SQ SEQUENCE 399 AA; 43888 MW; 910BCAFB10659EDD CRC64;

Query Match 40.9%; Score 184; DB 6; Length 399;
 Best Local Similarity 100.0%; Pred. No. 2.4e-170;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLILFTFGNALVILAVLTSRLAPQNLFLVSLAADIIVATLIIIPSLANELIGYW 78
 DB 6 ITFLILFTFGNALVILAVLTSRLAPQNLFLVSLAADIIVATLIIIPSLANELIGYW 65
 QY 79 YFRTWCEVYLAADVLFCTSSIVHLCAISIDRYAVASRALEYNSKRTPRRIKCIITLTVWL 138
 DB 66 YFRTWCEVYLAADVLFCTSSIVHLCAISIDRYAVASRALEYNSKRTPRRIKCIITLTVWL 125
 QY 139 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYIILASSIGSFAPCLIMILVLRITLYI 198
 DB 126 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYIILASSIGSFAPCLIMILVLRITLYI 185
 QY 199 AKRS 202
 DB 186 AKRS 189

RESULT 7

Q9GL18 PRELIMINARY; PRT; 388 AA.
 ID Q9GL18
 AC Q9GL18; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Alpha adrenergic receptor 2B (Fragment).
 GN AAR2B.
 OS Dicerops bicornis (Black rhinoceros).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Dicerops.
 NCBI_TaxID=9805;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082081; PubMed=11214318;
 RA Madsen O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
 RA Amrine H., Stanhope M., de Jong W., Springer M.;
 RT "Parallel adaptive radiations in two major clades of placental
 mammals";
 RL Nature 409:610-614(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ251184; CAC16666.1; -

DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; Tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1.
DR PROSITE; PS00262; G_PROTEIN_RECPT_F2_1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1 1
FT NON_TER 388 388
SQ SEQUENCE 388 AA; 42546 MW; 14EB08C6F8C5371 CRC64;
Query Match
Best Local Similarity 100.0%; Score 171; DB 6; Length 388;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 LVTLAVTSRSLRAPONTLVSLAADIIVATLIIIPSLANELLGYWFRRTWCEVIAL 91
DB 19 LVTLAVTSRSLRAPONTLVSLAADIIVATLIIIPSLANELLGYWFRRTWCEVIAL 78
QY 92 DVLEFCTSSIVHCAISLDRYWAVSRALRYNSKRTPRRIKCIITLVWLIAAVISLPLIYK 151
DB 79 DVLEFCTSSIVHCAISLDRYWAVSRALRYNSKRTPRRIKCIITLVWLIAAVISLPLIYK 138
QY 152 GDGQPPRGRPOCKINOEWYLLASISGFAPCLIMLVYLRVYIAKRS 202
DB 139 GDGQPPRGRPOCKINOEWYLLASISGFAPCLIMLVYLRVYIAKRS 189
RESULT 8
Q8BK45 PRELIMINARY; PRT; 401 AA.
AC Q8BK45;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN ADRA2B.
OS Tapirus terrestris (Lowland tapir) (Brazilian tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9601;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21608557; PubMed=11743200;
RA Murphy W.J., Elzirik E., O'Brien S.J., Madsen O., Scally M.,
RA Douady C.J., Teeling E., Ryder O.A., Stanhope M.J., de Jong W.W.,
RA Springer M.S.;
RT "Resolution of the early placental mammal radiation using Bayesian
RT phylogenetics";
RL Science 294:2348-2351 (2001).
DR EMBL; AJ315939; CAC87003.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; Tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECPT_F2_1; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 401 401
SQ SEQUENCE 401 AA; 43835 MW; 8D01F4C2548FE86 CRC64;
Query Match
Best Local Similarity 100.0%; Score 159; DB 6; Length 401;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 ITFTLFTFGNALVIAVLTSLRAPONTLVSLAADIIVATLIIIPSLANELLGYW 78
DB 6 ITFTLFTFGNALVIAVLTSLRAPONTLVSLAADIIVATLIIIPSLANELLGYW 65
QY 79 YFRRTWCEVIALDVLEFCTSSIVHCAISLDRYWAVSRALRYNSKRTPRRIKCIITLVWL 138
DB 66 YFRRTWCEVIALDVLEFCTSSIVHCAISLDRYWAVSRALRYNSKRTPRRIKCIITLVWL 125
QY 139 IAAVISLPLIYKDGQPPRGRPOCKINOEWYLLAS 177

DB 126 IAAVISLPLIYKDGQPPRGRPOCKINOEWYLLAS 164
RESULT 9
Q8BK43 PRELIMINARY; PRT; 392 AA.
AC Q8BK43;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN A2AB.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., Stanhope M.,
RA Carzeffis F., de Jong W.W., Douady C.J.,
RT "Rodent phylogeny and a timescale for the evolution of Glires:
RT evidence from an extensive taxon sampling using three nuclear genes";
RL Mol. Biol. Evol. 0:0-0 (2002).
DR EMBL; AJ427255; CAD20293.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; Tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECPT_F2_1; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 392 392
SQ SEQUENCE 392 AA; 42811 MW; 3F75BC33DA390587 CRC64;
Query Match
Best Local Similarity 100.0%; Score 145; DB 11; Length 392;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 AIAAATLFTLFTFGNALVIAVLTSLRAPONTLVSLAADIIVATLIIIPSLANE 73
DB 1 AIAAATLFTLFTFGNALVIAVLTSLRAPONTLVSLAADIIVATLIIIPSLANE 60
QY 74 LLGYWFRRTWCEVIALDVLEFCTSSIVHCAISLDRYWAVSRALRYNSKRTPRRIKCI 133
DB 61 LLGYWFRRTWCEVIALDVLEFCTSSIVHCAISLDRYWAVSRALRYNSKRTPRRIKCI 120
QY 134 LTWLIAAVISLPLIYKDGQPP 158
DB 121 LTWLIAAVISLPLIYKDGQPP 145
RESULT 10
Q8K4Y3 PRELIMINARY; PRT; 392 AA.
AC Q8K4Y3;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN ADRA2B.
OS Sciurus vulgaris (Red squirrel).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OX NCBI_TaxID=55149;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21608557; PubMed=11743200;
RA Murphy W.J., Elzirik E., O'Brien S.J., Madsen O., Scally M.,
RA Douady C.J., Teeling E., Ryder O.A., Stanhope M.J., de Jong W.W.,
RA Springer M.S.;

RT "Resolution of the early placental mammal radiation using Bayesian
phylogenetics.";
RL Science 294:2348-2351(2001).
DR EMBL: AJ315942; CAC87006.1; "-"
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECCEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECCEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 392
SQ SEQUENCE 392 AA; 42713 MW; 24894FD9B2E84D6 CRC64;
Query Match 32.2%; Score 145; DB 11; Length 392;
Best Local Similarity 100.0%; Pred. No. 2.2e-132;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 AIAAATFTLFTFGNALVILAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANE 73
DB 1 AIAAATFTLFTFGNALVILAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANE 60
QY 74 LGGYWRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALEYSKRTPRRIKCI 133
DB 61 LGGYWRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALEYSKRTPRRIKCI 120
QY 134 LTVWLIAAVTSPLIYKGDGQPOP 158
DB 121 LTVWLIAAVTSPLIYKGDGQPOP 145
RESULT 11
08K3R7 PRELIMINARY; PRT; 391 AA.
AC 08K3R7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN A2AB.
OS Aplodontia rufa (Mountain beaver).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Aplodontidae; Aplodontia.
OX NCBI_Taxid=51342;
RN [1]
RP SEQUENCE FROM N.A.
RA Huchon D., Maden O., Sibbald M.J.J.B., Ament K., Stanhope M.,
RA Catzeffis F., de Jong W.W., Douzery E.J.P.;
RT "Rodent phylogeny and a timescale for the evolution of Glites:
RT evidence from an extensive taxon sampling using three nuclear genes";
RL Mol. Biol. Evol. 010-01(2002).
DR EMBL: AJ427256; CAD20294.1; "-"
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECCEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECCEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 391
SQ SEQUENCE 391 AA; 42710 MW; B6244DDF3936DB82 CRC64;
Query Match 31.6%; Score 142; DB 11; Length 391;
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Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 AATFTLFTFGNALVILAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANELLG 60
QY 77 YWYFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALEYSKRTPRRIKCI 136
DB 61 YWYFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALEYSKRTPRRIKCI 120

QY 137 WLIAAVISLPLIYKGDGQPOP 158
DB 121 WLIAAVISLPLIYKGDGQPOP 142
RESULT 12
09GL20 PRELIMINARY; PRT; 389 AA.
AC 09GL20;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Cynopernus sphinx (Indian short-nosed fruit bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
OC Pteropodidae; Cynopterus.
OX NCBI_Taxid=9400;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21082081; Pubmed=11214318;
RA Maden O., Scally M., Donady C., Kao D., Debry R., Adkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer M.;
RT "Parallel adaptive radiations in two major clades of placental
RT mammals";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ251181; CAC16684.1; "-"
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECCEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECCEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
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SQ SEQUENCE 383 AA; 41945 MW; C135809087196294 CRC64;
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Best Local Similarity 100.0%; Pred. No. 1.6e-127;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 6 ITFTLFTFGNALVILAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANELLGYW 65
QY 79 YFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALEYSKRTPRRIKCI 138
DB 66 YFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALEYSKRTPRRIKCI 125
QY 139 IAAVVISLPLIYKGDGQPOP 158
DB 126 IAAVVISLPLIYKGDGQPOP 145
RESULT 13
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AC 09GL07;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCBI_Taxid=9720;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=21082081; PubMed=11214318;
RA Maden O., Scally M., Douady C., Kao D., DeBry R., Adkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer M.,
RT "Parallel adaptive radiations in two major clades of placental
RL mammalia."
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ251176; CAC16696.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 389
SQ SEQUENCE 389 AA; 42278 MW; E42F17873FE47FF CRC64;

Query Match
Best Local Similarity 31.1%; Score 140; DB 6; Length 389;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLILFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIPPSLANELLGYW 78
DB 6 ITFLILFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIPPSLANELLGYW 65
QY 79 YFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYWAVSRALVNSKRTPRRIKCIITLTVWL 138
DB 66 YFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYWAVSRALVNSKRTPRRIKCIITLTVWL 125
QY 139 IAAVISLPPILYKDGQGP 158
DB 126 IAAVISLPPILYKDGQGP 145

RESULT 14
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ID O8K1W8 PRELIMINARY; PRT; 389 AA.
AC O8K1W8;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN A2AB.
OS Batyergus suillus (Cape dune mole-rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Batyergidae;
OC Batyergus.
NCBI_TaxID=10172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5234;
RA Huchon D., Maden O., Sibbald M.J.J.B., Ament K., Stanhope M.,
RA Catzeffis F., de Jong W.W., Douzery E.J.P.;
RT "Rodent phylogeny and a timescale for the evolution of Glires:
RT evidence from an extensive taxon sampling using three nuclear genes.";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL: AJ427252; CAD20290.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 389
SQ SEQUENCE 389 AA; 42728 MW; F731C298F5FD81BC CRC64;

Query Match
Best Local Similarity 31.1%; Score 140; DB 11; Length 389;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 19 ITFLILFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIPPSLANELLGYW 78
DB 6 ITFLILFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIPPSLANELLGYW 65
QY 79 YFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYWAVSRALVNSKRTPRRIKCIITLTVWL 138
DB 66 YFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYWAVSRALVNSKRTPRRIKCIITLTVWL 125
QY 139 IAAVISLPPILYKDGQGP 158
DB 126 IAAVISLPPILYKDGQGP 145

RESULT 15
O8CG78
ID O8CG78 PRELIMINARY; PRT; 389 AA.
AC O8CG78;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN A2AB.
OS Chinchilla lanigera.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Chinchillidae;
OC Chinchilla.
NCBI_TaxID=34839;
RN [1]
RP SEQUENCE FROM N.A.
RC Huchon D., Maden O., Sibbald M.J.J.B., Ament K., Stanhope M.,
RA Catzeffis F., de Jong W.W., Douzery E.J.P.;
RT "Rodent phylogeny and a timescale for the evolution of Glires:
RT evidence from an extensive taxon sampling using three nuclear genes.";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL: AJ427271; CAD20309.1;
KW Receptor.
FT NON_TER 1
FT NON_TER 389
SQ SEQUENCE 389 AA; 42657 MW; 826AB4A7F4F7E901 CRC64;

Query Match
Best Local Similarity 31.1%; Score 140; DB 11; Length 389;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Job time : 34.1104 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:50:45 / Search time 38.1271 Seconds
(without alignments)
1873.391 Million cell updates/sec

Title: US-09-692-077D-7

Perfect score: 2378
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2378	100.0	450	22	AAW52117 Human alpha-2BAR t
2	2378	100.0	450	22	AAE00990 Human alpha2B-adre
3	2378	100.0	450	23	AAE26634 Human alpha-2B-adr
4	2370	99.7	450	24	ABP81780 Human alpha-2B-adr
5	2351.5	98.9	447	22	AAW52118 Human alpha-2BAR t
6	2351.5	98.9	447	22	AAE00989 Human alpha2B-adre
7	2351.5	98.9	447	23	AAE26633 Human alpha-2B-adr
8	2329	97.9	487	12	AAAI4149 Human alpha 2 beta
9	2329	97.9	487	18	AAW11804 Human alpha-2b adr

10	1624.5	68.3	330	15	AA48699	G-protein coupled
11	1624.5	68.3	330	17	AAW02671	G-protein coupled
12	1126.5	47.4	450	22	AAW52123	Human alpha-2BAR v
13	1124.5	47.3	450	22	AAW52122	Human alpha-2BAR p
14	1117.5	47.0	450	24	ABP81779	Human alpha 2a-adr
15	1079.5	45.4	457	22	AAW52126	Human alpha-2CAR v
16	1078.5	45.4	461	22	AAW52124	Human alpha-2CAR p
17	1078.5	45.4	461	24	ABP81781	Human alpha 2C-adr
18	1077	45.3	458	15	AA484834	Human derived adre
19	1027.5	43.2	334	15	AA4848701	G-protein coupled
20	1027.5	43.2	334	17	AAW02673	G-protein coupled
21	1001.5	42.1	330	15	AA48700	G-protein coupled
22	1001.5	42.1	330	17	AAW02672	G-protein coupled
23	990.5	41.7	324	10	AA490552	Hamster beta-2 -ad
24	985	41.4	330	15	AA484838	G-protein coupled
25	985	41.4	330	17	AAW02670	G-protein coupled
26	956	40.2	307	24	ABG73558	Human alpha2-adren
27	954	40.1	307	22	AAU08334	Human alpha 2 adre
28	651	27.4	601	13	AA481931	D.melanogaster oct
29	651	27.4	601	22	ABW63318	Drosophila melanog
30	651	27.4	601	23	AA480701	D. melanogaster oc
31	651	27.4	601	23	AA4817036	Drosophila melanog
32	645.5	27.1	379	18	AAW3185	Corn barnacle G-pr
33	598	25.1	476	18	AAW24089	Balanus amphitrite
34	594.5	25.0	467	24	ABP81811	Human dopamine rec
35	592	24.9	415	24	ABG73546	Rat dopamine D2 re
36	589	24.8	415	11	AA480539	Rat D2 dopamine re
37	589	24.8	415	20	AAV01598	Rat D2 dopamine re
38	588.5	24.7	467	15	AA484850	Sequence encoded b
39	588.5	24.7	467	15	AA484850	Recombinant human
40	588	24.7	415	17	AAW09388	Mouse dopamine D2
41	587.5	24.7	515	15	AA480995	Human/rat alpha-1B
42	587.5	24.7	520	15	AA480041	Human/rat hybrid a
43	586.5	24.7	520	15	AA482831	Sequence of human
44	585.5	24.6	515	22	AAU05408	Human adrenoceptor
45	585.5	24.6	517	21	AAV57169	Sequence of HnAlph

ALIGNMENTS

RESULT 1	
AAW52117	standard; Protein: 450 AA.
ID	AAW52117
XX	AAW52117;
AC	18-FEB-2002 (first entry)
XX	
XX	Human alpha-2BAR third intracellular loop.
XX	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2BAR.
XX	
OS	Homo sapiens.
XX	
XX	
FT	Key
FT	Location/Qualifiers
FT	/note= "featured in figure 2"
FT	170..193
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FT	301..303
FT	/label= polymorphic_site
FT	/note= "Polymorphic site absent in the variant protein (AAW52118)"
FT	Region
FT	310..312
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PN	W0200179561-A2.

XX 25-OCT-2001.
 XX 17-APR-2001, 2001WO-US12575.
 PF 17-APR-2000, 2000US-0531744.
 PR 10-APR-2000, 2000US-0636259.
 PR 19-OCT-2000, 2000US-0692077.
 XX (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX Liggett SB, Small KM;
 PI WPI: 2001-611728/70.
 DR N-PSDB; AAI99905.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 20, Page 146-147, 163pp; English.
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 or (IIIV)
 CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcgggcg) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlates to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfazine, idazoxan, tolazoline, phentolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC level(s)). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR protein, the sequence includes 3 amino acid
 CC polymorphic site at residues 301-303 (EEF), absent in the alpha-2BAR
 CC variant protein (AAM52118).
 XX
 SQ Sequence 450 AA;
 Query Match 100.0%; Score 2378; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2,2e-194;
 Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDHOPYSVQATTAIAAATFTLITFTFGNALVTLAVTSRSRAQONFLVLSAAADTL 60
 DB 1 MDHOPYSVQATTAIAAATFTLITFTFGNALVTLAVTSRSRAQONFLVLSAAADTL 60
 QY 61 VATTIIPSLANELLGYVYFRRRTWCERYTALDVLCFTSSIVHLCAISLDRYAAVRALEY 120
 DB 61 VATTIIPSLANELLGYVYFRRRTWCERYTALDVLCFTSSIVHLCAISLDRYAAVRALEY 120
 QY 121 NSKTPPRRIKTIITLWVLAIAVISLPLIYKGGQPGPGRPOCKLQNGEAWYIIASSIGS 180
 DB 121 NSKTPPRRIKTIITLWVLAIAVISLPLIYKGGQPGPGRPOCKLQNGEAWYIIASSIGS 180
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 DB 181 FFAPCLIMILVYRIYIAKRSNRBRPAKGGPQGGESKOPRPHGALAAKIPALASV 240
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DB 241 ASAREVNGSKSTGEKEGETPEDTGTALPSSMAALPNSGQGGKEGVCASPEDAEERE 300
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 DB 301 EEEEEECEPQAVVSPASACSPPLQPGQSRVLTLRQVLLGSGVAILGGQWRRR 360
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 DB 361 AQLTEKRTFTVLAIVIGVFLCWPPPPFYSLGALCPKXCKVPHGLFQFFWIGYCNSS 420
 QY 421 LNPVYITTFNODFRAFRRLICRPWTOTAW 450
 DB 421 LNPVYITTFNODFRAFRRLICRPWTOTAW 450
 RESULT 2
 AAE00990
 ID AAE00990 standard; Protein: 450 AA.
 AC AAE00990;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human alpha2B-adrenoceptor (alpha2B-AR) protein.
 XX
 KW Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Prinzmetal's variant.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 298..309
 FT /note="Glutamic acid repeat"
 PN MO200129082-A1.
 XX
 PD 26-APR-2001.
 XX
 PF 20-OCT-2000; 2000WO-F100913.
 XX
 PR 22-OCT-1999; 99US-0422985.
 XX
 PA (JIVA-) JUVANTIA PHARMA LTD OY.
 PI Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulou M, Pesonen U;
 PI Scheinin M, Salonen JT, Tuominen T, Lakka TA, Nyssönen K;
 PI Salonen R, Kaunonen J, Valkonen V;
 DR WPI: 2001-300318/31.
 DR N-PSDB; AAD04762.
 XX
 PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -
 XX
 PS Disclosure; Page 29-31, 37pp; English.
 XX
 CC The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) protein.
 CC alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of
 CC 12 glutamates, in an acidic stretch of 18 amino acids (amino acids
 CC 294-311), located in the third intracellular loop of the receptor
 CC polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR
 CC mediate many of the physiological effects of the catecholamines,
 CC norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is
 CC useful for treating a mammal suffering from vascular contraction of
 CC coronary arteries and a disease involving vascular contraction of
 CC coronary arteries which is clinically expressed as coronary heart disease
 CC (CHD), unstable chronic angina pectoris which is clinically expressed as

CC Primazetel's variant form or acute myocardial infarction (AMI).
CC Alpha2B-AR gene is used in gene therapy.
XX
SQ Sequence 450 AA;

Query Match 100.0%; Score 2378; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.2e-194;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHDPYSVQATATAIAAIFTLFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIL 60
DB 1 MDHDPYSVQATATAIAAIFTLFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIL 60
QY 61 VATLIIFSLANELGTYWFRRTWCEVYALDVLFCSTSYVHLCAISLDRYMAVSRALEY 120
DB 61 VATLIIFSLANELGTYWFRRTWCEVYALDVLFCSTSYVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKIIITWMLIAAVISLPLIYKDGQPPRGRPOCKLQEAAYIIASSIGS 180
DB 121 NSKRTPRRIKIIITWMLIAAVISLPLIYKDGQPPRGRPOCKLQEAAYIIASSIGS 180
QY 181 FPAACLMILVYLRITVLIARSNRGRPAKGPQGSKOPRPHGALASAKI.PALASV 240
DB 181 FPAACLMILVYLRITVLIARSNRGRPAKGPQGSKOPRPHGALASAKI.PALASV 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWALPNSGQGEVCGASPEDEABEE 300
DB 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWALPNSGQGEVCGASPEDEABEE 300
QY 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSVTLATLRQVLLGRGVGAIIGQWRRR 360
DB 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSVTLATLRQVLLGRGVGAIIGQWRRR 360
QY 361 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGAIQPKCKVPHGLFQFFFWIIGYCNSS 420
DB 361 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGAIQPKCKVPHGLFQFFFWIIGYCNSS 420
QY 421 LNPVIYTIIFNODFRARFRILCRPMTOTAW 450
DB 421 LNPVIYTIIFNODFRARFRILCRPMTOTAW 450

RESULT 3

AAE26634
ID AAE26634 standard; Protein: 450 AA.

AC AAE26634;

DT 13-DEC-2002 (first entry)

XX Human alpha-2B-adrenoceptor protein.

XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;

KM hypertension; hypotensive.

OS Homo sapiens.

XX WO200266617-A1.

PD 29-AUG-2002.

PF 13-FEB-2002; 2002WO-FI00113.

XX 20-FEB-2001; 2001FI-0000323.

PA (JURI-) JURILAB LTD OY.

PI Salonen J;

XX WPI; 2002-667063/71.

DR N-PSDB; AAD26634.

PT Detecting a risk of hypertension and targeting treatment in a subject

PT by determining the pattern of alleles encoding a variant
PT alpha-2-adrenoceptor
XX
PS Disclosure; Page 30-31; 35pp; English.

XX The invention relates to a method for detecting a risk of hypertension
CC by determining the pattern of alleles encoding a variant alpha-2B-
CC adrenoceptor (AR) protein. The methods and compositions of the invention
CC are useful for detecting risks and targeting treatment for hypertension.
CC The kit is also useful for selecting for clinical drug trials testing
CC the antihypertensive effect of compounds. The present sequence is human
CC alpha-2B-adrenoceptor protein.

SQ Sequence 450 AA;

Query Match 100.0%; Score 2378; DB 23; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.2e-194;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHDPYSVQATATAIAAIFTLFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIL 60
DB 1 MDHDPYSVQATATAIAAIFTLFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIL 60
QY 61 VATLIIFSLANELGTYWFRRTWCEVYALDVLFCSTSYVHLCAISLDRYMAVSRALEY 120
DB 61 VATLIIFSLANELGTYWFRRTWCEVYALDVLFCSTSYVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKIIITWMLIAAVISLPLIYKDGQPPRGRPOCKLQEAAYIIASSIGS 180
DB 121 NSKRTPRRIKIIITWMLIAAVISLPLIYKDGQPPRGRPOCKLQEAAYIIASSIGS 180
QY 181 FPAACLMILVYLRITVLIARSNRGRPAKGPQGSKOPRPHGALASAKI.PALASV 240
DB 181 FPAACLMILVYLRITVLIARSNRGRPAKGPQGSKOPRPHGALASAKI.PALASV 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWALPNSGQGEVCGASPEDEABEE 300
DB 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWALPNSGQGEVCGASPEDEABEE 300
QY 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSVTLATLRQVLLGRGVGAIIGQWRRR 360
DB 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSVTLATLRQVLLGRGVGAIIGQWRRR 360
QY 361 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGAIQPKCKVPHGLFQFFFWIIGYCNSS 420
DB 361 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGAIQPKCKVPHGLFQFFFWIIGYCNSS 420
QY 421 LNPVIYTIIFNODFRARFRILCRPMTOTAW 450
DB 421 LNPVIYTIIFNODFRARFRILCRPMTOTAW 450

RESULT 4

ABP81780
ID ABP81780 standard; Protein: 450 AA.

AC ABP81780;

DT 04-MAR-2003 (first entry)

XX Human alpha 2b-adrenoceptor protein SEQ ID NO:42.

XX G protein-coupled receptor; GPCR; anti-genic peptide; gene therapy;

KM G protein-coupled receptor; modulator; antibody; immune-related disease;

KM growth-related disease; cell regeneration-related disease; AIDS; cancer;

KM immunological-related cell proliferative disease; autoimmune disease;

KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KM osteoporosis; cardiovascular; inflammation; Crohn's disease; diabetes;

KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KM ulcer.

XX Homo sapiens.
 OS
 XX WO200261087-A2.
 PN
 XX 08-AUG-2002.
 PD
 XX 19-DEC-2001; 2001WO-US50107.
 PF
 XX 19-DEC-2000; 2000US-257144P.
 PR
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA
 XX Burner GC, Roush CL, Brown JP;
 PI
 XX WPI; 2003-046718/04.
 DR
 XX N-PSDB; AB242624.
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases
 XX
 XX Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising:
 (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 acids. Also described: (1) an assay for the detection of a particular
 G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 and (2) an isolated antibody having high specificity and high affinity
 or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related diseases, cell
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 450 AA;

Query Match 99.7%; Score 2370; DB 24; Length 450;
 Best Local Similarity 99.6%; Pred. NO. 1e-193;
 Matches 448; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDHODPYSVQATAIAAITEFLITFGNALVILAVTSRSIRAPONTFLVSLAADI 60
 DB 1 MDHODPYSVQATAIAAITEFLITFGNALVILAVTSRSIRAPONTFLVSLAADI 60
 QY 61 VATLIIPSLANELLGWYFRRTWCEVYALADVICTSSIVHLCAISLDRYNAVSRLEY 120
 DB 61 VATLIIPSLANELLGWYFRRTWCEVYALADVICTSSIVHLCAISLDRYNAVSRLEY 120
 QY 121 NSKTPPRIKCIITLWVLAIVSLPLIYKSGOGPOPRRPOCKKNQENAWYTLASIS 180
 DB 121 NSKTPPRIKCIITLWVLAIVSLPLIYKSGOGPOPRRPOCKKNQENAWYTLASIS 180
 QY 181 FPAACLMILVYRIYIYIAKSNRGRGAFSGQESKQPRPDHGAALASAKLPAALASY 240
 DB 181 FPAACLMILVYRIYIYIAKSNRGRGAFSGQESKQPRPDHGAALASAKLPAALASY 240

QY 241 ASAREVNGHSKSTGKEKGETPEDTGTALPSPMAIPNSGQCKEGYCGASPEDAE 300
 DB 241 ASAREVNGHSKSTGKEKGETPEDTGTALPSPMAIPNSGQCKEGYCGASPEDAE 300
 QY 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRVLTATLRGOVLGRGVAGIGOMWRR 360
 DB 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRVLTATLRGOVLGRGVAGIGOMWRR 360
 QY 361 AQLTRKRFETFLAVVIGVFLCMFPFFESYSGAICPKKCKVPHGLPOFFWIGYCNSS 420
 DB 361 AHTREKRFETFLAVVIGVFLCMFPFFESYSGAICPKKCKVPHGLPOFFWIGYCNSS 420
 QY 421 LNPVITYTFNODFRARFRILCRPMTOTAW 450
 DB 421 LNPVITYTFNODFRARFRILCRPMTOTAW 450

RESULT 5

AM52118
 ID AM52118 standard; Protein; 447 AA.

AC AM52118;

DT 18-FEB-2002 (first entry)

XX Human alpha-2BAR third intracellular loop variant.

XX Human, genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 XX phosphorylation; inositol phosphate; alpha-2BAR.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Domain 170..193
 /label= transmembrane_domain

FT Region 307..309
 /label= polymorphic_site

FT Domain 370..393
 /label= transmembrane_domain

XX WO200179561-A2.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-US12575.

XX 17-APR-2000; 2000US-0551744.

XX 10-AUG-2000; 2000US-0636259.

XX 19-OCT-2000; 2000US-0692077.

XX (LIGG/) LIGGETT S B.

XX (SMAL/) SMALL K M.

XX Liggett SB, Small KM;

XX WPI; 2001-611728/70.

XX N-PSDB; AA199906.

XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -

XX Claim 20; Page 147-149; 163pp; English.

XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (III)

CC or a site comprising (A) (9999CG9999CG) or (B) (9999CG9999CG) at
 CC positions 961-972 of (iii). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR variant protein, the sequence is deleted for the 3
 CC amino acid polymorphic site at residues 301-303 (EEE) of the wildtype
 CC protein (AA052117).

SO Sequence 447 AA;

Query Match 98.9%; Score 2351.5; DB 22; Length 447;
 Best Local Similarity 99.3%; Pred. No. 3.9e-192;
 Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MDHDDPSVQATATAIAAIFLLIFFTFGNALVILAVITSRSLAPQNLFLVSLAADIL 60
 DB 1 MDHDDPSVQATATAIAAIFLLIFFTFGNALVILAVITSRSLAPQNLFLVSLAADIL 60
 QY 61 VATLIIPFSLANELLGWYFRRRTCEVYALADVLFCTTSIVHLCAISLDRYMAVSRALEY 120
 DB 61 VATLIIPFSLANELLGWYFRRRTCEVYALADVLFCTTSIVHLCAISLDRYMAVSRALEY 120
 QY 121 NSKRTPRRIKIIITWVLIAAVISLPLIYKDGQPPGRGPOCKLQNEAWYIIASSIGS 180
 DB 121 NSKRTPRRIKIIITWVLIAAVISLPLIYKDGQPPGRGPOCKLQNEAWYIIASSIGS 180
 QY 181 PFACCLIMILVYLRILYIYIAKSNRGRPRAGKGPQGGESKQRPDHGALASAKIIPALASV 240
 DB 181 PFACCLIMILVYLRILYIYIAKSNRGRPRAGKGPQGGESKQRPDHGALASAKIIPALASV 240
 QY 241 ASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEABEE 300
 DB 241 ASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEABEE 300
 QY 301 EEEEEECEPQAVPVSPASACSPPLQPGQSRVLTATLRGQVILGRGVALIGQWMMRR 360
 DB 301 EEEEEECEPQAVPVSPASACSPPLQPGQSRVLTATLRGQVILGRGVALIGQWMMRR 360
 QY 361 AQLTRERKFTVLAIVGVFLCWFPPFFSYSLGALCKKCKVPHGLFQFFFWIGYCNS 420
 DB 361 AQLTRERKFTVLAIVGVFLCWFPPFFSYSLGALCKKCKVPHGLFQFFFWIGYCNS 420
 QY 421 LNPVIYITIFNODFRAPRILCRPMTOTAM 450
 DB 421 LNPVIYITIFNODFRAPRILCRPMTOTAM 450
 QY 418 LNPVIYITIFNODFRAPRILCRPMTOTAM 447
 DB 418 LNPVIYITIFNODFRAPRILCRPMTOTAM 447

RESULT 6
 AAE00989 ID AAE00989 standard; Protein: 447 AA.

XX AC AAE00989,
 XX DT 04-JUL-2001 (first entry)

DE Human alpha2B-adrenoceptor (alpha2B-AR) variant protein.

XX Human, cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;

KW acute myocardial infarction; AMI; Prinzmetal's variant.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 298..306
 FT /note="Glutamic acid repeat"

PM W0200129082-AL.

PD 26-APR-2001.

XX 20-OCT-2000; 2000WO-F100913.

XX 22-OCT-1999; 99US-0422985.

XX (JUVN-) JUVANTIA PHARMA LTD OY.

PI Snajir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
 PI Schein M, Salonen JT, Tuomainen T, Lakka TA, Myllysoenen K;
 PI Salonen R, Kaunonen J, Valkonen V;

XX WPI; 2001-300318/31.

DR N-PSDB; AAD04761.

PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -

PS Claim 8; Page 26-27; 37pp; English.

XX The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) variant
 CC protein. Alpha2B-AR has a glutamic acid repeat element (amino acids
 CC 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino
 CC acids 294-311), located in the third intracellular loop of the receptor
 CC polypeptide. The variant is obtained by deletion of three glutamates from
 CC the glu repeat (amino acids 307-309). Alpha2B-AR gene is located on
 CC chromosome 2. Alpha2-AR mediates many of the physiological effects of the
 CC catecholamines, norepinephrine and epinephrine. An antagonist of
 CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
 CC vascular contraction of coronary arteries and a disease involving
 CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
 CC clinically expressed as Prinzmetal's variant form or acute myocardial
 CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.

SO Sequence 447 AA;

Query Match 98.9%; Score 2351.5; DB 22; Length 447;
 Best Local Similarity 99.3%; Pred. No. 3.9e-192;
 Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MDHDDPSVQATATAIAAIFLLIFFTFGNALVILAVITSRSLAPQNLFLVSLAADIL 60
 DB 1 MDHDDPSVQATATAIAAIFLLIFFTFGNALVILAVITSRSLAPQNLFLVSLAADIL 60
 QY 61 VATLIIPFSLANELLGWYFRRRTCEVYALADVLFCTTSIVHLCAISLDRYMAVSRALEY 120
 DB 61 VATLIIPFSLANELLGWYFRRRTCEVYALADVLFCTTSIVHLCAISLDRYMAVSRALEY 120
 QY 121 NSKRTPRRIKIIITWVLIAAVISLPLIYKDGQPPGRGPOCKLQNEAWYIIASSIGS 180
 DB 121 NSKRTPRRIKIIITWVLIAAVISLPLIYKDGQPPGRGPOCKLQNEAWYIIASSIGS 180
 QY 181 PFACCLIMILVYLRILYIYIAKSNRGRPRAGKGPQGGESKQRPDHGALASAKIIPALASV 240
 DB 181 PFACCLIMILVYLRILYIYIAKSNRGRPRAGKGPQGGESKQRPDHGALASAKIIPALASV 240
 QY 241 ASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEABEE 300
 DB 241 ASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEABEE 300
 QY 241 ASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEABEE 297
 DB 241 ASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEABEE 297

QY 301 EEEEEEECEPQAVPVPSPASCSPTLOPQGSRLVATLRGVTLGRGVGALIGQWRRR 360
 DB 298 EEEEEEECEPQAVPVPSPASCSPTLOPQGSRLVATLRGVTLGRGVGALIGQWRRR 357
 QY 361 AQLTRKRTFTFLAVVIGVFLCMFPFFFSYSLGALCPKCKVPHGLFQFFFWIGYCNSS 420
 DB 358 AQLTRKRTFTFLAVVIGVFLCMFPFFFSYSLGALCPKCKVPHGLFQFFFWIGYCNSS 417
 QY 421 LNPVITYTFNQDFRRAFRRLICRPWTQTAM 450
 DB 418 LNPVITYTFNQDFRRAFRRLICRPWTQTAM 447

RESULT 7

AAE26633
 ID AAE26633 standard; Protein; 447 AA.
 AC AAE26633;
 DT 13-DEC-2002 (first entry)

DE Human alpha-2B-adrenoceptor variant.
 KM Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive.
 KW hypertension; hypotensive; variant.
 XX Homo sapiens.
 OS Synthetic.
 PN WO200266617-A1.
 XX 29-AUG-2002.
 PD 13-FEB-2002; 2002WO-F100113.
 PF 20-FEB-2001; 2001FI-0000323.
 PR (JURI-) JURILAB LTD OY.
 PA Salomon J;
 PI Salomon J;
 XX MPI; 2002-667063/71.
 DR N-PSDB; AAD44388.
 XX

PT Detecting a risk of hypertension and targeting treatment in a subject
 PT by determining the pattern of alleles encoding a variant
 PT alpha-2-adrenoceptor

PS Disclosure; Page 26-27; 35pp; English.

CC The invention relates to a method for detecting a risk of hypertension
 CC by determining the pattern of alleles encoding a variant alpha-2B-
 CC adrenoceptor (AR) protein. The methods and compositions of the invention
 CC are useful for detecting risks and targeting treatments for hypertension.
 CC The kit is also useful for selecting for clinical drug trials testing
 CC the antihypertensive effect of compounds. The present sequence is human
 CC alpha-2B-adrenoceptor variant.
 XX

SO Sequence 447 AA;

Query Match 98.9%; Score 2351.5; DB 23; Length 447;
 Best Local Similarity 99.3%; Pred. No. 3.9e-192;
 Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MDHODPYSVQATTAIAAATFTLFTFGNALVTLAVTSRSRAPONTFLVSLAADI 60
 DB 1 MDHODPYSVQATTAIAAATFTLFTFGNALVTLAVTSRSRAPONTFLVSLAADI 60
 QY 61 VATLIIFSLANELLGYWFRFTWCEVYALDVLFCFTSSVHLCAISLDYWAASRALEY 120
 DB 61 VATLIIFSLANELLGYWFRFTWCEVYALDVLFCFTSSVHLCAISLDYWAASRALEY 120
 QY 121 NSKTRPRRIKCIILTWLAAVSLDPLIYKDGQPGPRGPOCKLNGEAWTILASSIGS 180

DB 121 NSKTRPRRIKCIILTWLAAVSLDPLIYKDGQPGPRGPOCKLNGEAWTILASSIGS 180
 QY 181 FFAPLILMILYLYLRIYLIANKSNRRGPRAKGPGQGSKOPRDPHGALASAKLPALASY 240
 DB 181 FFAPLILMILYLYLRIYLIANKSNRRGPRAKGPGQGSKOPRDPHGALASAKLPALASY 240
 QY 241 ASAREVNHGSKSTGEKEGETPEDTGTALPSPMAALPNSGQCKGVCASFEDEAEE 300
 DB 241 ASAREVNHGSKSTGEKEGETPEDTGTALPSPMAALPNSGQCKGVCASFEDEAEE 297
 QY 301 EEEEEEECEPQAVPVPSPASCSPTLOPQGSRLVATLRGVTLGRGVGALIGQWRRR 360
 DB 298 EEEEEEECEPQAVPVPSPASCSPTLOPQGSRLVATLRGVTLGRGVGALIGQWRRR 357
 QY 361 AQLTRKRTFTFLAVVIGVFLCMFPFFFSYSLGALCPKCKVPHGLFQFFFWIGYCNSS 420
 DB 358 AQLTRKRTFTFLAVVIGVFLCMFPFFFSYSLGALCPKCKVPHGLFQFFFWIGYCNSS 417
 QY 421 LNPVITYTFNQDFRRAFRRLICRPWTQTAM 450
 DB 418 LNPVITYTFNQDFRRAFRRLICRPWTQTAM 447

RESULT 8

AAE14149
 ID AAE14149 standard; Protein; 487 AA.
 AC AAE14149;
 DT 06-JAN-1992 (first entry)

DE Human alpha 2 beta adrenergic receptor.
 KM Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta.
 KW Homo sapiens.
 OS US053337-A.
 PN 01-OCT-1991.
 PD 30-OCT-1989; 89US-0428856.
 PF 30-OCT-1989; 89US-0428856.
 PR 30-OCT-1989; 89US-0428856.
 PA (NEUR-) NEUROGENETIC CORP.
 XX
 PI Weinschenk RL, Hartig PR;
 XX
 DR MPI; 1991-310087/42.
 DR N-PSDB; AAQ14151.
 XX

PT Isolated DNA encoding human adrenergic receptor - for detecting
 PT nucleic acids encoding alpha, 2-beta adrenergic receptor, for
 PT screening drugs.
 PT
 PS Disclosure; Fig 2; 15pp; English.

CC Clone NGC-alpha2beta was isolated from a human spleen genomic
 CC library by screening with a fragment of the human 5-HT1A receptor
 CC gene. The gene was used to express recombinant receptor protein
 CC which can be used to produce antibodies for inhibition of receptor
 CC function.
 XX

SO Sequence 487 AA;

Query Match 97.9%; Score 2329; DB 12; Length 487;
 Best Local Similarity 98.2%; Pred. No. 3.6e-190;
 Matches 442; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDHODPYSVQATTAIAAATFTLFTFGNALVTLAVTSRSRAPONTFLVSLAADI 60

Db 38 MDHDPYSVQATATAAATFLIFTFGNALVILAVITSRSWAPQNLFLVSLAADIL 97
 Qy 61 VATLIIPPSLANELLGYWYFRRTWCEVYLAIDVLECTSSIVHLCALISDRYMAVSRALEY 120
 Db 98 VATLIIPCSLANELLGYWYFRRTWQVYLAIDVLECTSSIVHLCALISDRYMAVSRALEY 157
 Qy 121 NSKTRPRRIKCIILTWMLIAAVISLPLIYKGDGPGRGRPOCKLNOEAMYTIIASSIGS 180
 Db 158 NSKTRPRRIKCIILTWMLIAAVISLPLIYKGDGPGRGRPOCKLNOEAMYTIIASSIGS 217
 Qy 181 FFAPCLIMILVYLRITVLIKRSNRGPRKAGPGQGESKOPRPHGALASAKLPALASV 240
 Db 218 FFAPCLIMILVYLRITVLIKRSNRGPRKAGPGQGESKOPRPHGALASAKLPALASV 277
 Qy 241 ASAREVNGSHSKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEAEE 300
 Db 278 ASAREVNGSHSKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEAEE 337
 Qy 301 EEEEEECEPQAVPVSPASACSPPLQPGGSRYLATLRGQVLLGRGVGAIGQWMRRR 360
 Db 338 EEEEEECEPQAVPVSPASACSPPLQPGGSRYLATLRGQVLLGRGVGAIGQWMRRR 397
 Qy 361 AQLTRERKFTFVLAVVIGVFLCMFPFFSYSLGALCPKHCKVPHGLFOFFFWIGYCNS 420
 Db 398 AHTREKRFITVLAVVIGVFLCMFPFFSYSLGALCPKHCKVPHGLFOFFFWIGYCNS 457
 Qy 421 LNPVIYITIFNODFFRFRRLICRPMWTQTA 450
 Db 458 LNPVIYITIFNODFFRFRRLICRPMWTQTA 487

RESULT 9
 AAM1804
 ID AAM1804 standard; Protein; 487 AA.

AC AAM1804;
 XX 25-MAR-2003 (updated)
 DT 06-MAY-1997 (first entry)
 XX
 DE Human alpha-2b adrenergic receptor.
 XX
 KW alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
 KM epinephrine; signal transduction; neurotransmitter; ligand.
 OS Homo sapiens.
 XX
 PN US5595880-A.
 XX 21-JAN-1997.
 PD
 XX 22-OCT-1992; 92US-0965040.
 PF
 XX 30-OCT-1989; 89US-0428856.
 PR 30-MAY-1991; 91US-0707604.
 PR 22-OCT-1992; 92US-0965040.
 XX
 PA (SYNA-) SYNAPTIC PHARM CORP.
 XX
 PI Hartig PR, Weinschenk RL;
 XX
 DR WPI; 1997-107576/10.
 DR N-PSDB; AAT59499.
 XX
 PT Assay for alpha-2b adrenergic receptor ligands - using membranes of
 PT cells expressing recombinant receptor
 XX
 PS Disclosure; Fig 2A-E; 16pp; English.
 PS
 CC Human alpha-2b adrenergic receptor (AAM1804) is a member of the
 CC rhodopsin-like signal transducer family. Its amino acid sequence
 CC was deduced from a genomic DNA clone (AAT59499) obt'd. from a human
 CC spleen DNA library. Vectors have been adapted to allow prodn. of

CC alpha-2b adrenoceptor in bacterial, yeast or mammalian cells;
 CC transfected Ltk- cells, designated L-NGC-alpha-2b, are deposited as
 CC ATCC CRL 10275. Membranes of transfected mammalian cells can used
 CC in novel methods to identify drugs which specifically interact
 CC with, and bind to, the alpha-2b adrenergic receptor.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 487 AA;

Query Match 97.9%; Score 2329; DB 18; Length 487;
 Best Local Similarity 98.2%; Pred. No. 3.6e-190;
 Matches 442; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MDHDPYSVQATATAAATFLIFTFGNALVILAVITSRSLAPQNLFLVSLAADIL 60
 Db 38 MDHDPYSVQATATAAATFLIFTFGNALVILAVITSRSWAPQNLFLVSLAADIL 97
 Qy 61 VATLIIPPSLANELLGYWYFRRTWCEVYLAIDVLECTSSIVHLCALISDRYMAVSRALEY 120
 Db 98 VATLIIPCSLANELLGYWYFRRTWQVYLAIDVLECTSSIVHLCALISDRYMAVSRALEY 157
 Qy 121 NSKTRPRRIKCIILTWMLIAAVISLPLIYKGDGPGRGRPOCKLNOEAMYTIIASSIGS 180
 Db 158 NSKTRPRRIKCIILTWMLIAAVISLPLIYKGDGPGRGRPOCKLNOEAMYTIIASSIGS 217
 Qy 181 FFAPCLIMILVYLRITVLIKRSNRGPRKAGPGQGESKOPRPHGALASAKLPALASV 240
 Db 218 FFAPCLIMILVYLRITVLIKRSNRGPRKAGPGQGESKOPRPHGALASAKLPALASV 277
 Qy 241 ASAREVNGSHSKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEAEE 300
 Db 278 ASAREVNGSHSKSTGEKEGETPEDTGTALPPSWAALPNSGQGEVCGASPEDEAEE 337
 Qy 301 EEEEEECEPQAVPVSPASACSPPLQPGGSRYLATLRGQVLLGRGVGAIGQWMRRR 360
 Db 338 EEEEEECEPQAVPVSPASACSPPLQPGGSRYLATLRGQVLLGRGVGAIGQWMRRR 397
 Qy 361 AQLTRERKFTFVLAVVIGVFLCMFPFFSYSLGALCPKHCKVPHGLFOFFFWIGYCNS 420
 Db 398 AHTREKRFITVLAVVIGVFLCMFPFFSYSLGALCPKHCKVPHGLFOFFFWIGYCNS 457
 Qy 421 LNPVIYITIFNODFFRFRRLICRPMWTQTA 450
 Db 458 LNPVIYITIFNODFFRFRRLICRPMWTQTA 487

RESULT 10

AAR48699

ID AAR48699 standard; Protein; 330 AA.

XX AAR48699;

XX 05-JUN-1996 (first entry)

DE G-protein coupled human alpha-2 C2 adrenergic receptor protein.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotic disorder; schizophrenia; dopamine; CAMF; adenosine; thrombin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomegalo virus.

XX Homo sapiens.

XX W09405695-A1.

XX 17-MAR-1994.

XX 09-SEP-1993; 93WO-US08528.

XX 10-SEP-1992; 92US-0943236.

XX (UYNV) UNIV NEW YORK STATE.

PI Murphy RB, Schuster DI;
 XX WPI: 1994-101120/12.
 DR
 XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 PT binding GPR ligands or modulating GPR binding
 XX
 PS Disclosure; Page 72-73; 160pp; English.
 XX
 CC Proteins AAR4865-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from GPR, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
 CC of polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 XX
 XX Sequence 330 AA;
 SQ
 Query Match 68.3%; Score 1624.5; DB 15; Length 330;
 Best Local Similarity 73.1%; Pred. No. 2.8e-130;
 Matches 321; Conservative 6; Mismatches 3; Indels 109; Gaps 4;
 QY 12 TAAIAAATFTLFTFGNALVILAVITSSIRAPQNLFLVSLAADIIVATLIIIPSLA 71
 DB 1 TAAIAAATFTLFTFGNALVILAVITSSIRAPQNLFLVSLAADIIVATLIIIPSLA 60
 QY 72 NELGWWFRRTRWCEVYALDVLFTCTSSIVHCAISLDRYVAVSRALEYNSKRTPRRIKC 131
 DB 61 NELGWWFRRTRWCEVYALDVLFTCTSSIVHCAISLDRYVAVSRALEYNSKRTPRRIKC 120
 QY 132 IILTWMLAAVITSLPPLIYKDGQOPRGRPOCKLQNGEAWYIIASSIGSFAPCLIMILV 191
 DB 121 IILTWMLAAVITSLPPLIYKDGQOPRGRPOCKLQNGEAWYII-SSIGSFAPCLIL-LIV 178
 QY 192 YLRITVLIAKSNRRGPRAKGPGQGESKOPRPHDGAALASAKLPALASVASAREVNGHSK 251
 DB 179 YLRITVLIAKSNRRGPRAKGPGQGESKOPRPHDGAALASAKLPALAS- 226
 QY 252 STGEKEGETPEDTGTALPSPMAALPNSGGQKEGVCASPEDAESEEEEEEEBCE 311
 DB 227 ----- 226
 QY 312 POAVVSPASACSPPLQOPQGSRLVATLRGVILGRGVGAIIGQWRRRAQLTREKRTF 371
 DB 227 -----GRGVGAIIGQWRRRAVHTREKRTF 252
 QY 372 VLAIVIGFVLCWPPFFSISLGAICPKGCKVPHGLFOFFFWIGYCNSLNPVIYITINQ 431
 DB 253 VLAIVIGFVLCWPPFFSISLGAICPKGCKVPHGLFOFFFWIGYCNSLNPVIYITINQ 312
 QY 432 DFRRAFRRIICRPWTOTAW 450
 DB 313 DFRRAFRRIICRPWTOTAW 330
 RESULT 11
 AAM02671 standard; peptide; 330 AA.
 AC AAM02671;
 XX
 XX 25-MAR-2003 (updated)
 DT 12-NOV-1996 (first entry)
 DE G-protein coupled human alpha-2 C2 adrenergic receptor.
 XX G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW

KW schizophrenia; dopamine; CAMP; adenosine, thrombin, adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomagalovirus; serotonergic.
 XX
 OS Homo sapiens.
 XX
 PN US5508384-A.
 XX
 PD 16-APR-1996.
 XX
 PF 09-SEP-1993; 93US-0118270.
 XX
 PR 09-SEP-1993; 93US-0118270.
 PR 10-SEP-1992; 92US-0943236.
 XX
 PA (UNIV) UNIV NEW YORK STATE.
 XX
 PI Murphy RB, Schuster DI;
 XX WPI: 1996-208785/21.
 DR
 XX
 PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrenia
 XX
 PS Disclosure; Column 69-72; 184pp; English.
 XX
 CC Proteins AAM02657-W02720 represent a range of G-protein coupled receptor
 CC (GPR) proteins selected from GPR, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other GPR proteins. The receptor proteins
 CC were used to design polypeptides, pref. based on the transmembrane
 CC domains, for use in G-protein coupled receptor ligand binding assays.
 CC The polypeptide fragments retain biological activity such as binding a
 CC GPR ligand or modulating GPR ligand binding to a GPR (see
 CC AAM02747-W02899 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 330 AA;
 SQ
 Query Match 68.3%; Score 1624.5; DB 17; Length 330;
 Best Local Similarity 73.1%; Pred. No. 2.8e-130;
 Matches 321; Conservative 6; Mismatches 3; Indels 109; Gaps 4;
 QY 12 TAAIAAATFTLFTFGNALVILAVITSSIRAPQNLFLVSLAADIIVATLIIIPSLA 71
 DB 1 TAAIAAATFTLFTFGNALVILAVITSSIRAPQNLFLVSLAADIIVATLIIIPSLA 60
 QY 72 NELGWWFRRTRWCEVYALDVLFTCTSSIVHCAISLDRYVAVSRALEYNSKRTPRRIKC 131
 DB 61 NELGWWFRRTRWCEVYALDVLFTCTSSIVHCAISLDRYVAVSRALEYNSKRTPRRIKC 120
 QY 132 IILTWMLAAVITSLPPLIYKDGQOPRGRPOCKLQNGEAWYIIASSIGSFAPCLIMILV 191
 DB 121 IILTWMLAAVITSLPPLIYKDGQOPRGRPOCKLQNGEAWYII-SSIGSFAPCLIL-LIV 178
 QY 192 YLRITVLIAKSNRRGPRAKGPGQGESKOPRPHDGAALASAKLPALASVASAREVNGHSK 251
 DB 179 YLRITVLIAKSNRRGPRAKGPGQGESKOPRPHDGAALASAKLPALAS- 226
 QY 252 STGEKEGETPEDTGTALPSPMAALPNSGGQKEGVCASPEDAESEEEEEEEBCE 311
 DB 227 ----- 226
 QY 312 POAVVSPASACSPPLQOPQGSRLVATLRGVILGRGVGAIIGQWRRRAQLTREKRTF 371
 DB 227 -----GRGVGAIIGQWRRRAVHTREKRTF 252
 QY 372 VLAIVIGFVLCWPPFFSISLGAICPKGCKVPHGLFOFFFWIGYCNSLNPVIYITINQ 431
 DB 253 VLAIVIGFVLCWPPFFSISLGAICPKGCKVPHGLFOFFFWIGYCNSLNPVIYITINQ 312

Query Match 47.0%; Score 1117.5; DB 24; Length 450;
Best Local Similarity 52.7%; Pred. No. 7.1e-87;
Matches 241; Conservative 52; Mismatches 105; Indels 59; Gaps 13;

```
QY 6 PYSVQATAAIAATFLFTFTFGNALVTLVTSRSRAPQNTFLVSLAADIIVATLI 65
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 PYSVQATAAIAATFLFTFTFGNALVTLVTSRSRAPQNTFLVSLAADIIVATLI 86
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 66 IFFSLANELGMYFRRTWCEVYLAIDLFCSTSSIVHCAISLDRYMVASALENSKRT 125
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 IFFSLANELGMYFRRTWCEVYLAIDLFCSTSSIVHCAISLDRYMVASALENSKRT 146
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 126 PRRKCIITLWTLIAAVISLPLI---YKDGQPPQPRGRPOCKLNOAWYTIASSISGF 181
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 PRRKCIITLWTLIAAVISLPLI---YKDGQPPQPRGRPOCKLNOAWYTIASSISGF 205
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 PAPCLIMLVLYRIYLAIR---SNRGRPAKGGPGOGSSKOPR---PHGALASAK 233
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 206 PAPCLIMLVLYRIYLAIR---SNRGRPAKGGPGOGSSKOPR---PHGALASAK 265
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 234 LPALASVASAREVNGHSTGEKEGEPEDTGTALPPSWALPNSGOGKEGVCASP 293
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 266 AEPILPT---QLNG---APGEPAPA-GPRTDALDLES-----SS 298
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 294 EDEABE-----EEEEECEPQAPVPSPASCSPPLOQPGSRVLTATLNGVLLRGV 349
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 299 SDHAEPRPPGRPRGRPGKAKARASOVKPDLSLGRAGRGRRG-----GRLLQGR 351
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 350 GAIGGQWRRRAQL---TREKRFTFVLAIVIGVFLCMPPFFSYSIGALCPKCKVPHG 406
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 352 SASGLP---RRRAGAGGQVLEKRFVLAIVIGVFLCMPPFFFTYTLAV---GCSVPT 406
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 407 LFOFFFWIGYCNSSLNPIYITITFNODPRRARRLICR 443
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 407 LKFFFWFGYCNSSLNPIYITITFNODPRRARRLICR 443
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 15

AAMS2126
ID AAMS2126 standard; Protein; 457 AA.

AC AAMS2126;

DT 18-FEB-2002 (first entry)

DE Human alpha-2CAR variant protein.

XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;

KM polymorphic site; allelic variant; cardiovascular disease;

KM central nervous system disease; adenylyl cyclase; MAP kinase activity;

KM phosphorylation; inositol phosphate; alpha-2CAR.

OS Homo sapiens.

XX Key location/Qualifiers

FT Domain 208..231

FT Domain /label= transmembrane_domain

FT Domain 379..402

FT Domain /label= transmembrane_domain

PN WO200179561-A2.

PD 25-OCT-2001.

XX 17-APR-2001; 2001WO-US12575.

XX 17-APR-2000; 2000US-0551744.

PR 10-AUG-2000; 2000US-0636259.

PR 19-OCT-2000; 2000US-0692077.

XX (LIGG/) LIGGETT S B.

PA (SMAL/) SMALL K M.

XX LIGGETT SB, Small KM;
PI WPI: 2001-611728/70.
XX N-PSDB; AA199933.

PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
determining whether an individual is at increased risk of developing a
disease associated with the corresponding receptor comprises detecting
a polymorphic site -

Claim 78; Page 160-162; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
receptor gene (I)-(III) by detecting a polymorphic site, comprising:
(a) obtaining a sample having a polynucleotide encoding an alpha-2B,
alpha-2A or alpha-2C or fragment or complement of; and
(b) detecting a polymorphic site comprising nucleotide positions 901-909
of (I), a site comprising cytosine or guanine at position 753 of (II)
or a site comprising (A) (ggggcgggcg) or (B) (ggggcgggcg) at
positions 961-972 of (III). The method may be used for genotyping an
alpha-2B, alpha-2A or alpha-2C receptor gene and further used to determine
whether an individual is at increased risk of developing a disease
associated with alpha-2B, alpha-2A or alpha-2C, comprising detecting a
polymorphic site which correlate to disease selected from cardiovascular
disease, central nervous system disease and combinations of these. In
addition, the technique may be used to predict an individual's response
to an alpha-2B, alpha-2A, or alpha-2C agonist (e.g. epinephrine,
norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
ranolazine, idazoxan, tolazoline, phenolamine and combinations of
these) by detecting the polymorphic site and correlating the site to a
predetermined response (where the response is correlated to adenylyl
cyclase, MAP kinase activity, phosphorylation or inositol phosphate
levels). The present sequence is that of the human alpha-2CAR variant
protein, deleted for a 4 amino acid polymorphic site at residues 321-324
of the wildtype protein (AAMS2124).

XX Sequence 457 AA;

Query Match 45.4%; Score 1079.5; DB 22; Length 457;
Best Local Similarity 52.2%; Pred. No. 1.3e-83;
Matches 240; Conservative 40; Mismatches 101; Indels 79; Gaps 12;

```
QY 7 YSVQATAAIAATFLFTFTFGNALVTLVTSRSRAPQNTFLVSLAADIIVATLI 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 46 YSVQATAAIAATFLFTFTFGNALVTLVTSRSRAPQNTFLVSLAADIIVATLI 105
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 PFSIANELGMYFRRTWCEVYLAIDLFCSTSSIVHCAISLDRYMVASALENSKRT 126
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 106 PFSIANELGMYFRRTWCEVYLAIDLFCSTSSIVHCAISLDRYMVASALENSKRT 165
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 127 RRIKCIITLWTLIAAVISLPLI---YKDGQPPQPRGR---POCKLNOAWYTIASSISGF 182
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166 RRIKCIITLWTLIAAVISLPLI---YKDGQPPQPRGR---POCKLNOAWYTIASSISGF 220
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 APCLIMLVLYRIYLAIR---SNRGRPAKGGPGOGSSKOPR---PHGALASAK 242
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 221 APCLIMLVLYRIYLAIR---SNRGRPAKGGPGOGSSKOPR---PHGALASAK 257
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 AREVNGHSTGEKEBETPEDTGT-RALPSW-----AALPNSG-----QCG 284
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 258 PTFENGAGAAAGAR-----TGTARPRPTWRTTAQPRGAGAPLRRGRRRAGA 310
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 285 KEVCGASPEDEABE-----EEEEECEPQAPVPSPASCSPPLOQPGSRVLTATLNGV 343
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 311 KEVCGASPEDEABE-----EEEEECEPQAPVPSPASCSPPLOQPGSRVLTATLNGV 350
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 344 LIGGVALIGGQWRRRAQLTREKRFTFVLAIVIGVFLCMPPFFSYSIGALCPKCKV 403
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 351 LIGGVALIGGQWRRRAQLTREKRFTFVLAIVIGVFLCMPPFFSYSIGALCPKCKV 409
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 404 PHGLFQFFFWIGYCNSSLNPIYITITFNODPRRARRLICR 443
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Mon Feb 9 08:28:44 2004

us-09-692-077d-7.rag

Db 410 PGPLFKFFWIGYCNSSLNPFVITVFNQDFRPSFKHLLR 449

Search completed: February 6, 2004, 18:17:31
Job time : 40.1271 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: February 6, 2004, 18:16:11 ; Search time 15.0502 Seconds
(without alignments)
1265.095 Million cell updates/sec

Title: US-09-692-077D-7

Perfect score: 2378
Sequence: 1 MDHDPYSVQATTAIAAAT.....ODFRRAFRRLICRPTOTAW 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA.*
2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep.*
7: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1624.5	68.3	330	1 US-08-118-270-20	Sequence 20, Appl
2	1624.5	68.3	330	5 PCT-US93-08528-20	Sequence 20, Appl
3	1130.5	47.5	450	1 US-08-194-338-5	Sequence 5, Appl
4	1132.5	47.2	450	1 US-08-444-734A-8	Sequence 8, Appl
5	1063.5	44.7	461	1 US-08-194-338-4	Sequence 4, Appl
6	1027.5	43.2	334	1 US-08-118-270-22	Sequence 22, Appl
7	1027.5	43.2	334	5 PCT-US93-08528-22	Sequence 22, Appl
8	1025.5	43.1	358	2 US-08-465-971B-4	Sequence 4, Appl
9	1001.5	42.1	330	1 US-08-118-270-21	Sequence 21, Appl
10	1001.5	42.1	330	5 PCT-US93-08528-21	Sequence 21, Appl
11	985	41.4	330	1 US-08-118-270-19	Sequence 19, Appl
12	985	41.4	330	5 PCT-US93-08528-19	Sequence 19, Appl
13	950.5	40.0	450	1 US-08-196-989B-11	Sequence 11, Appl
14	950.5	40.0	450	2 US-08-760-936-11	Sequence 11, Appl
15	950.5	40.0	450	4 US-09-225-024-11	Sequence 11, Appl
16	651	27.4	601	1 US-07-676-174A-2	Sequence 2, Appl
17	594	25.0	415	1 US-08-194-338-10	Sequence 10, Appl
18	588.5	24.7	467	1 US-08-056-051-6	Sequence 6, Appl
19	588.5	24.7	467	2 US-07-928-611-22	Sequence 22, Appl
20	588.5	24.7	467	2 US-08-487-811A-22	Sequence 22, Appl
21	588.5	24.7	467	3 US-09-060-694-22	Sequence 22, Appl
22	588.5	24.7	467	4 US-09-378-074-22	Sequence 22, Appl
23	588.5	24.7	467	5 PCT-US93-07370-22	Sequence 22, Appl
24	587.5	24.6	515	1 US-08-722-001-25	Sequence 25, Appl
25	585.5	24.6	517	2 US-08-467-568-10	Sequence 10, Appl
26	585.5	24.6	517	2 US-09-030-582-10	Sequence 10, Appl
27	584.5	24.6	515	1 US-08-444-734A-7	Sequence 7, Appl

28	584.5	24.6	515	2 US-08-406-855A-22	Sequence 22, Appl
29	584.5	24.6	515	3 US-09-206-899-22	Sequence 22, Appl
30	584.5	24.6	520	1 US-08-334-698-4	Sequence 4, Appl
31	584.5	24.6	520	1 US-08-228-932-4	Sequence 4, Appl
32	584.5	24.6	520	1 US-08-468-939-4	Sequence 4, Appl
33	584.5	24.6	520	2 US-08-406-855A-4	Sequence 4, Appl
34	584.5	24.6	520	2 US-08-722-190-4	Sequence 4, Appl
35	584.5	24.6	520	3 US-08-244-354-4	Sequence 4, Appl
36	584.5	24.6	520	3 US-09-206-899-4	Sequence 4, Appl
37	584.5	24.6	520	4 US-09-444-783-4	Sequence 4, Appl
38	584.5	24.6	520	4 US-09-688-415-4	Sequence 4, Appl
39	584.5	24.6	520	5 PCT-US93-04203-4	Sequence 4, Appl
40	583.5	24.5	515	4 US-09-688-415-10	Sequence 10, Appl
41	582.5	24.5	419	1 US-08-056-051-4	Sequence 4, Appl
42	582.5	24.5	419	1 US-07-928-611-20	Sequence 20, Appl
43	582.5	24.5	419	2 US-08-487-811A-20	Sequence 20, Appl
44	582.5	24.5	419	3 US-09-060-694-20	Sequence 20, Appl
45	582.5	24.5	419	3 US-09-378-074-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-118-270-20
Sequence 20, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROMIDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-20

Query Match 68.3%; Score 1624.5; DB 1; Length 330;
Best Local Similarity 73.1%; Pred. No. 5.9e-100;
Matches 321; Conservative 6; Mismatches 3; Indels 109; Gaps 4;
CY 12 TAAIAATITFLITFGNLVLAIVTSRSLRAPQNLFLVSLAAADIVATLIPSLA 71

|||||
Db 1 TAAIAAATFTLLFTFGNALVITIAVITSRSLRAPOQLFVLSIAADILVATLLIPFSLA 60
Qy 72 NELGMYWFRRTWCVEVIALDVLFTCTSSIVHLCAISLDRYWASRALEYNKRTPRRIKC 131
Db 61 NELGMYWFRRTWCVEVIALDVLFTCTSSIVHLCAISLDRYWASRALEYNKRTPRRIKC 120
Qy 132 IILTWMLIAAVISLPPLIYKGDGQPGPRGPOCKLNOEAWYILASISGFFAPCLIMILV 191
Db 121 IILTWMLIAAVISLPPLIYKGDGQPGPRGPOCKLNOEAWYIL--SSIGSFAPCLILV 178
Qy 192 YLRIYLIAKSNRRGPRAKGPGQGESKOPRPHGALASAKLPALASVASAREVNGHSK 251
Db 179 YLRIYLIAKSNRRGPRAKGPGQGESKOPRPHGALASAKLPALAS-- 226
Qy 252 STGEKEGETPDTGTALPSPMALPNSGQGQKGVGASPEDAESEEEEEEEBCE 311
Db 227 ----- 226
Qy 312 PQAVVSPASACSPPLQPGSRVLATLRGQVLLGRGVGAIGGQWRRRAQLTREKRTF 371
Db 227 -----GRGVGAIGGQWRRRAVHTREKRTF 252
Qy 372 VLAIVGVFLCWPFPPFSYSLGALCPKHCKVPHGLFQFPFWIGYCNLSNPVITYTFNQ 431
Db 253 VLAIVGVFLCWPFPPFSYSLGALCPKHCKVPHGLFQFPFWIGYCNLSNPVITYTFNQ 312
Qy 432 DFRAPFRILCRPWTOTAM 450
Db 313 DFRAPFRILCRPWTOTAM 330

RESULT 2

PCT-US93-08528-20
Sequence 20, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF.
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

PCT-US93-08528-20

Query Match 68.3%; Score 1624.5; DB 5; Length 330;
Best Local Similarity 73.1%; Pred. No. 5.9e-100;
Matches 321; Conservative 6; Mismatches 3; Indels 109; Gaps 4;

Qy 12 TAAIAAATFTLLFTFGNALVITIAVITSRSLRAPOQLFVLSIAADILVATLLIPFSLA 71
Db 1 TAAIAAATFTLLFTFGNALVITIAVITSRSLRAPOQLFVLSIAADILVATLLIPFSLA 60
Qy 72 NELGMYWFRRTWCVEVIALDVLFTCTSSIVHLCAISLDRYWASRALEYNKRTPRRIKC 131
Db 61 NELGMYWFRRTWCVEVIALDVLFTCTSSIVHLCAISLDRYWASRALEYNKRTPRRIKC 120
Qy 132 IILTWMLIAAVISLPPLIYKGDGQPGPRGPOCKLNOEAWYILASISGFFAPCLIMILV 191
Db 121 IILTWMLIAAVISLPPLIYKGDGQPGPRGPOCKLNOEAWYIL--SSIGSFAPCLILV 178
Qy 192 YLRIYLIAKSNRRGPRAKGPGQGESKOPRPHGALASAKLPALASVASAREVNGHSK 251
Db 179 YLRIYLIAKSNRRGPRAKGPGQGESKOPRPHGALASAKLPALAS-- 226
Qy 252 STGEKEGETPDTGTALPSPMALPNSGQGQKGVGASPEDAESEEEEEEEBCE 311
Db 227 ----- 226
Qy 312 PQAVVSPASACSPPLQPGSRVLATLRGQVLLGRGVGAIGGQWRRRAQLTREKRTF 371
Db 227 -----GRGVGAIGGQWRRRAVHTREKRTF 252
Qy 372 VLAIVGVFLCWPFPPFSYSLGALCPKHCKVPHGLFQFPFWIGYCNLSNPVITYTFNQ 431
Db 253 VLAIVGVFLCWPFPPFSYSLGALCPKHCKVPHGLFQFPFWIGYCNLSNPVITYTFNQ 312
Qy 432 DFRAPFRILCRPWTOTAM 450
Db 313 DFRAPFRILCRPWTOTAM 330

RESULT 3

US-08-194-338-5
Sequence 5, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McComb, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH01.001DVL
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 US-08-194-338-5

Query Match 47.5%; Score 1130.5; DB 1; Length 450;
 Best Local Similarity: 53.2%; Pred. No. 2.7e-67;
 Matches 243; Conservative 52; Mismatches 103; Indels 59; Gaps 13;

QY 6 PYSVQATTAIAAATLFTLFTFGNALVILAVTSRSLRAPQNFVLSLAADILVATLI 65
 DB 27 PYSQVTLTVCLAGLMLTLVFGNVLYITAVTSRLKAPQNFVLSLAADILVATLV 86
 QY 66 IPFSLANELLGYWFRRTWCEVYALDVLFTCTSSIVHLCASIDRYAVASRALEYSKRT 125
 DB 87 IPFSLANENVGWYFGKTWCEIYALDVLFTCTSSIVHLCASIDRYAVASITQAIENYKRT 146
 QY 126 PRRIKIIITVWLIAVVISLPELI-----YKDGQPGPRGRPOCKLQNGEAMVTLASISGSF 181
 DB 147 PRRIKIIITVWLVISAVISFPLISIEKKGCGGPGP-AEPRCEINDQKMWIVASISGSF 205
 QY 182 FAPCLIMILVLYRIYLAIR-----SNRGRPRAGGPGQESKQPR---PDHGALASAK 233
 DB 206 FAPCLIMILVYVRIYQAKRTRVPSRRGPDVAAPGCTERRPGLGPRRSAGPGAG 265
 QY 234 LPALASVASAREVNGHSGTGEKEGETPEDTGTALPPSWALPNSGQCKEGVCGASP 293
 DB 266 AEPLPT-----QLNG---APGERAPA-GRDITDALDEES-----SS 298
 QY 294 EDEAE-----EEEEEEECPEQAVVSPASCPPLQOPQSGRVATLIRGQVLLGRV 349
 DB 299 SDHAERPPGRRPRGRGKARASQVKGPSDLRGAGRGGRS-----GRLLQGRGR 351
 QY 350 GATGGQWRRRAQL---TREKRTFVLAVYGVVLCWFPFYSYSGAICPKKCKVPHG 406
 DB 352 SASGLP--RRRAGAGGQNRKRTFVLAVYGVVLCWFPFYSYSGAICPKKCKVPHG 406
 QY 407 LPOFFFWIGYCNSSLNPIVYITIFNODPRRAFRIILCR 443
 DB 407 LFKFFFWIGYCNSSLNPIVYITIFNODPRRAFRIILCR 443

RESULT 4
 US-08-444-734A-8
 ; Sequence 8, Application US/08444734A
 ; Patent No. 5610282
 ; GENERAL INFORMATION:
 ; APPLICANT: Sibley, David R.
 ; APPLICANT: Monema, Frederick J.
 ; APPLICANT: Mahan, Lawrence C.
 ; APPLICANT: McVittie, Louis D.
 ; TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
 ; TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and
 ; TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
 ; TITLE OF INVENTION: cell lines
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobe, Martens, Olson and Bear
 ; STREET: 620 Newport Center Drive, Sixteenth Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/444,734A
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/029,917
 FILING DATE: 03-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/548,714
 FILING DATE: 06-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Altman, Daniel E.
 REGISTRATION NUMBER: 34,115
 REFERENCE/DOCKET NUMBER: NIH065.001FW1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (714) 760-0404
 TELEFAX: (714) 760-9502
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 US-08-444-734A-8

Query Match 47.2%; Score 1122.5; DB 1; Length 450;
 Best Local Similarity: 52.7%; Pred. No. 9.1e-67;
 Matches 241; Conservative 53; Mismatches 104; Indels 59; Gaps 13;

QY 6 PYSVQATTAIAAATLFTLFTFGNALVILAVTSRSLRAPQNFVLSLAADILVATLI 65
 DB 27 PYSQVTLTVCLAGLMLTLVFGNVLYITAVTSRLKAPQNFVLSLAADILVATLV 86
 QY 66 IPFSLANELLGYWFRRTWCEVYALDVLFTCTSSIVHLCASIDRYAVASRALEYSKRT 125
 DB 87 IPFSLANENVGWYFGKTWCEIYALDVLFTCTSSIVHLCASIDRYAVASITQAIENYKRT 146
 QY 126 PRRIKIIITVWLIAVVISLPELI-----YKDGQPGPRGRPOCKLQNGEAMVTLASISGSF 181
 DB 147 PRRIKIIITVWLVISAVISFPLISIEKKGCGGPGP-AEPRCEINDQKMWIVASISGSF 205
 QY 182 FAPCLIMILVLYRIYLAIR-----SNRGRPRAGGPGQESKQPR---PDHGALASAK 233
 DB 206 FAPCLIMILVYVRIYQAKRTRVPSRRGPDVAAPGCTERRPGLGPRRSAGPGAG 265
 QY 234 LPALASVASAREVNGHSGTGEKEGETPEDTGTALPPSWALPNSGQCKEGVCGASP 293
 DB 266 AEPLPT-----QLNG---APGERAPA-GRDITDALDEES-----SS 298
 QY 294 EDEAE-----EEEEEEECPEQAVVSPASCPPLQOPQSGRVATLIRGQVLLGRV 349
 DB 299 SDHAERPPGRRPRGRGKARASQVKGPSDLRGAGRGGRS-----GRLLQGRGR 351
 QY 350 GATGGQWRRRAQL---TREKRTFVLAVYGVVLCWFPFYSYSGAICPKKCKVPHG 406
 DB 352 SASGLP--RRRAGAGGQNRKRTFVLAVYGVVLCWFPFYSYSGAICPKKCKVPHG 406
 QY 407 LPOFFFWIGYCNSSLNPIVYITIFNODPRRAFRIILCR 443
 DB 407 LFKFFFWIGYCNSSLNPIVYITIFNODPRRAFRIILCR 443

RESULT 5
 US-08-194-338-4
 ; Sequence 4, Application US/08194338

```

/ Patent No. 5474898
/ GENERAL INFORMATION:
/ APPLICANT: Venter, John C.
/ APPLICANT: Praeger, Claire M.
/ APPLICANT: McCombie, William R.
/ TITLE OF INVENTION: OCTOPAMINE RECEPTOR
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson and Bear
/ STREET: 620 Newport Center Drive, Sixteenth floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/194,338
/ FILING DATE: 08-FEB-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/676,174
/ FILING DATE: 28-MAR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Israelson, Ned A.
/ REGISTRATION NUMBER: 29,655
/ REFERENCE/DOCKET NUMBER: NIH101.001DV1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 235-8550
/ TELEFAX: (619) 235-0176
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 461 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ US-08-194-338-4

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Query Match 44.7%; Score 1063.5; DB 1; Length 461;
Best Local Similarity 51.3%; Pred. No. 7.2e-63;
Matches 236; Conservative 43; Mismatches 106; Indels 75; Gaps 12;

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QY 7 YSVQATAIAAATFLFTIFGNAVLAVITSRSLRAPONFLVSLAADIIVATLIT 66
DB 46 YSAGAVAGLAAVGFLVFTVGNVLAVITSRALRAPONFLVSLASADILVATIVM 105
QY 67 PSLINELIGYFRRTWCEVYALDVLEFCTSIYHCAISLDRYAVASALEYNSKRP 126
DB 106 PSLINELIMAVYFQVWGVYALDVLEFCTSIYHCAISLDRYMSVGAIVNKRTP 165
QY 127 RRIKIIITVWLIAVSLPLI--YKGDGQPOGRG--PQCKLNGEAWYIIASISGSFF 182
DB 166 RRVKATIVAVMISIVISFPPLVSLR-----QPDGAAYPCQGLINDETYIILSSCIQSF 220
QY 183 APCIMITIVYRIYLIARSNRRGPRAKGPGGSGESKOPRPHDGLASAKIPALASVAS 242
DB 221 APCIMGLVAVIRIVAKRRTR-----TLSEKRAPVGPDDAS 257
QY 243 AREVNGSKSTGKEBEGTEPEDGT--RALPRSWAL-----PNSG-----OGQ 284
DB 258 PTENGGLAAGAR-----TGTAAPRPPTWARTRAQRPRGAPGLRRGRRAGA 310
QY 285 KEVGCGASPEDDAEBEEEEEECEPOAVVSPASACSPPLQPOGSRVLAITLKG-QV 343
DB 311 EGAGGA-----DGGAGPGAAGSALITASRSP--GPGRLSRASSRSVER 354

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QY 344 LIGRGVGAIGQWMBRRAQLREKFTFVLAVYGVFLCMFPFSSYSGAICPKHCKV 403
DB 355 FLSRRRRASSVCRRKAVQ-AREKFTFVLAVWGVFLCMFPFFYSYLGICREACGV 413
QY 404 PHGLQFFPWGICVNSSINPIYITFNODFFRARFRILCR 443
DB 414 FGLPFFFWGICVNSSINPIYITFNODFFRASKILLFR 453

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RESULT 6

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US-08-118-270-22
/ Sequence 22, Application US/08118270
/ Patent No. 5508384
/ GENERAL INFORMATION:
/ APPLICANT: Murphy, Randall B.
/ APPLICANT: Schuster, David I.
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEWMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004

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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/118,270
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY-2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 334 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-118-270-22

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Query Match 43.2%; Score 1027.5; DB 1; Length 334;
Best Local Similarity 47.3%; Pred. No. 1.2e-60;
Matches 210; Conservative 46; Mismatches 59; Indels 129; Gaps 8;

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QY 12 TAAIAAATFLFTIFGNAVLAVITSRSLRAPONFLVSLAADIIVATLITPSLA 71
DB 1 TLTVLCIAGLIMLVFVFGNVLAVITSRALKAPONFLVSLASADILVATIVTIPSLA 60
QY 72 NELLGWYFRRTWCEVYALDVLEFCTSIYHCAISLDRYAVASALEYNSKRPRIK 131
DB 61 NEWM-YWYFGKWCBIYALDVLEFCTSIYHCAISLDRYMSVGAIVNKRTPRIRA 119
QY 132 IITVWLIAVSLPLIY-----KGDGQPOGRGPOCKLNGEAWYIIASISGSFFAPCI 187
DB 120 IITVWVIAVSLPPLISITKKGAGGQGPAPBPCKINDQKVIYISSISGSFFAPCI 179
QY 188 MLIVYLRITLIAR-----SNRRGPRAKGPGGSGESKOPR-----PDHGLASAKIPALAS 239
DB 180 NMLVYVRIYQIARRKRTVPPSRGPDACAPPGAGLRIRNNAVGPENAGCTA----- 230

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QY 240 VASAREVNGSHKSTGEKEGETPEDTGTALPSPMALPNSGQKGVCSPEDEAE 299
DB 231 -----GGQGE----- 236
QY 300 EEEEEEECEPQAVPSPASCSPLQOPQGSRLATLGRGVALIGQWRR 359
DB 237 -----RAGAKASRW--- 246
QY 360 RAQLTREKRTFTFLAVVIGVFLCWFPPFFSYSIGALCPKCKVPHGLFOFFFIIGVNS 419
DB 247 RGRNREKRTFTFLAVVIGVFLCWFPPFFSYSIGALCPKCKVPHGLFOFFFIIGVNS 419
QY 420 SLNPVITITFMDPRRAFKILCR 443
DB 304 SLNPVITITFMDPRRAFKILCR 327

RESULT 7
PCT-US93-08528-22
Sequence 22, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-22

Query Match 43.2%; Score 1027.5; DB 5; Length 334;
Best Local Similarity 47.3%; Pred. No. 1.2e-60;
Matches 210; Conservative 46; Mismatches 59; Indels 129; Gaps 8;

QY 12 TAAIAAATFLITFTFGNALVILAVLTSRSRAPOMFLVSLAADIIVTLIPSLA 71
DB 1 TLTIVCAGLIMLTIVGNAVITIAVFSRLAKAPOMFLVSLAADIIVTLIPSLA 60
QY 72 NELLGMYFRRTTCEVYIALDVLCSTSSIVHLCAISLDRYVAASRALEYSKTPRIK 131
DB 61 NEMV-YVYFGKWEIYLAIDVLCSTSSIVHLCAISLDRYVSIQALEYNLKRPRIKA 119

QY 132 ILTVMILIAVISLIPPLY-----KGQGPQPRGRPOCKLNOEAYIILASSIGSFAPCLI 187
DB 120 ILTVVIAVISLIPPLYLISIEKKAGCGQOPAPPSCKINDOKKYVLISSISGFAPCLI 179
QY 188 MILVYIAIYLIAR-----SNRRGPRAKGGPGQESQPR---PDHGALASALIPALAS 239
DB 180 NMLVYVRIYQIAKRTVPSPRRGPDACSAPPGADRRPNVAVGERAGTA----- 230
QY 240 VASAREVNGSHKSTGEKEGETPEDTGTALPSPMALPNSGQKGVCSPEDEAE 299
DB 231 -----GGQGE----- 236
QY 300 EEEEEEECEPQAVPSPASCSPLQOPQGSRLATLGRGVALIGQWRR 359
DB 237 -----RAGAKASRW--- 246
QY 360 RAQLTREKRTFTFLAVVIGVFLCWFPPFFSYSIGALCPKCKVPHGLFOFFFIIGVNS 419
DB 247 RGRNREKRTFTFLAVVIGVFLCWFPPFFSYSIGALCPKCKVPHGLFOFFFIIGVNS 419
QY 420 SLNPVITITFMDPRRAFKILCR 443
DB 304 SLNPVITITFMDPRRAFKILCR 327

RESULT 8
US-08-465-971B-4
Sequence 4, Application US/08465971B
Patent No. 5942414
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBBF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PFI87)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-465-971B-4

Query Match 43.1%; Score 1025.5; DB 2; Length 358;
Best Local Similarity 48.4%; Pred. No. 1.8e-60;
Matches 218; Conservative 39; Mismatches 56; Indels 137; Gaps 10;

QY 6 PYSVQATAAIAAATFLITFTFGNALVILAVLTSRSRAPOMFLVSLAADIIVA-- 62
DB 27 PYSIQVTLTVCLAGLMLTIVGNAVITIAVFSRLAKAPOMFLVXSLASADIIVAXX 86

QY 63 TLIIIPSLANELLGYWYPRRTWCCEVYLLADVLCTSSIVHCAISLDRYVAASRALEYNS 122
DB 87 TLVIIPSLANEMGWTYFGKACETYLALDVLCTSSIVHCAISLDRYVSIQALEYNL 146
QY 123 KETPRRIKIIITWLVIAVITSLPPLI-----YKGQGPQPRGRPOCKLNOEAWYILAS 176
DB 147 KETPRRIKIIITWLVIAVITSLPPLI-----YKGQGPQPRGRPOCKLNOEAWYILAS 205
QY 177 SIGSFAPCLIMILVYIRIYILAKSRNRGRPRAGGQGESKQPRPDHGALASAKLPA 236
DB 206 CIGSFAPCLIMILVYIRIYILAKSRNRGRPRAGGQGESKQPRPDHGALASAKLPA 240
QY 237 LASVASAREVNGSHKSTGEKEGETPDTGTRALPSSMAALPNSGQGEKGVCGASPRDE 296
DB 241 -----PDVAAPPGGGLQGRGASG----- 260
QY 297 AEEEEEEEEEECEPQAVVSPASACSPPLQOPGSRVLAITRGQVLLGRGVAGIGQW 356
DB 261 -----LPRRAGA-GGQ- 271
QY 357 WRRRAQLTRKRTFLAVVIGVFLCWPFFFSYLSAICPKGKVPHGILFOFFWITGY 416
DB 272 -----NREKRTFLAVVIGVFLCWPFFFSYLSAICPKGKVPHGILFOFFWITGY 416
QY 417 CNSLNPVITYITFNODFRAPRI---LCR 443
DB 322 CNSLNPVITYITFNODFRAPRI---LCR 443

RESULT 9

US-08-118-270-21
Sequence 21, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-118-270-21
Query Match 42.1%; Score 1001.5; DB 1; Length 330;
Best Local Similarity 50.1%; Pred. No. 6,36-59;
Matches 214; Conservative 40; Mismatches 48; Indels 125; Gaps 12;
QY 26 TIFGNALVILAVITSRSLAPQNLFIIVSLAADILVATLIIIPSLANELLGYWYPRRTWC 85
DB 13 TIFGNALVILAVITSRSLAPQNLFIIVSLAADILVATLIIIPSLANELLGYWYPRRTWC 85
QY 86 EYIALDLVCTSSIVHCAISLDRYVAASRALEYNSKTRPRRIKIIITWLVIAVITSL 145
DB 72 EYIALDLVCTSSIVHCAISLDRYVAASRALEYNSKTRPRRIKIIITWLVIAVITSL 131
QY 146 PPLI-----YKGQGPQPRGRPOCKLNOEAWYILASISGSEFAPCLIMILVYIRIYILAKR 201
DB 132 PPLI-----YKGQGPQPRGRPOCKLNOEAWYILASISGSEFAPCLIMILVYIRIYILAKR 189
QY 202 -----SNRGRPRAGGQGESKQPRPDHGALASAKLPALASVASAREVNGSHKSTGEK 256
DB 190 RTRVPRRRPDVAAPPGGTERRP-----NG----- 216
QY 257 EGGTPTDTGTRALPSSMAALPNSGQGEKGVCGASPRDEAEEEEEEBCEPQAVP 316
DB 217 -----LGRSAGPGGGR- 231
QY 317 VSPASACSPPLQOPGSRVLAITRGQVLLGRGVAGIGQWRRRAQLTRKRTFLVAV 376
DB 232 -----SASGLP-----RRRAGA-GGQ-----NREKRTFLVAV 259
QY 377 IGVFLCWPFFFSYLSAICPKGKVPHGILFOFFWITGNSLNPVITYITFNODFRRA 436
DB 260 IGVFLCWPFFFSYLSAICPKGKVPHGILFOFFWITGNSLNPVITYITFNODFRRA 436
QY 437 FRRILCR 443
DB 317 FRRILCR 323

RESULT 10

PCT-US93-08528-21
Sequence 21, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-21

Query Match 42.1%; Score 1001.5; DB 5; Length 330;
Best Local Similarity 50.1%; Pred. No. 6.3e-59;
Matches 214; Conservative 40; Mismatches 48; Indels 125; Gaps 12;

26 TIFGNALVILAVLTSSIRAPQNLFLVSLAADIIVATLIIPFSLANELLGYWFRFRWC 85
13 TIFGNVILVILAVLTSSIRAPQNLFLVSLAADIIVATLIIPFSLANELLGYWFRFRWC 71
86 EVYALDVLFTSSIVHICAIISLDRYMAVSRALEYNKRTPRIKCIITVWLIAAVISL 145
72 EYVALDVLFTSSIVHICAIISLDRYMSITQAIENLKRTPRIKCIITVWLVSAVISF 131
146 PRLI-----YKGDQGPGRGRPOCKLNOAWYILASISGFFAPCLIMLVLYRIYLAKR 201
132 PRLISIEKKGSGGPQP-AEPRCEINDQKWYVSSIGSFAPCLIM-LVYVRIYOLAKR 189
202 -----SNRGRPAKGGPGQESKOPRPHDGALASAKLPALASVASAREVNGHSKSTGEK 256
190 RTRVPVRDRDDVAAPPGCTERRP-----NG----- 216
257 BEGETPDTGTALRPSWALPNSGQGEKVCASPEDEAEDEEEDEEEDEECPQAVP 316
217 -----IGPERSAGPGGGRGR----- 231
317 VSPASACSPPLQOGSSRVLTATLGGVILGRGVAIGQWRRRAQLTREKFTFVLAIV 376
232 ---SASGLP-----RRRAGA-GGQ-----NRRKRFTEVLAIV 259
377 IGVFLVLCMPFFPFSYSLGAIQPKHCKVPHGLFQFFFWIGYCNSSLNPIYITIFNDPFRRA 436
260 IGVFLVLCMPFFPFSYSLGAIQPKHCKVPHGLFQFFFWIGYCNSSLNPIYITIFNDPFRRA 316
437 FRRILCR 443
317 FRRILCR 323

RESULT 11
US-08-118-270-19
Sequence 19, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-19

Query Match 41.4%; Score 985; DB 1; Length 330;
Best Local Similarity 48.3%; Pred. No. 7.6e-58;
Matches 210; Conservative 41; Mismatches 66; Indels 118; Gaps 9;

13 AIAAATFLILFTIFGNALVILAVLTSSIRAPQNLFLVSLAADIIVATLIIPFSLAN 72
2 AGLAAVGFLVFTVGNVILVILAVLTSSIRAPQNLFLVSLAADIIVATLVMPFSIAN 61
73 ELIGWYFRRTWCYVALADVLFTSSIVHICAIISLDRYMAVSRALEYNKRTPRIKCI 132
62 EIM-YWYFGWCGVVALADVLFTSSIVHICAIISLDRYMSITQAVEYNLKRTPRVAT 120
133 ILTVWLIAAVISLPLI--YKGDQGPGRGR--POCKLNOAWYILASISGFFAPCLIM 188
121 IVANWLVSAVISFPLVSLR-----QPDGAAYQCGINDEWYILSSIGSFAPCLIM 175
189 ILVYRIYLAIRKSNRRPRAKGGPGQESKOPRPHDGALASAKLPALASVASAREVNG 248
176 LLYVARIYRAKRRTR-----TLSEKRAVGPDGASPTIENG 212
249 HSKSTGEKEGETPDTGTALRPSWALPNSGQGEKVCASPEDEAEDEEEDEE 308
213 LGAAAGEAR-----TGT-----ARFLSRRRASSVC----- 239
309 ECEPQAVPVSASACSPPLQOGSSRVLTATLGGVILGRGVAIGQWRRRAQLTREK 368
240 -----RRKVAQAEKR 250
369 FTFVLAIVGVFLVLCMPFFPFSYSLGAIQPKHCKVPHGLFQFFFWIGYCNSSLNPIYIT 428
251 FTFVLAIVGVFLVLCMPFFPFSYSLGAIQPKHCKVPHGLFQFFFWIGYCNSSLNPIYIT 307
429 FNDPFRAPRILCR 443
308 FNDPFRAPRILCR 322

RESULT 12
PCT-US93-08528-19
Sequence 19, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: PCT/US93/08528
 APPLICATION NUMBER: PCT/US93/08528
 FILING DATE: 09-SEP-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MCRPHY=2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 330 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US93-08528-19

Query Match 41.4%; Score 985; DB 5; Length 330;
 Best Local Similarity 48.3%; Pred. No. 7,6e-58;
 Matches 210; Conservative 41; Mismatches 66; Indels 118; Gaps 9;

13 AATAATPFLIFLIFGNALVILAVLTSRLAPQNLPLVSLAADIIVATLIIPSLAN 72
 2 AGLAAVGFLIVTGVNVLVAVLALPSRALPQNLPLVSLAADIIVATLIIPSLAN 61
 73 ELIGWYFRTTCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRALEYSKRTPRICI 132
 62 EIM-YWFGVQWGVYALDVLFTCTSSIVHLCAISLDRYMAVSRALEYSKRTPRICI 120
 133 ILTWMLIAVYISLPLI--YKGGQGPGR--POCKLNOEWYLLASSIGSFAPCLIM 188
 121 IVAVWILSAVISLPLVLSYLR---QPDGAAYPOGGLNDETWYLLSSIGSFAPCLIT 175
 189 ILVYLRIYLIARNSNRGRPRAGKGPQGESKQPRDHGALASALPLASVASAREVNG 248
 176 LLYVAIYIVAKKRR-----TISKRAVGPQGCASPTTENG 212
 249 HSKSGEKEGETPDTGTALPPSMALPNSGGQKEGVCASPEDEAESEEESEEB 308
 213 LGAAAGEAR-----TGT-----ARFLSRRRARRSSVC----- 239
 309 ECEPOAVPVSPASACSPLOQPOGSRVLATLRGVLLGRGVALGGQWRRRAQLTREKR 368
 240 -----RKKVAQAREKR 250
 369 FTPLAVAVIGVPLVLCWPFPPFSYSLGALCPKHKVPHGLFOFPFMWIGYCNSSLNPIYTI 428
 251 FTFVIAL---VFLVLCWPFPPFSYSLGALCPKHKVPHGLFOFPFMWIGYCNSSLNPIYTI 307
 429 FNQDFRRAFRRIICR 443
 308 FNQDFRPSFKHILFR 322

RESULT 13
 US-08-196-989B-11
 ; Sequence 11, Application US/08196989B
 ; Patent No. 5585476
 ; GENERAL INFORMATION:
 ; APPLICANT: MacLennan, A. John
 ; TITLE OF INVENTION: Molecular Cloning and Expression of
 ; NUMBER OF INVENTIONS: G-Protein Coupled Receptors
 ; CORRESPONDENCE ADDRESS: 14
 ; ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: US
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/196,989B
 FILING DATE: 15-FEB-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MAC-100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-08-196-989B-11

Query Match 40.0%; Score 950.5; DB 1; Length 450;
 Best Local Similarity 45.8%; Pred. No. 1,9e-55;
 Matches 202; Conservative 36; Mismatches 174; Indels 29; Gaps 4;

6 PYSVQATAAIAAIFLIFLIFGNALVILAVLTSRLAPQNLPLVSLAADIIVATLI 65
 27 PYSIQTLVTLVCLAGLMLTLVFGVAVIIVITSRALKAKQNLPLVSLAADIIVATLI 86
 66 IPESLANELGWRRTTCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRALEYSKRT 125
 87 IPESLANELGWRRTTCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRALEYSKRT 146
 126 PRKICILTWMLIAVYISLPLI--YKGGQGPGR--POCKLNOEWYLLASSIGSF 181
 147 PRKIALITVWVIAVISLPLVLSYLR---QPDGAAYPOGGLNDETWYLLSSIGSF 205
 182 PAPCLIMILVYRIYLIARNSNRGRPRAGKGPQGESKQPRDHGALASAKLPALASVA 241
 206 PAPCLIMILVYRIYLIARNSNRGRPRAGKGPQGESKQPRDHGALASAKLPALASVA 244
 242 SAREVNGSKSTGEKEGETPDTGTALPPSMALPNSGGQKEGVCASPEDEAESE 301
 245 XXX 304
 302 EEESECEPOAVPVSPASACSPLOQPOGSRVLATLRGVLLGRGVALGGQWRRRA 361
 305 XXX 364
 362 QUTREKRTFTPLAVAVIGVPLVLCWPFPPFSYSLGALCPKHKVPHGLFOFPFMWIGYCNSSL 421
 365 XXXREKRTFTPLAVAVIGVPLVLCWPFPPFSYSLGALCPKHKVPHGLFOFPFMWIGYCNSSL 421
 422 NPVIYTIFFNDFRRAFRRIIC 442
 422 NPVIYTIFFNDFRRAFRRIIC 442

RESULT 14
 US-08-760-936-11
 ; Sequence 11, Application US/08760936
 ; Patent No. 5856443
 ; GENERAL INFORMATION:
 ; APPLICANT: MacLennan, A. John

TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936
FILING DATE: December 6, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-760-936-11

Query Match 40.0%; Score 950.5; DB 2; Length 450;
Best Local Similarity 45.8%; Pred. No. 1.9e-55;
Matches 202; Conservative 36; Mismatches 174; Indels 29; Gaps 4;

QY 6 PYSVQATTAATAATPILFTIFGNALVILAVLTSRLRAPQNFVLSLAADTLVATLI 65
DB 27 PYSIQVTLTVCLAGLMLTLVFGNVILVAVFTSRALKAPQNFVLSASADTLVATLV 86
QY 66 IPFSLANELLGYWFRRTWCENVLALDVLCTSSIVHLCASLDRIYASTOAIETNLKRT 125
DB 87 IPFSLANELLGYWFRRTWCENVLALDVLCTSSIVHLCASLDRIYASTOAIETNLKRT 146
QY 126 PRRICKIILTWMLAAVLSPLI---YKDGQPGPRGRPOCKLNOEAWYILASISGSF 181
DB 147 PRRIKAIITITVWISAVISPPPLISIEKGGGGGPGP-ABRCEINDQKMWISSICGSF 205
QY 182 FAPCLIMILVLYRILYIAKRSNRGRPAKGGPGGSGSKOPRPHGALASAKLPALASVA 241
DB 206 FAPCLIMILVLYRILYIAKRSNRGRPAKGGPGGSGSKOPRPHGALASAKLPALASVA 244
QY 242 SARVNHGHSKSTGKEBGETPEDTGTALPPSWAALPNSGQGGQKEGVCGASPEDAEABEE 301
DB 245 SARVNHGHSKSTGKEBGETPEDTGTALPPSWAALPNSGQGGQKEGVCGASPEDAEABEE 304
QY 302 EEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRGQVLLGRGVAIGQWMBRRA 361
DB 305 EEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRGQVLLGRGVAIGQWMBRRA 364
QY 362 QLTREKPTFLVAVIGVFLCMFPFFSLSGLAI CPHGCVPRGLFQFFWIGYCNSSL 421
DB 365 XXXXREKFTFLVAVIGVFLCMFPFFSLSGLAI CPHGCVPRGLFQFFWIGYCNSSL 421
QY 422 NPVITYTIFNODRRAFRILC 442
DB 422 NPVITYTIFNODRRAFRILC 442

RESULT 15

US-09-225-024-11
Sequence 11, Application US/09225024
Patent No. 6518414
GENERAL INFORMATION:
APPLICANT: Macleaman, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,024
FILING DATE: 04-JAN-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,936
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/196,989
FILING DATE: 15-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-225-024-11

Query Match 40.0%; Score 950.5; DB 4; Length 450;
Best Local Similarity 45.8%; Pred. No. 1.9e-55;
Matches 202; Conservative 36; Mismatches 174; Indels 29; Gaps 4;

QY 6 PYSVQATTAATAATPILFTIFGNALVILAVLTSRLRAPQNFVLSLAADTLVATLI 65
DB 27 PYSIQVTLTVCLAGLMLTLVFGNVILVAVFTSRALKAPQNFVLSASADTLVATLV 86
QY 66 IPFSLANELLGYWFRRTWCENVLALDVLCTSSIVHLCASLDRIYASTOAIETNLKRT 125
DB 87 IPFSLANELLGYWFRRTWCENVLALDVLCTSSIVHLCASLDRIYASTOAIETNLKRT 146
QY 126 PRRICKIILTWMLAAVLSPLI---YKDGQPGPRGRPOCKLNOEAWYILASISGSF 181
DB 147 PRRIKAIITITVWISAVISPPPLISIEKGGGGGPGP-ABRCEINDQKMWISSICGSF 205
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DB 206 FAPCLIMILVLYRILYIAKRSNRGRPAKGGPGGSGSKOPRPHGALASAKLPALASVA 244
QY 242 SARVNHGHSKSTGKEBGETPEDTGTALPPSWAALPNSGQGGQKEGVCGASPEDAEABEE 301
DB 245 SARVNHGHSKSTGKEBGETPEDTGTALPPSWAALPNSGQGGQKEGVCGASPEDAEABEE 304
QY 302 EEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRGQVLLGRGVAIGQWMBRRA 361
DB 305 EEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRGQVLLGRGVAIGQWMBRRA 364

Oy	362	QUTREKRFTEVLAVVIGVFLCMPPFPFSYLGAI	CPKHCKVPHGLFOFPFWIGYCNSSL	421
Db	365	XXXXREKRFTEVLAVVIGVFLCMPPFPFTYTLTA	V--GCSVPRTLFKFPFMFGYCNSSL	421
Oy	422	NPVIYTFINQDFRAFRRLC		442
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Search completed: February 6, 2004, 18:20:51
 Job time : 17.0502 secs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: February 6, 2004, 18:17:36 ; Search time 30.1003 Seconds
(without alignments)
3130.265 Million cell updates/sec

Title: US-09-692-077D-7
Perfect score: 2378
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2378	100.0	450	9	US-09-825-923-4
2	2378	100.0	450	15	US-10-077-870-4
3	2378	100.0	450	15	US-10-001-073-7
4	2370	99.7	450	15	US-10-225-567A-42
5	2351.5	98.9	447	9	US-09-825-923-2
6	2351.5	98.9	447	15	US-10-077-870-2
7	2351.5	98.9	447	15	US-10-001-073-8
8	1126.5	47.4	450	15	US-10-001-073-27
9	1124.5	47.3	450	15	US-10-001-073-26
10	1117.5	47.0	450	15	US-10-225-567A-40
11	1078.5	45.4	461	15	US-10-225-567A-44
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14	959	40.3	307	15	US-10-060-795B-4
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18	594.5	25.0	467	15	US-10-225-567A-106	Sequence 106, App
19	589	24.8	415	15	US-10-060-795B-2	Sequence 2, Appli
20	588.5	24.7	467	15	US-10-224-260-22	Sequence 22, Appli
21	587.5	24.7	419	12	US-10-292-798-460	Sequence 460, App
22	585.5	24.6	517	10	US-09-951-622-10	Sequence 10, Appli
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25	584.5	24.6	497	14	US-10-052-589-2	Sequence 2, Appli
26	584.5	24.6	520	15	US-10-185-991-4	Sequence 4, Appli
27	584.5	24.6	520	15	US-10-238-129-4	Sequence 4, Appli
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29	584.5	24.6	520	15	US-10-225-567A-36	Sequence 36, Appli
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31	583.5	24.5	515	15	US-10-238-667-20	Sequence 10, Appli
32	582.5	24.5	419	15	US-10-224-260-20	Sequence 20, Appli
33	581.5	24.5	462	12	US-10-017-161-754	Sequence 754, App
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38	578.5	24.3	515	15	US-10-054-616A-3	Sequence 3, Appli
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40	578	24.3	443	15	US-10-060-795B-11	Sequence 11, Appli
41	578	24.3	443	15	US-10-157-031-78	Sequence 78, Appli
42	578	24.3	443	15	US-10-325-567A-102	Sequence 102, App
43	578	24.3	445	12	US-10-292-798-658	Sequence 658, App
44	577.5	24.3	422	12	US-10-118-804-13	Sequence 13, Appli
45	577.5	24.3	422	12	US-10-318-661-10	Sequence 10, Appli

ALIGNMENTS

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RESULT 1
US-09-825-923-4
Sequence 4, Application US/09825923
Patent No. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Tuomainen, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Myrskanen, Kristina
APPLICANT: Salonen, Riitta
APPLICANT: Kauppinen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825, 923
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-923-4
Query Match 100.0%; Score 2378; DB 9; Length 450;
Best Local Similarity 100.0%; Pred. No. 8, 7e-162;
Matches 450; Conservative 0; Mismatches 0; Indels 0;
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DB 1 MDHDPYSVQATAAIAAATFLIFTIFGNALVTLAVTSRSLRAPONLFLVSLAAADIL 60
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DB 361 AQLTREKRFTEVLAVVIGVFLCMFPFFFSYSLGALCPKCKVPHGLFOFFFWIGYCNSS 420
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DB 421 LNPVITYITFNODFRARFRILICRPWTOTAW 450

RESULT 2
US-10-077-870-4
Sequence 4, Application US/10077870
Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salomon, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 4
LENGTH: 450
TYPE: PRF
ORGANISM: Homo sapiens
US-10-077-870-4

Query Match 100.0%; Score 2378; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 8,7e-162;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 FFAFCLIMLVLYLRIYLIYIAKRSNRGRPRAGKGPQGSGSKOPRPHDGALASAKLPALASV 240

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DB 421 LNPVITYITFNODFRARFRILICRPWTOTAW 450

RESULT 3
US-10-001-073-7
Sequence 7, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Small, Kirsten
FILE REFERENCE: 11073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 450
TYPE: PRF
ORGANISM: Homo sapiens
US-10-001-073-7

Query Match 100.0%; Score 2378; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 8,7e-162;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 VATLIIPSLANELLGMYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
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DB 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKDGOPRGRPOCKLNOEAWYTLASISGS 180
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RESULT 4
US-10-225-567A-42
; Sequence 42, Application US/10225567A
; Publication No. US2003013798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 42
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-42

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Best Local Similarity 99.6%; Pred. No. 3.2e-161;
Matches 448; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 421 LNPVIYITFNODFRRAFRILCRPWTOTAW 450
DB 421 LNPVIYITFNODFRRAFRILCRPWTOTAW 450

RESULT 5
US-09-825-923-2
; Sequence 2, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapfit, Amkr
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhonen, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulou, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
```

```
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakkia, Timo A
; APPLICANT: Myyssen, Kristina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kaunonen, Uuseli
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-2

Query Match      98.9%; Score 2351.5; DB 9; Length 447;
Best Local Similarity 99.3%; Pred. No. 6.7e-160;
Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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DB 61 VATLIIPSLANELLGYVYFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRALEY 120
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DB 181 FFAFLIMILVLYLRILYLAJRSNRGPRAKGPGGSGSKORPRDHGALASAKLPALASV 240
QY 241 ASAREVNHSGSTGKEGGETPEDTGTALPPSMALPNSGQGQKEGVCGASPEDAEAE 300
DB 241 ASAREVNHSGSTGKEGGETPEDTGTALPPSMALPNSGQGQKEGVCGASPEDAEAE 300
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DB 361 AQLTRKRFVLAIVGVFVLCWPFPPFSYSLGAIKPKHCKVPHGLQFFFWIGYCNSS 420
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RESULT 6
US-10-077-870-2
; Sequence 2, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 2
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LENGTH: 447
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-077-870-2

Query Match
 Best Local Similarity 98.9%; Score 2351.5; DB 15; Length 447;
 Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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DB 1 MDHODPYVQATAIAAATFTLFTFGNALVILAVTSRLAPQNLFLVSLAAADIL 60
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DB 61 VATTLPESLANELLGYWFRRTWCEVYALDVLFCTSSIVHCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIITLFWLIAAVISLPPLIKGDDGPPQGRPOCKLNOEAWYILASSIGS 180
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DB 181 FAPCLIMILVYRIYLIARNSNRGPRAGKPGQGESKOPRPHDGALASAKLPALASV 240
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DB 241 ASAREVNGSKSTGEKEGETPEDTGTALPPSMALPNSGQCKEVCASPEDAE 297
QY 301 EEEEEECEPOAVPVSPASACSPLOQPOGSRVLTATLRGQVLLGRGVGALGQWRRR 360
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DB 361 AQLTRERFTVLAVVIGVFLCWPFFFSYSLGAIKPKHCKVPHGLPOFFWIGYCNS 420
QY 421 LNPVIYITFNODFRAPRRIICRPWTOTAM 450
DB 421 LNPVIYITFNODFRAPRRIICRPWTOTAM 450

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RESULT 7

US-10-001-073-8
 Sequence 8, Application US/10001073
 Publication No. US20030113725A1
 GENERAL INFORMATION:
 APPLICANT: Liggett, Stephen
 TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
 FILE REFERENCE: 13073-PCT
 CURRENT APPLICATION NUMBER: US/10/001,073
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 8
 LENGTH: 447
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-001-073-8

Query Match
 Best Local Similarity 98.9%; Score 2351.5; DB 15; Length 447;
 Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

```

QY 1 MDHODPYVQATAIAAATFTLFTFGNALVILAVTSRLAPQNLFLVSLAAADIL 60
DB 1 MDHODPYVQATAIAAATFTLFTFGNALVILAVTSRLAPQNLFLVSLAAADIL 60
QY 61 VATTLPESLANELLGYWFRRTWCEVYALDVLFCTSSIVHCAISLDRYMAVSRALEY 120
DB 61 VATTLPESLANELLGYWFRRTWCEVYALDVLFCTSSIVHCAISLDRYMAVSRALEY 120

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QY 121 NSKRTPRRIKCIITLFWLIAAVISLPPLIKGDDGPPQGRPOCKLNOEAWYILASSIGS 180
DB 121 NSKRTPRRIKCIITLFWLIAAVISLPPLIKGDDGPPQGRPOCKLNOEAWYILASSIGS 180
QY 181 FAPCLIMILVYRIYLIARNSNRGPRAGKPGQGESKOPRPHDGALASAKLPALASV 240
DB 181 FAPCLIMILVYRIYLIARNSNRGPRAGKPGQGESKOPRPHDGALASAKLPALASV 240
QY 241 ASAREVNGSKSTGEKEGETPEDTGTALPPSMALPNSGQCKEVCASPEDAE 297
DB 241 ASAREVNGSKSTGEKEGETPEDTGTALPPSMALPNSGQCKEVCASPEDAE 297
QY 301 EEEEEECEPOAVPVSPASACSPLOQPOGSRVLTATLRGQVLLGRGVGALGQWRRR 360
DB 301 EEEEEECEPOAVPVSPASACSPLOQPOGSRVLTATLRGQVLLGRGVGALGQWRRR 360
QY 361 AQLTRERFTVLAVVIGVFLCWPFFFSYSLGAIKPKHCKVPHGLPOFFWIGYCNS 420
DB 361 AQLTRERFTVLAVVIGVFLCWPFFFSYSLGAIKPKHCKVPHGLPOFFWIGYCNS 420
QY 421 LNPVIYITFNODFRAPRRIICRPWTOTAM 450
DB 421 LNPVIYITFNODFRAPRRIICRPWTOTAM 450

```

RESULT 8

US-10-001-073-27
 Sequence 27, Application US/10001073
 Publication No. US20030113725A1
 GENERAL INFORMATION:
 APPLICANT: Liggett, Stephen
 TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
 FILE REFERENCE: 13073-PCT
 CURRENT APPLICATION NUMBER: US/10/001,073
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 27
 LENGTH: 450
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-001-073-27

Query Match
 Best Local Similarity 47.4%; Score 1126.5; DB 15; Length 450;
 Matches 243; Conservative 50; Mismatches 105; Indels 59; Gaps 14;

```

QY 6 PYSVQATAIAAATFTLFTFGNALVILAVTSRLAPQNLFLVSLAAADILVATTI 65
DB 6 PYSVQATAIAAATFTLFTFGNALVILAVTSRLAPQNLFLVSLAAADILVATTI 65
QY 27 PYSVQATAIAAATFTLFTFGNALVILAVTSRLAPQNLFLVSLAAADILVATTI 65
DB 27 PYSVQATAIAAATFTLFTFGNALVILAVTSRLAPQNLFLVSLAAADILVATTI 65
QY 66 IPESLANELLGYWFRRTWCEVYALDVLFCTSSIVHCAISLDRYMAVSRALEY 125
DB 66 IPESLANELLGYWFRRTWCEVYALDVLFCTSSIVHCAISLDRYMAVSRALEY 125
QY 87 IPESLANELLGYWFRRTWCEVYALDVLFCTSSIVHCAISLDRYMAVSRALEY 146
DB 87 IPESLANELLGYWFRRTWCEVYALDVLFCTSSIVHCAISLDRYMAVSRALEY 146
QY 126 PRRKCIITLFWLIAAVISLPPLIKGDDGPPQGRPOCKLNOEAWYILASSIGS 181
DB 126 PRRKCIITLFWLIAAVISLPPLIKGDDGPPQGRPOCKLNOEAWYILASSIGS 181
QY 147 PRRKCIITLFWLIAAVISLPPLIKGDDGPPQGRPOCKLNOEAWYILASSIGS 205
DB 147 PRRKCIITLFWLIAAVISLPPLIKGDDGPPQGRPOCKLNOEAWYILASSIGS 205
QY 182 FAPCLIMILVYRIYLIARNSNRGPRAGKPGQGESKOPRPHDGALASAKLPALASV 240
DB 182 FAPCLIMILVYRIYLIARNSNRGPRAGKPGQGESKOPRPHDGALASAKLPALASV 240
QY 241 ASAREVNGSKSTGEKEGETPEDTGTALPPSMALPNSGQCKEVCASPEDAE 297
DB 241 ASAREVNGSKSTGEKEGETPEDTGTALPPSMALPNSGQCKEVCASPEDAE 297
QY 301 EEEEEECEPOAVPVSPASACSPLOQPOGSRVLTATLRGQVLLGRGVGALGQWRRR 360
DB 301 EEEEEECEPOAVPVSPASACSPLOQPOGSRVLTATLRGQVLLGRGVGALGQWRRR 360
QY 361 AQLTRERFTVLAVVIGVFLCWPFFFSYSLGAIKPKHCKVPHGLPOFFWIGYCNS 420
DB 361 AQLTRERFTVLAVVIGVFLCWPFFFSYSLGAIKPKHCKVPHGLPOFFWIGYCNS 420
QY 421 LNPVIYITFNODFRAPRRIICRPWTOTAM 450
DB 421 LNPVIYITFNODFRAPRRIICRPWTOTAM 450

```

Db 352 ERVAAKASRWGQ--NREKRFVLAIVGVFWCMFPFFTYTLAV---GCSVPRT 406
Qy 407 LFOFFWIGYCNSSLNPIVYITIFNODFRRAFRILCR 443
Db 407 LKFFFWFGYCNSSLNPIVYITIFNODFRRAFRILCR 443

RESULT 9
US-10-001-073-26

; Sequence 26, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001.073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-073-26

Query Match 47.3%; Score 1124.5; DB 15; Length 450;
Best Local Similarity 53.2%; Pred. No. 2.6e-72;
Matches 241; Conservative 49; Mismatches 106; Indels 59; Gaps 14;

Qy 6 PYSVQATPAIAAATTFILFTIFGNALVILAVLTSRSRAPONLFLVSLAADIIVATLI 65
Db 27 PYSQVTLTVCLAGLMLTVFGNVLIIVFTSRALKAPQNFVLSASADILVATLV 86
Qy 66 IPFSLANELGYWYFRRTWCEVYIALDVLFTCTSSIVHLCAISLDRYAASRALEYSKRT 125
Db 87 IPFSLANEMVWGYWYFGKMWCEIYIALDVLFTCTSSIVHLCAISLDRYMSITQAIENLKRT 146
Qy 126 PRKRCITLTVWLAIVSLPPLI---YKGDQOPGRGRPOCKLQDEAWYTLASISGSF 181
Db 147 PRKRCITLTVWLAIVSLPPLI---YKGDQOPGRGRPOCKLQDEAWYTLASISGSF 205
Qy 147 PRKRCITLTVWLAIVSLPPLI---YKGDQOPGRGRPOCKLQDEAWYTLASISGSF 205
Db 147 PRKRCITLTVWLAIVSLPPLI---YKGDQOPGRGRPOCKLQDEAWYTLASISGSF 205
Qy 182 FAPCLIMILVYLRILYIAKR-----SNRGRPRAGGQGESKOPR---PDHGALASAK 233
Db 206 FAPCLIMILVYLRILYIAKR-----SNRGRPRAGGQGESKOPR---PDHGALASAK 265
Qy 234 LPALASVASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQCKEGVCGASP 293
Db 266 AEPLPT-----QNG--APGEPA--GPRDTDALDEES-----SS 298
Qy 294 EDEAEF---EEEEEEBCEPOAVPVSPASCPPLQOPQSGRVLATLRGQVLLRG- 348
Db 299 SDHAERPPGRRPRGRGKAKASQVKPGD--SLPRRG--ATGIGTPAAGPGE 351
Qy 349 --VGAIGQWRRRAQLTREKRFVLAIVGVFLVCMPPFFSYSGAICPKKCKVPHG 406
Db 352 ERVGAASRRKRGQ--NREKRFVLAIVGVFWCMFPFFTYTLAV---GCSVPRT 406
Qy 407 LFOFFWIGYCNSSLNPIVYITIFNODFRRAFRILCR 443
Db 407 LKFFFWFGYCNSSLNPIVYITIFNODFRRAFRILCR 443

RESULT 10
US-10-225-567A-40
; Sequence 40, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-40

Query Match 47.0%; Score 1117.5; DB 15; Length 450;
Best Local Similarity 52.7%; Pred. No. 8.2e-72;
Matches 241; Conservative 52; Mismatches 105; Indels 59; Gaps 13;

Qy 6 PYSVQATPAIAAATTFILFTIFGNALVILAVLTSRSRAPONLFLVSLAADIIVATLI 65
Db 27 PYSQVTLTVCLAGLMLTVFGNVLIIVFTSRALKAPQNFVLSASADILVATLV 86
Qy 66 IPFSLANELGYWYFRRTWCEVYIALDVLFTCTSSIVHLCAISLDRYAASRALEYSKRT 125
Db 87 IPFSLANEMVWGYWYFGKMWCEIYIALDVLFTCTSSIVHLCAISLDRYMSITQAIENLKRT 146
Qy 126 PRKRCITLTVWLAIVSLPPLI---YKGDQOPGRGRPOCKLQDEAWYTLASISGSF 181
Db 147 PRKRCITLTVWLAIVSLPPLI---YKGDQOPGRGRPOCKLQDEAWYTLASISGSF 205
Qy 182 FAPCLIMILVYLRILYIAKR-----SNRGRPRAGGQGESKOPR---PDHGALASAK 233
Db 206 FAPCLIMILVYLRILYIAKR-----SNRGRPRAGGQGESKOPR---PDHGALASAK 265
Qy 234 LPALASVASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQCKEGVCGASP 293
Db 266 AEPLPT-----QNG--APGEPA--GPRDTDALDEES-----SS 298
Qy 294 EDEAEF---EEEEEEBCEPOAVPVSPASCPPLQOPQSGRVLATLRGQVLLRGV 349
Db 299 SDHAERPPGRRPRGRGKAKASQVKPGD--SLRGARRRG-----GRLQGRGR 351
Qy 350 GAIGQWRRRAQL--TREKRFVLAIVGVFLVCMPPFFSYSGAICPKKCKVPHG 406
Db 352 SASGLP--RRRAGGQNLKRTFTVLAIVGVFWCMFPFFTYTLAV---GCSVPRT 406
Qy 407 LFOFFWIGYCNSSLNPIVYITIFNODFRRAFRILCR 443
Db 407 LKFFFWFGYCNSSLNPIVYITIFNODFRRAFRILCR 443

RESULT 11
US-10-225-567A-44
; Sequence 44, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-44

Query Match 45.4%; Score 1078.5; DB 15; Length 461;
 Best Local Similarity 52.2%; Pred. No. 5.1e-69;
 Matches 240; Conservative 41; Mismatches 104; Indels 75; Gaps 12;

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OY 7 YSVQATTAIAAATITLFTTIFGNALVLAVALTSRLRAPQNLFLVSLAADIIVATLTI 66
DB 46 YSAGAVAGLAAVGFLIVFTVGNVLAVALTSRLRAPQNLFLVSLAADIIVATLTI 105
OY 67 PPSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISIDRYWAVSRALVENSRTKP 126
DB 106 PPSLANELLMAVYFGQWCGVYALDVLFCTSSIVHLCAISIDRYWAVSRALVENSRTKP 165
OY 127 RRIKCIITLWMLAAVYSLPPLI--YKDGQGPQGR--POCKLNOAMTYIASISGSFF 182
DB 166 RRVKATIVAAVWLISAVISFPLVSLYR-----QPDGAAYPOCGLANDETWTYLLSSCIGSFF 220
OY 183 APCLMILVLYRIYILAKSNRGRPRAGGPGQESKOPRBDHGALASAKLPALASVAS 242
DB 221 APCLMIGLVYARIYVAVAKRTR-----TLSEKRAPVPPDGAS 257
OY 243 AREVNGHSKSGEKEGETPEDTGT--RALPPSW-----AALPPSG-----QSQ 284
DB 258 PTTENGGLGAAAGEAR-----TGTARPREPTWSTRRAQRGAPGELRGRARRAGA 310
OY 285 KEGVCGASPEDEAESEEESECEPQAVPVSASCSPPLOQPGSRVATLNG--QV 343
DB 311 EGGAGGA-----DQGAGPGAAQSGALTYASRSP--GPGGRLSRASRSVEF 354
OY 344 ILGKGVGAIGQWRRRAQLTREKRTFLAVVIGVFLCMFPFFSYSGAICPQKCKV 403
DB 355 FLSSRRRARSVCRRKVAQ--AREKRTFVLAVWGVFLCMFPFFYSYLSYICREACV 413
OY 404 PHGFPOFFWICGNSLNPIYITIFNODFRRAFRILCR 443
DB 414 PGPLFFPFWIGCNSLNPIYITVFNODFRPSFKHILFR 453

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RESULT 12
 US-10-001-073-46

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/ Sequence 46, Application US/10001073
/ Publication No. US20030113725A1
/ GENERAL INFORMATION:
/ APPLICANT: Liggett, Stephen
/ TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
/ FILE REFERENCE: 13073-PCR
/ CURRENT APPLICATION NUMBER: US/10/001.073
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 46
/ LENGTH: 458
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-001-073-46

```

Query Match 45.0%; Score 1071; DB 15; Length 458;
 Best Local Similarity 53.6%; Pred. No. 1.7e-68;
 Matches 241; Conservative 44; Mismatches 107; Indels 58; Gaps 14;

```

OY 7 YSVQATTAIAAATITLFTTIFGNALVLAVALTSRLRAPQNLFLVSLAADIIVATLTI 66
DB 46 YSAGAVAGLAAVGFLIVFTVGNVLAVALTSRLRAPQNLFLVSLAADIIVATLTI 105
OY 67 PPSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISIDRYWAVSRALVENSRTKP 126
DB 106 PPSLANELLMAVYFGQWCGVYALDVLFCTSSIVHLCAISIDRYWAVSRALVENSRTKP 165
OY 127 RRIKCIITLWMLAAVYSLPPLI--YKDGQGPQGR--POCKLNOAMTYIASISGSFF 182
DB 166 RRVKATIVAAVWLISAVISFPLVSLYR-----QPDGAAYPOCGLANDETWTYLLSSCIGSFF 220

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OY 183 APCLMILVLYRIYILAKSNR--RPRAGGPGQESKOPRBDHGALASAKLPALASV 240
DB 221 APCLMIGLVYARIYVAVAKRTRTLSEKRAPVPP-----DASPTTENG-----LGAA 267
OY 241 ASAREVNGH-----SKSGEKEGETPEDTGTALPPSMALPNSQO-----GQKEGVGASPE 294
DB 268 AGAGE--NGHCAPPADVEDESSAAAEERRRR-----GALRRGRRRAGAGGAGADGQ 321
OY 295 DEAESEEESECEPQAVPVSASCSPPLOQPGSRVATLNG--QVILGRGVGATG 353
DB 322 GAAS-----GALTYASRSP--GPGGRLSRASRSVEFPLSRRRARS 361
OY 354 GQWRRRAQLTREKRTFVLAVVIGVFLCMFPFFSYSGAICPQKCKVPHGLQOFFFW 413
DB 362 SVCRKRVAG--AREKRTFVLAVWGVFLCMFPFFYSYLSYICRBACQVPPGLFKFFFW 420
OY 414 IGYCNSLNPIYITIFNODFRRAFRILCR 443
DB 421 IGYCNSLNPIYITVFNODFRPSFKHILFR 450

```

RESULT 13
 US-10-001-073-44

```

/ Sequence 44, Application US/10001073
/ Publication No. US20030113725A1
/ GENERAL INFORMATION:
/ APPLICANT: Liggett, Stephen
/ TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
/ FILE REFERENCE: 13073-PCR
/ CURRENT APPLICATION NUMBER: US/10/001.073
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 44
/ LENGTH: 462
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-001-073-44

```

Query Match 45.0%; Score 1070; DB 15; Length 462;
 Best Local Similarity 53.6%; Pred. No. 2.1e-68;
 Matches 241; Conservative 45; Mismatches 110; Indels 54; Gaps 14;

```

OY 7 YSVQATTAIAAATITLFTTIFGNALVLAVALTSRLRAPQNLFLVSLAADIIVATLTI 66
DB 46 YSAGAVAGLAAVGFLIVFTVGNVLAVALTSRLRAPQNLFLVSLAADIIVATLTI 105
OY 67 PPSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISIDRYWAVSRALVENSRTKP 126
DB 106 PPSLANELLMAVYFGQWCGVYALDVLFCTSSIVHLCAISIDRYWAVSRALVENSRTKP 165
OY 127 RRIKCIITLWMLAAVYSLPPLI--YKDGQGPQGR--POCKLNOAMTYIASISGSFF 182
DB 166 RRVKATIVAAVWLISAVISFPLVSLYR-----QPDGAAYPOCGLANDETWTYLLSSCIGSFF 220
OY 183 APCLMILVLYRIYILAKSNR--RPRAGGPGQESKOPRBDHGALASAKLPALASV 240
DB 221 APCLMIGLVYARIYVAVAKRTRTLSEKRAPVPP-----DASPTTENG-----LGAA 267
OY 241 ASAREVNGH-----SKSGEKEGETPEDTGTALPPSMALPNSQO-----GQKEGVGASPE 294
DB 268 AGAGE--NGHCAPPADVEDESSAAAEERRRR-----GALRRGRRRAGAGGAGAGA--- 318
OY 295 DEAESEEESECEPQAVPVSASCSPPLOQPGSRVATLNG--QVILGRGVGATG 353
DB 319 -----DQGAGPGAAQSGALTYASRSP--GPGGRLSRASRSVEFPLSRRRARS 365
OY 354 GQWRRRAQLTREKRTFVLAVVIGVFLCMFPFFSYSGAICPQKCKVPHGLQOFFFW 413
DB 366 SVCRKRVAG--AREKRTFVLAVWGVFLCMFPFFYSYLSYICRBACQVPPGLFKFFFW 424
OY 414 IGYCNSLNPIYITIFNODFRRAFRILCR 443

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Db 425 IGCNSSLNPVITYVFNODFRSPFGLILFR 454

RESULT 14
US-10-060-795B-4

; Sequence 4, Application US/10060795B
; Publication No. US20030040022A1
; GENERAL INFORMATION:
; APPLICANT: Civelis, Olivier
; APPLICANT: Bunzow, James R.
; APPLICANT: Grandy, David K.
; APPLICANT: Machida, Curtis A.
; TITLE OF INVENTION: Dopamine Receptors and Genes
; FILE REFERENCE: 90-1092-CCC
; CURRENT APPLICATION NUMBER: US/10/060,795B
; CURRENT FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: 09/238977
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 08/474892
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/973588
; PRIOR FILING DATE: 1992-11-09
; PRIOR APPLICATION NUMBER: 07/438544
; PRIOR FILING DATE: 1989-11-20
; PRIOR APPLICATION NUMBER: 07/27373
; PRIOR FILING DATE: 1988-11-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-795B-4

Query Match 40.3%; Score 959; DB 15; Length 307;
Best Local Similarity 43.9%; Pred. No. 1,1e-60;
Matches 194; Conservative 42; Mismatches 40; Indels 166; Gaps 4;

QY 6 PYSQATNAIAATFLITFLITFGNALVITLVSRSRAPQNFVLSLAADILVATLI 65
DB 27 PYSQAVTLTVLACLAGLMLTLVFGNVVITLVFTSSRALKAPQNFIVLSADILVATLV 86
QY 66 IPFSLANELLGYWFRRTWCEVYALDVLCTSSIVHLCAISLDRYAVASRALEYSKRT 125
DB 87 LPFSLANENVQWTFGKTCWCIYALDVLCTSSIVHLCAISLDQRYSTISITPAIEYMLKRT 146
QY 126 PRRKICITLTVWLTAAVLSLPPLI-----YKGDGQPPRGRPOCKLNOEAWYILASSIGSF 181
DB 147 PRRKAIITITWVLSAVISFPPLISIEKGGGGGPPF-AEPRCHINQKMWVVISCTGSF 205
QY 182 PAPCLMILVYLRITLAKSNRRGPRKGGPGGSGKQPPDHGALASAKLPALASVA 241
DB 206 FAPLLIMLVYVRYOIAK----- 224
QY 242 SARVNHGHSKSTGKEBGETPEDTGTALPPSMAALPNSGGQKQGVGASPEDEABEE 301
DB 225 ----- 224
QY 302 EEEBEEBEEBOAVPVSPASCSPPLOQPOGSRVLTALRGVLLGRGVAIGQMMWRRA 361
DB 225 -----RT 227
QY 362 QLTREKPTFVLAIVGVFVLCMPFPFSPSLSGALICPRGKCVPRGLFOFPFWIYCNSSL 421
DB 228 RVPREKFTFVLAVIGVFWCMPPFFFTYTLTAV---GCSVPRTLKFPFMPYCNSSL 284
QY 422 NPVITYTENDPRAFRILCR 443
DB 285 NPVITYTLFNHDFRRAFWILCR 306

RESULT 15

US-09-782-980-84
; Sequence 84, Application US/09782980
; Patent No. US20020072089A1
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran M.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Buefield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIPE, TRASH, BGSF, LRSG, AND
; TITLE OF INVENTION: STMT PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: NMI-121CP
; CURRENT APPLICATION NUMBER: US/09/782,980
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/014,348
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/086,892
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/296,208
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 09/063,950
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 09/561,381
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,810
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/087,121
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/672,721
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/049,799
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-980-84

Query Match 27.4%; Score 651; DB 9; Length 601;
Best Local Similarity 33.1%; Pred. No. 2,2e-38;
Matches 164; Conservative 72; Mismatches 181; Indels 78; Gaps 10;

QY 16 AATFLITFLITFGNALVITLVSRLAPQNFVLSLAADILVATLIIPFSLANELL 75
DB 113 ALVIVITVITIGNITLVISVFTYKPLRIVQNFIVSLAVADLVALLVLPFVAVSIL 172
QY 76 GYWFRRTWCEVYALDVLCTSSIVHLCAISLDRYAVASRALEYSKRTPRRKICITLT 135
DB 173 GRWFFGHLCKLWLTCTVLCCTSSIMLCAIALDRYVAITDPINVAOKRTVGRVLLISG 232
QY 136 VWLIAVVISLPPLIYKGDGQPPRGRPOCKLNOEAWYILASSIGSPAPCLIMTVYIRI 195
DB 233 VWLSTLISSPPLIGANDWDEFTSATPCETLSQRGVITYISLGSFFIPLAINTVYIRI 292
QY 196 YL-----IAKSNRRGPRKGGPG----- 214
DB 293 FVATRRRLRRARANKNTIALKSTELPMANSPVAANSNGSKRLSLAGWLCGRDRAQ 352

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QY 215 -----QGESKQPRPD-----HGALASAK-----LPALASVASAREVNGHSKS 252
Db 353 FATPMI QNDQESISSETHQPODSSKAGPHGNSDPQOQHVVVLYKSRRAKTDSIKHKT 412
QY 253 TG--EKEGETPEDTGTTRALPPSWALPNSGQ--OKEGVCA SPEDAE EEEEEEE 307
Db 413 RGRKRSOSSSTCEPHGEQOL-----LPAGDGGSCQPGGHSGGKSDAISTESGSDP 466
QY 308 ECEPQAVPVSPASACSPPLQOPQGSRYLATLRGQVLLGRGVGAI GCMRRRAQLTREK 367
Db 467 KGC-IQVCVTQADQCTSLKLPPOSSTGVAAVSVEPLOKKTSGVNQFIEKXISLSKER 525
QY 368 RFTVLA VITGVFVLCWFPPEFSYSLGAI CPKHCKVPHGLFQ-FFWTGYCNSLNPVY 426
Db 526 RAARTLGIIMGVFVLCWLPPEFLMYVILPFCQTC--PTMKXNFTTWLGYTNSGILNPVY 583
QY 427 TIFNODPRRAFRRL 441
Db 584 TIFNLDYRRRAFRRL 598

```

Search Completed: February 6, 2004, 18:22:04
 Job time : 32.1003 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 18:13:11 ; Search time 16.5552 Seconds
(without alignments)
2614.040 Million cell updates/sec

Title: US-09-692-077D-7

Perfect score: 2378
Sequence: 1 MDHDPYSVQNTAIAAAIT.....QDFRRAPRRILCRPWTQTAW 450

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2370	99.7	450	2 A37223	alpha-2B-adrenergic
2	1984	83.4	448	2 151883	alpha-2B-adrenergic
3	1981	83.3	453	2 A35642	alpha-2B-adrenergic
4	1940	81.6	455	2 S28221	alpha-2-C2 adrener
5	1425.5	59.9	276	2 153161	alpha-2-adrenergic
6	1148.5	48.3	450	2 B40392	alpha-2-adrenergic
7	1141.5	48.0	450	2 149481	alpha-2-adrenergic
8	1124.5	47.3	450	2 A34169	alpha-2A-adrenergic
9	1118.5	47.0	450	2 A38316	alpha-2-adrenocpt
10	1106.5	46.5	432	2 150829	alpha-2-adrenocpt
11	1091.5	45.9	450	2 JH0190	alpha-2-adrenergic
12	1083	45.5	458	2 A40392	alpha-2-adrenergic
13	1082	45.5	458	2 149480	alpha-2-adrenergic
14	1079	45.4	458	2 A48392	alpha-2C4 adrenoce
15	1078.5	45.4	461	2 A31237	alpha-2C4-adrenergic
16	1074	45.2	458	2 A37869	alpha-2B-adrenergic
17	685	28.8	484	2 S58868	G protein-coupled
18	651	27.4	601	2 S12004	tyramine receptor
19	651	27.4	601	2 JH0170	octopamine receptor
20	645.5	27.1	379	2 JG6178	serotonin receptor
21	598	25.1	476	2 JG5042	G protein-coupled
22	589	24.8	422	2 JH0315	serotonin receptor
23	585.5	24.6	511	2 C56849	dopamine receptor
24	585.5	24.6	517	2 A45121	alpha-1B adrenergi
25	585	24.6	444	1 D1B0D2	dopamine receptor
26	584.5	24.6	421	2 149375	serotonin receptor
27	584.5	24.6	515	2 A40491	alpha-1-adrenergic
28	582.5	24.5	442	1 D1XLD2	dopamine receptor
29	582.5	24.5	564	2 A38271	serotonin receptor

30	581.5	24.5	514	2 D56849	dopamine receptor-
31	578.5	24.3	387	1 D1HSD4	dopamine receptor
32	578.5	24.3	444	1 DYMDU2	dopamine receptor
33	578.5	24.3	444	1 S08146	dopamine receptor
34	578	24.3	443	1 D1HSD2	dopamine receptor
35	577.5	24.3	422	2 138209	serotonin receptor
36	577.5	24.3	560	2 A38731	serotonin receptor
37	576	24.2	509	2 A47174	serotonin receptor
38	574.5	24.2	515	2 JG1525	alpha-1B-adrenergic
39	573.5	24.1	377	2 B30341	G protein-coupled
40	571.5	24.0	377	2 S68423	serotonin receptor
41	568.5	23.9	572	2 139369	alpha-1A-adrenergic
42	565.5	23.8	501	2 JH0447	alpha-1A-adrenergic
43	565.5	23.8	501	2 138653	hypothetical prote
44	564.5	23.7	430	2 T16079	hypothetical prote
45	555.5	23.4	377	2 A53279	serotonin receptor

ALIGNMENTS

RESULT 1
A37223
alpha-2B-adrenergic receptor - human
N:Alternate names: alpha-2C2-adrenergic receptor
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 29-Oct-1999
C:Accession: A37223, J39407, S14308, A36158
R:Weinshank, R.L.; Zgombick, J.M.; Macchi, M.; Adham, N.; Lichtblau, H.; Branchek, T.A.; Mol. Pharmacol. 38, 681-688, 1990
A:Title: Cloning, expression, and pharmacological characterization of a human alpha-2B-adrenergic receptor
A:Reference number: A37223; MUID:91042469; PMID:2172775
A:Accession: A37223
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-450 <MB>
R:Romasney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, T.L.; Caron, R.; Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S. FEBS Lett. 280, 241-244, 1991
A:Title: Identification of an additional gene belonging to the alpha(2) adrennergic receptor family
A:Reference number: J39407; MUID:90311349; PMID:2164221
A:Accession: S14308
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 56-185 <CH>
A:Cross-references: GB:X59684; NID:928635
A:Note: this translation is not annotated in GenBank entry HSALPH218, release 111.0
R:Chang, A.C.; Ho, T.F.; Chang, N.C. Biochem. Biophys. Res. Commun. 172, 817-823, 1990
A:Title: In vitro amplification by polymerase chain reaction of a partial gene encoding the alpha-2B-adrennergic receptor
A:Reference number: A36158; MUID:91054503; PMID:2173582
A:Accession: A36158
A:Molecule type: DNA
A:Residues: 95-361, 'OL', 364-389 <CHA>
A:Cross-references: GB:M8742; NID:9177867; PIDN:AAA62823.1; PID:9177868
C:Genetics:
A:Gene: GDB:ADRA2B; ADRA2B; ADRA2B1; ADRA2B1
A:Cross-references: GDB:120539; OMIM:104260
A:Map position: 2p13-2q13
C:Superfamily: G protein-coupled receptor; glycoprotein; transmembrane protein
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
Query Match 99.7%; Score 2370; DB 2; Length 450;
Best Local Similarity 99.6%; Pred. No. 3.3e-154;
Matches 448; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY      1 MDHDPYSVQATTAIAAATITLLFTIFGNALVLAVALTSRSIRAPONLFLVSLAADI 60
DB      1 MDHDPYSVQATTAIAAATITLLFTIFGNALVLAVALTSRSIRAPONLFLVSLAADI 60
QY      61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLCFTSSIVHLCALSLDRYMAVSRALEY 120
DB      61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLCFTSSIVHLCALSLDRYMAVSRALEY 120
QY      121 NSKRTPRRIKCIITLWMLAAVLSLPLIYKDGQPPRGRPOCKLNOEAMWYLLASISGS 180
DB      121 NSKRTPRRIKCIITLWMLAAVLSLPLIYKDGQPPRGRPOCKLNOEAMWYLLASISGS 180
QY      181 FFAPCLIMILVYLRIRYIAKRSNRGRPRAGKGGGSGKOPRPHGALASAKLPALASV 240
DB      181 FFAPCLIMILVYLRIRYIAKRSNRGRPRAGKGGGSGKOPRPHGALASAKLPALASV 240
QY      241 ASARRENVGHSKSTGKEGEGTPEDTGTALPPSWAALPNSGQGGKEGVCGASPEDAEAE 300
DB      241 ASARRENVGHSKSTGKEGEGTPEDTGTALPPSWAALPNSGQGGKEGVCGASPEDAEAE 300
QY      301 EEEEEECEEPQAVPVSPASCPPLQOPQGSRLVATLRGQVTLGRGVGALGGQWRRR 360
DB      301 EEEEEECEEPQAVPVSPASCPPLQOPQGSRLVATLRGQVTLGRGVGALGGQWRRR 360
QY      361 AQLTERKFTFLAVAVIGFVLCWPFPPFSYSLGALCPKCKVPHGLFOFFFWIGYCNS 420
DB      361 AQLTERKFTFLAVAVIGFVLCWPFPPFSYSLGALCPKCKVPHGLFOFFFWIGYCNS 420
QY      421 LNPVITYTFENDFRARRRILCRPWTOTAW 450
DB      421 LNPVITYTFENDFRARRRILCRPWTOTAW 450

```

RESULT 2

```

151883
alpha-2B-adrenergic receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #ext_change 13-Aug-1999
C/Accession: I51883
R/Le Joesec, M.; Cloix, J.F.; Pecquery, R.; Giudicelli, Y.; Dause, J.P.
A/Title: Differential sodium regulation between salt-sensitive and salt-resistant Sabra
A/Reference number: I51883; MUID:95275492; PMID:7755946
A/Accession: I51883
A/Molecule type: DNA
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-448 <RES>
A/Cross-references: EMBL:X74400; NID:9840862; PIDN:CAA52411.1; PID:940816
C/Superfamily: vertebrate rhodopsin
C/Keywords: neurotransmitter receptor

```

Query Match 83.4%; Score 1984; DB 2; Length 448;
Best Local Similarity 83.8%; Pred. No. 6.5e-128;

Matches 378; Conservative 24; Mismatches 45; Indels 4; Gaps 2;

```

QY      1 MDHDPYSVQATTAIAAATITLLFTIFGNALVLAVALTSRSIRAPONLFLVSLAADI 60
DB      1 MDHDPYSVQATTAIAAATITLLFTIFGNALVLAVALTSRSIRAPONLFLVSLAADI 60
QY      61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLCFTSSIVHLCALSLDRYMAVSRALEY 120
DB      61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLCFTSSIVHLCALSLDRYMAVSRALEY 120
QY      121 NSKRTPRRIKCIITLWMLAAVLSLPLIYKDGQPPRGRPOCKLNOEAMWYLLASISGS 180
DB      121 NSKRTPRRIKCIITLWMLAAVLSLPLIYKDGQPPRGRPOCKLNOEAMWYLLASISGS 180
QY      181 FFAPCLIMILVYLRIRYIAKRSNRGRPRAGKGGGSGKOPRPHGALASAKLPALAS- 239
DB      181 FFAPCLIMILVYLRIRYIAKRSNRGRPRAGKGGGSGKOPRPHGALASAKLPALAS- 239
QY      240 VASARENVGHSKSTGKEGEGTPEDTGTALPPSWAALPNSGQGGKEGVCGASPEDAEAE 299
DB      240 VASARENVGHSKSTGKEGEGTPEDTGTALPPSWAALPNSGQGGKEGVCGASPEDAEAE 299

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DB      241 LSSVGEANGHPKPREXEGEGTPEDEARALPPTMSALPRSOGQKGTGATNE---EG 297
QY      300 EEEEEECEEPQAVPVSPASCPPLQOPQGSRLVATLRGQVTLGRGVGALGGQWRRR 359
DB      298 XEEDEEVECEEPQAVPVSPASCPPLQOPQGSRLVATLRGQVTLGRGVGALGGQWRRR 357
QY      360 RAQLTERKFTFLAVAVIGFVLCWPFPPFSYSLGALCPKCKVPHGLFOFFFWIGYCNS 419
DB      358 RTQLSREKFTFLAVAVIGFVLCWPFPPFSYSLGALCPKCKVPHGLFOFFFWIGYCNS 417
QY      420 SLNPVITYTFENDFRARRRILCRPWTOTAW 450
DB      418 SLNPVITYTFENDFRARRRILCRPWTOTAW 448

```

RESULT 3

```

A35642
alpha-2B-adrenergic receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #ext_change 13-Aug-1999
C/Accession: A35642
R/Zeng, D.; Harrison, J.K.; D'Angelo, D.D.; Barber, C.M.; Tucker, A.L.; Lu, Z.; Lynch, K
A/Title: Molecular characterization of a rat alpha-2B-adrenergic receptor.
A/Reference number: A35642; MUID:90222177; PMID:2158103
A/Accession: A35642
A/Molecule type: mRNA
A/Residues: 1-453 <ZEN>
A/Cross-references: GB:M32061; NID:9202589; PIDN:AAA0635.1; PID:9202590
A/Note: 169-Phe was also found
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

```

Query Match 83.3%; Score 1981; DB 2; Length 453;
Best Local Similarity 83.8%; Pred. No. 1.1e-127;

Matches 378; Conservative 24; Mismatches 45; Indels 4; Gaps 2;

```

QY      1 MDHDPYSVQATTAIAAATITLLFTIFGNALVLAVALTSRSIRAPONLFLVSLAADI 60
DB      6 MDHDPYSVQATTAIAAATITLLFTIFGNALVLAVALTSRSIRAPONLFLVSLAADI 65
QY      61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLCFTSSIVHLCALSLDRYMAVSRALEY 120
DB      66 VATLIIPFSLANELLGWYFRRTWCEVYALDVLCFTSSIVHLCALSLDRYMAVSRALEY 125
QY      121 NSKRTPRRIKCIITLWMLAAVLSLPLIYKDGQPPRGRPOCKLNOEAMWYLLASISGS 180
DB      126 NSKRTPRRIKCIITLWMLAAVLSLPLIYKDGQPPRGRPOCKLNOEAMWYLLASISGS 185
QY      181 FFAPCLIMILVYLRIRYIAKRSNRGRPRAGKGGGSGKOPRPHGALASAKLPALAS- 239
DB      186 FFAPCLIMILVYLRIRYIAKRSNRGRPRAGKGGGSGKOPRPHGALASAKLPALAS- 239
QY      240 VASARENVGHSKSTGKEGEGTPEDTGTALPPSWAALPNSGQGGKEGVCGASPEDAEAE 299
DB      246 LSSVGEANGHPKPREXEGEGTPEDEARALPPTMSALPRSOGQKGTGATNE---EG 302
QY      300 EEEEEECEEPQAVPVSPASCPPLQOPQGSRLVATLRGQVTLGRGVGALGGQWRRR 359
DB      303 DEEDDEVECEEPQAVPVSPASCPPLQOPQGSRLVATLRGQVTLGRGVGALGGQWRRR 362
QY      360 RAQLTERKFTFLAVAVIGFVLCWPFPPFSYSLGALCPKCKVPHGLFOFFFWIGYCNS 419
DB      363 RTQLSREKFTFLAVAVIGFVLCWPFPPFSYSLGALCPKCKVPHGLFOFFFWIGYCNS 422
QY      420 SLNPVITYTFENDFRARRRILCRPWTOTAW 450
DB      423 SLNPVITYTFENDFRARRRILCRPWTOTAW 453

```

RESULT 4

S28221

alpha-2-C2 adrenergic receptor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
 C/Accession: S88221; JH0693
 R/Chen, W.M.; Chang, A.C.; Shie, B.J.; Chang, Y.H.; Chang, N.C.A.
 Biochim. Biophys. Acta 1171, 219-223, 1992
 A/Title: Molecular cloning and characterization of a mouse alpha(2)C2 adrenoceptor subty
 A/Reference number: S88221; MUID:93129625; PMID:1336396
 A/Accession: S88221
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-455 <CH>
 A/Cross-references: EMBL:M94583
 A/Note: the authors translated the codon CCA for residue 161 as Phe, ACT for residue 337
 R/Christie, A.J.; Link, R.E.; Dault, D.A.; Barsh, G.S.; Kobilka, B.K.
 Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992
 A/Title: Cloning and expression of the mouse homolog of the human alpha2-C2 adrenergic r
 A/Reference number: JH0693; MUID:92378586; PMID:1354956
 A/Accession: JH0693
 A/Molecule type: DNA
 A/Residues: 6-228, 231-455 <CH>
 A/Cross-references: GB:L00979; NID:G191547; PIDN:AAA37131.1; PID:G191548
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein
 F/18-43/Domain: transmembrane #status predicted <TM1>
 F/55-81/Domain: transmembrane #status predicted <TM2>
 F/90-115/Domain: transmembrane #status predicted <TM3>
 F/134-158/Domain: transmembrane #status predicted <TM4>
 F/173-199/Domain: transmembrane #status predicted <TM5>
 F/377-402/Domain: transmembrane #status predicted <TM6>
 F/410-435/Domain: transmembrane #status predicted <TM7>

Query Match 81.6%; Score 1940; DB 2; Length 455;
 Best Local Similarity 83.0%; Pred. No. 6-6e-15;
 Matches 376; Conservative 22; Mismatches 49; Indels 6; Gaps 3;

QY 1 MDHDPYSVQATAIAAATFLILFTFGNALVTLAVTSRSLRAPQNLPLVSLAAADIL 60
 DB 6 MVHDEPYSVQATAIAAATFLILFTFGNALVTLAVTSRSLRAPQNLPLVSLAAADIL 65

QY 61 VATTIIPPSLANELLGVIYFRRTWCEVYALADVLFTSSIVHLCAISIDRYMAVSRALEY 120
 DB 66 VATTIIPPSLANELLGVIYFRRTWCEVYALADVLFTSSIVHLCAISIDRYMAVSRALEY 125

QY 121 NSKRTPRRIKIIITLWMLIAVISLPLIYKGDGPQPRGPOCKNDQEAAYIIASSIGS 180
 DB 126 NSKRTPRRIKIIITLWMLIAVISLPLIYKGDGPQPRGPOCKNDQEAAYIIASSIGS 185

QY 181 PFAPCLIMILVYLRIYLAIRKSNRGPRAKGPQSGSKOPRPD--HGALASAKLPALA 238
 DB 186 PFAPCLIMILVYLRIYLAIRKSNRGPRAKGPQSGSKOPRPD--HGALASAKLPALA 245

QY 239 S-VASAEVNGSHKSTGEKEGETPEDTGTALPPSMAALPNSGQKEGVGASPEDEA 297
 DB 246 SPLSSVGEANGHPKPREKEGETPEDPEALALPPNMSALPRSVQDDKGTGATKAKGA 305

QY 298 EEEEEEVEECPCQVAPVSPASACSPPLQPGSGRYLATLRQVILGRVCAIGGQW 357
 DB 306 ---EEDEEEVEECPCQVAPVSPASACSPPLQPGSGRYLATLRQVILGRVCAIGGQW 362

QY 358 RRRARQLREKRFVTLAVIGVFLCMPPFFSYSLGICPKHCKVPHGLPQFFWIGYC 417
 DB 363 RRRARQLREKRFVTLAVIGVFLCMPPFFSYSLGICPKHCKVPHGLPQFFWIGYC 422

QY 418 NSSLNPIYITIFNODPRRAFRRIICRPMTQTAM 450
 DB 423 NSSLNPIYITIFNODPRRAFRRIICRPMTQTAM 455

RESULT 5
 153161
 alpha-2-adrenergic receptor, isolets of Langerhans - rat (fragment)
 C/Species: Rattus sp. (rat)

C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 30-May-1997
 C/Accession: 153161
 R/Wang, S.Y.; Pilkey, D.T.
 Diabetes 43, 127-136, 1994
 A/Title: Identification in islets of Langerhans of a new rat alpha 2-adrenergic receptor
 A/Reference number: 153161; MUID:94085695; PMID:8262309
 A/Accession: 153161
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-276 <RES>
 A/Cross-references: GB:S67316; NID:G456949
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: neurotransmitter receptor

Query Match 59.9%; Score 1425.5; DB 2; Length 276;
 Best Local Similarity 98.2%; Pred. No. 4.5e-90;
 Matches 274; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 96 CTSSIVHLCAISIDRYMAVSRALEYNSKRTPRRIKIIITLWMLIAVISLPLIYKDDG 155
 DB 1 CTSSIVHLCAISIDRYMAVSRALEYNSKRTPRRIKIIITLWMLIAVISLPLIYKDDG 60

QY 156 PQRGRPOCKLNDQEAAYIIASSIGSPAPCLIMILVYLRIYLAIRKSNRGPRAKGPQ 215
 DB 61 PQRGRPOCKLNDQEAAYIIASSIGSPAPCLIMILVYLRIYLAIRKSNRGPRAKGPQ 120

QY 216 GESKOPRPHDGALASAKLPALASVASAREVNGSKSTGKEGETPEDTGTALPPSWA 275
 DB 121 GESKOPRPHDGALASAKLPALASVASAREVNGSKSTGKEGETPEDTGTALPPSWA 180

QY 276 ALPNSGQKEGVGASPEDAESEEESEECPCQVAPVSPASACSPPLQPGSGRY 335
 DB 181 ALPNSGQKEGVGASPEDAESEEESEECPCQVAPVSPASACSPPLQPGSGRY 237

QY 336 LATLRQVILGRVCAIGGQWRRRAQLTREKRTFYLA 374
 DB 238 LATLRQVILGRVCAIGGQWRRRAQLTREKRTFYLA 276

RESULT 6
 B40392
 alpha-2-adrenergic receptor (clone RG10) - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
 C/Accession: B40392
 R/Lanier, S.M.; Downing, S.; Duzic, B.; Homcy, C.J.
 J. Biol. Chem. 266, 10470-10478, 1991
 A/Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic rece
 A/Reference number: A40392; MUID:91244823; PMID:1645350
 A/Accession: B40392
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-450 <LAN>
 A/Cross-references: GB:M62372; NID:G206615; PIDN:AAA42034.1; PID:G206616
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 48.3%; Score 1148.5; DB 2; Length 450;
 Best Local Similarity 52.3%; Pred. No. 5.4e-71;
 Matches 243; Conservative 51; Mismatches 96; Indels 75; Gaps 12;

QY 6 PYSGVQATAIAAATFLILFTFGNALVTLAVTSRSLRAPQNLPLVSLAAADILVATLI 65
 DB 27 PYSGVQATAIAAATFLILFTFGNALVTLAVTSRSLRAPQNLPLVSLAAADILVATLI 86

QY 66 IFFSLANELLGVIYFRRTWCEVYALADVLFTSSIVHLCAISIDRYMAVSRALEYNSKRT 125
 DB 87 IFFSLANELLGVIYFRRTWCEVYALADVLFTSSIVHLCAISIDRYMAVSRALEYNSKRT 146

QY 126 PRRIKIIITLWMLIAVISLPLI---YKGDGPQPRGPOCKLNDQEAAYIIASSIGSF 182
 DB 147 PRRIKIIITLWMLIAVISLPLI---YKGDGPQPRGPOCKLNDQEAAYIIASSIGSF 206

QY 183 ACCLIMILVRLIYLIAK-----SNRGPRAKGGPGGSGKPR---PDHGALASAKT 234
 DB 207 APCLIMILVRLIYLIAKRRTRVPPSRGPDACSAPGADRRPNAVAPRGGAGTGAAGA 266
 QY 235 PALASVASAREVNGSHKSTGEKEGETPEDTGTALPSPMAALPNSGGQKEGVCGASPE 294
 DB 267 EPLPT-----QLNG-----APGE-----PAPT-----RPR 286
 QY 295 DEAEEREEEREEEREECPQAVPVPSPASCPPLQOGSRYLATLR-GQVLGRGVALG 353
 DB 287 DGDALDESSSSSEHARPPQGPQKBERG-----PRAKGTAKASQVKGDSLRRRGGCAAG 341
 QY 354 -----GQWRR-----RAQLTREKRTFTVLAVIGVPLCMFPFFSYSLGACIP 398
 DB 342 PGASGGSGEERAGAKASRWGRGRONREKRTFTVLAVIGVPLCMFPFFSYSLGACIP 398
 QY 399 KICKVPHGLFQFFPIGVCNSLNDVYTTTINODFRAPRILCR 443
 DB 400 -GCPVYQLFNFQFFWFGVCNSLNDVYTTTINODFRAPRILCR 443

RESULT 7
 149481
 alpha-2 adrenergic receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C:Accession: 149481
 R:Link, R.: Daunt, D.; Barb, G.S.; Chruscinski, A.; Kobilka, B.
 M1: Pharmacol. 42, 16-27, 1992
 A:Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and its
 A:Reference number: 149480; PMID:92342131; PMID:1355249
 A:Accession: 149481
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-450 <RES>
 A:Cross-references: GB:M99377; NID:G191882; PIDN:AAA37213.1; PID:G191883
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 48.0%; Score 1141.5; DB 2; Length 450;
 Best Local Similarity 52.4%; Pred. No. 1.6e-70;
 Matches 245; Conservative 42; Mismatches 100; Indels 81; Gaps 11;
 QY 6 PYSVQATAIAAATPFLIFLFTIRGNALVILAVTSRSLAPQNLPLVSLAADIIVATLI 65
 DB 27 PYSIQVTLTLVCLAGLMLFTFGNVLIIVFTSRALKAPQNLPLVSLAADIIVATLI 65
 QY 66 IFFSLANELGWYFRRTWCETVLAIDLVECTSSIVHLCAISLDRYMAVSRALFNYSKRT 125
 DB 87 IFFSLANELGWYFRRTWCETVLAIDLVECTSSIVHLCAISLDRYMAVSRALFNYSKRT 125
 QY 126 PPRIKCIILTVMLAAVYISLPLI---YKGDGQPPRGRPOCKLNOAWYTLASISGSF 182
 DB 147 PPRIKCIILTVMLAAVYISLPLI---YKGDGQPPRGRPOCKLNOAWYTLASISGSF 182
 QY 183 APCLIMILVRLIYLIAK-----SNRGPRAKGGPGGSGKPR---PDHGALASAKT 234
 DB 207 APCLIMILVRLIYLIAKRRTRVPPSRGPDACSAPGADRRPNAVAPRGGAGTGAAGA 266
 QY 235 PALASVASAREVNGSHKSTGEKEGETPEDTGTALPSPMAALPNSGGQKEGVCGASPE 294
 DB 267 EPLPT-----QLNG-----APGE-----PAPT-----RPR 286
 QY 295 DEAEEREEEREEEREECPQAVPVPSPASCPPLQOGSRYLATLR-GQVLGRGVALG 353
 DB 287 DGDALDESSSSSEHARPPQGPQKBERG-----PRAKGTAKASQVKGDSLRRRGGCAAG 341
 QY 354 -----GQWRR-----RAQLTREKRTFTVLAVIGVPLCMFPFFSYSLGACIP 398
 DB 342 PGASGGSGEERAGAKASRWGRGRONREKRTFTVLAVIGVPLCMFPFFSYSLGACIP 398
 QY 399 KICKVPHGLFQFFPIGVCNSLNDVYTTTINODFRAPRILCR 443
 DB 400 -GCPVYQLFNFQFFWFGVCNSLNDVYTTTINODFRAPRILCR 443

DB 399 V---GCPVYQLFNFQFFWFGVCNSLNDVYTTTINODFRAPRILCR 443

RESULT 8
 A34169
 alpha-2A-adrenergic receptor - human
 N:Alternate names: alpha-2C10-adrenergic receptor
 C:Species: Homo sapiens (man)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 29-Oct-1999
 C:Accession: A34169; A40132; S14311
 R:Fraser, C.M.; Arakawa, S.; McComb, W.R.; Venter, J.C.
 J. Biol. Chem. 264, 11754-11761, 1989
 A:Title: Cloning, sequence analysis, and permanent expression of a human alpha2-adrenergic
 A:Reference number: A34169; PMID:89308571; PMID:2568356
 A:Accession: A34169
 A:Molecule type: DNA
 A:Residues: 1-450 <PRA>
 A:Cross-references: GB:M23533; NID:G178195; PIDN:AAAS1665.1; PID:G178196
 R:Kobilka, B.K.; Matsui, H.; Kobilka, T.S.; Yang-Feng, T.L.; Francke, U.; Caron, M.G.;
 Science 238, 650-656, 1987
 A:Title: Cloning, sequencing, and expression of the gene coding for the human platelet a
 A:Reference number: A40132; PMID:88042789; PMID:2823389
 A:Accession: A40132
 A:Molecule type: DNA
 A:Residues: 1-103, 'T', 105-156, 'C', 158-367, 'T', 369-450 <KOB>
 A:Cross-references: GB:M16415; NID:G178191; PIDN:AAAS1664.1; PID:G178192
 A:Note: the authors translated the codon TGT for residue 157 as Val, and CTC for residue
 R:Chajlani, V.; Rangell, N.; Uhlen, S.; Wikberg, J.E.S.
 FEBS Lett. 280, 241-244, 1991
 A:Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept
 A:Reference number: S14308; MUID:91192139; PMID:1849485
 A:Accession: S14311
 A:Molecule type: DNA
 A:Residues: 77-123, 'P', 125-209 <CHH>
 C:Genes: GDB:ADRA2A; ADRA2; ADRA2R
 A:Cross-references: GDB:120538; OMIM:104210
 A:Map position: 10q25-10q25
 A:introns: #status absent
 C:Superfamily: G protein-coupled receptor; transmembrane protein
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 47.3%; Score 1124.5; DB 2; Length 450;
 Best Local Similarity 53.0%; Pred. No. 2.3e-69;
 Matches 242; Conservative 52; Mismatches 104; Indels 59; Gaps 13;
 QY 6 PYSVQATAIAAATPFLIFLFTIRGNALVILAVTSRSLAPQNLPLVSLAADIIVATLI 65
 DB 27 PYSIQVTLTLVCLAGLMLFTFGNVLIIVFTSRALKAPQNLPLVSLAADIIVATLI 65
 QY 66 IFFSLANELGWYFRRTWCETVLAIDLVECTSSIVHLCAISLDRYMAVSRALFNYSKRT 125
 DB 87 IFFSLANELGWYFRRTWCETVLAIDLVECTSSIVHLCAISLDRYMAVSRALFNYSKRT 125
 QY 126 PPRIKCIILTVMLAAVYISLPLI---YKGDGQPPRGRPOCKLNOAWYTLASISGSF 181
 DB 147 PPRIKCIILTVMLAAVYISLPLI---YKGDGQPPRGRPOCKLNOAWYTLASISGSF 181
 QY 182 PAPCLIMILVRLIYLIAK-----SNRGPRAKGGPGGSGKPR---PDHGALASAK 233
 DB 206 PAPCLIMILVRLIYLIAKRRTRVPPSRGPDACSAPGADRRPNAVAPRGGAGTGAAGA 265
 QY 234 LPLASVASAREVNGSHKSTGEKEGETPEDTGTALPSPMAALPNSGGQKEGVCGASP 293
 DB 266 AEPDPT-----QLNG-----APGEPAAP-GPRDTALDEES-----SS 298
 QY 294 EDEAE-----EEEREEEREECPQAVPVPSPASCPPLQOGSRYLATLRQVLLGRGV 349
 DB 299 SDHAEPRPPRRPPRPPRGGKAKASQVKGDSLRGAGGRGS-----GRRLOGRGR 351

Qy 350 GAIGQWRRRAQL---TREKRTFVLAVIGVFLVCMPEFFSYSLGALCPKCKVPHG 406
 Db 352 SASGLP--RRRAGAGGQRRKRFVLAIVGVFCMPFFFTYTLAV---GCSVPT 406
 Qy 407 LFOFPFWIGYCNSSLNPIYITITFNDFRRAFRILCR 443
 Db 407 LFKFFPFGYCNSSLNPIYITITFNDFRRAFRILCR 443

RESULT 9

A38316
 alpha-2-adrenergic receptor - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
 C/Accession: A38316
 R/Guyer: C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., E.J.; Lambird, L.E.
 J. Biol. Chem. 265, 17307-17317, 1990
 A/Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2-ad
 A/Reference number: A38316; MUID:91009167; PMID:2170371
 A/Accession: A38316
 A/Molecule type: DNA
 A/Residues: 1-450 <GVY>
 A/Cross-references: GB:J05652; NID:G164303; PIDN:AAA30984.1; PID:G164304
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 47.0%; Score 118.5; DB 2; Length 450;
 Best Local Similarity 52.6%; Pred. No. 5.9e-69;
 Matches 241; Conservative 46; Mismatches 110; Indels 61; Gaps 11;

Qy 6 PYSVQATAIAAATFLILFTIFGNALVILAVTSRSLRAPQNTFLVSLAADILVATLI 65
 Db 27 PYSVQATLTLVCLAGLMLFTVFGNVITIAVFTSRALKAQNTFLVSLAADILVATLV 86
 Qy 66 IPFSLANBLGMYPRRTWCEVYALDVLFTCTSSIVHLCAISLDRYAVASRLAENSKRT 125
 Db 87 IPFSLANBLGMYPRRTWCEVYALDVLFTCTSSIVHLCAISLDRYAVASRLAENSKRT 146
 Qy 126 PRRIKCIITLWLAIVSLPLI---YKDGQFQPRGRPOCKNOEMAYTLASISGFP 182
 Db 147 PRRIKCIITLWLAIVSLPLI---YKDGQFQPRGRPOCKNOEMAYTLASISGFP 206
 Qy 183 APCIMILVLYRIYLIARNSNRGRPRAGCGGQESKQPRPDHGAALASAKLPALASVAS 242
 Db 207 APCIMILVLYRIYLIARNSNRGRPRAGCGGQESKQPRPDHGAALASAKLPALASVAS 246
 Qy 243 AREVNGHSKSTGEKEBETPDGTTRALPPSMALPNSGQKQKGVCGASPEDEABEEBE 302
 Db 247 ERRPNGLGPERGVGVGALEA-----PLVQLNGAPGEPAPAGPRDADGLDLE 294
 Qy 303 EEEEBECE-----PQAVPVSASACSP-----PLQGP--QGSRLVATIRGQVLL 345
 Db 295 ESSSEHAERPPGRSEGRPRASKARASQVKGDSLPRGPAFPAGPATGAGE--- 351
 Qy 346 GRGGAIGGQWRRRAQLTREKRTFVLAVIGVFLVCMPEFFSYSLGALCPKCKVPH 405
 Db 352 ERGGAIAASR--RGRONREKRTFVLAVIGVFLVCMPEFFSYSLGALCPKCKVPH 405
 Qy 406 GLFQFPFWIGYCNSSLNPIYITITFNDFRRAFRILCR 443
 Db 406 TLFFKFFPFGYCNSSLNPIYITITFNDFRRAFRILCR 443

RESULT 10

I50829
 alpha-2-adrenoceptor - cuckoo wrasse
 C/Species: Labrus ocellatus (cuckoo wrasse)
 C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
 C/Accession: I50829
 R/Svensson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom, N.; Ala-Norila, S.; Scheinin,
 B.J. Pharmacol. 110, 54-60, 1993
 A/Title: Cloning and expression of a fish alpha-2-adrenoceptor.
 A/Reference number: I50829; MUID:94035926; PMID:7693288

A/Accession: I50829
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-432 <SVB>
 A/Cross-references: EMBL:U07743; NID:9467287; PIDN:AAA17386.1; PID:9467288
 C/Superfamily: vertebrate rhodopsin

Query Match 46.5%; Score 1106.5; DB 2; Length 432;
 Best Local Similarity 51.2%; Pred. No. 3.7e-68;
 Matches 232; Conservative 62; Mismatches 100; Indels 59; Gaps 11;

Qy 7 YSVQATAIAAATFLILFTIFGNALVILAVTSRSLRAPQNTFLVSLAADILVATLI 66
 Db 27 YSLAASIAALVAFLLIFTVGNILVIAVLTSLRALKAQNTFLVSLAADILVATLV 86
 Qy 67 PFSLANBLGMYPRRTWCEVYALDVLFTCTSSIVHLCAISLDRYAVASRLAENSKRT 126
 Db 87 PFSLANBLGMYPRRTWCEVYALDVLFTCTSSIVHLCAISLDRYAVASRLAENSKRT 146
 Qy 127 PRRIKCIITLWLAIVSLPLIYKDGQFQPRGRPOCKNOEMAYTLASISGFPAPCL 186
 Db 147 KRIVCIITVYWLISAFISSPPL-SIDSNNYISSQPCMLNDPIWYLLSSMASFPAPCL 205
 Qy 187 IMILVLYRIYLIARNSNRGRPRAGCGGQESKQPRPDHGAALASAKLPALASVASREV 246
 Db 206 IMILVLYRIYLIARNSNRGRPRAGCGGQESKQPRPDHGAALASAKLPALASVASREV 246
 Qy 247 NGHSKST---GEKEBETPDGTTRALPPSMALPNSGQKQKGVCGASPEDEABEEBE 302
 Db 240 NGILKANSPCGGRRENCHC-----OCPT-----PSQRTVITG-QQTDADNDES 283
 Qy 303 EEEEBECEPQAVPVSASACSPPLQGPQGSRLVATIRGQVLLGRGGAIGQWRRRAQ 362
 Db 284 FSEBKGAKFORQDSQAK--RELKKSISKQSA--RIRVNSKSVDLPAKRKRKRSS 339
 Qy 363 L-----TREKRTFVLAVIGVFLVCMPEFFSYSLGALCPKCKVPHGLFQFPFWIG 415
 Db 340 IAEKVSQAREKRTFVLAVIGVFLVCMPEFFSYSLGALCPKCKVPHGLFQFPFWIG 398
 Qy 416 YCNSSLNPIYITITFNDFRRAFRILCRPWTQT 448
 Db 399 YCNSSLNPIYITITFNDFRRAFRILCRPWTQT 431

RESULT 11

JH0190
 alpha-2-adrenergic receptor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
 C/Accession: JH0190
 R/Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.
 Mol. Cell. Biochem. 97, 161-172, 1990
 A/Title: Molecular cloning, sequencing and expression of an alpha-2-adrenergic receptor c
 A/Reference number: JH0190; MUID:91125329; PMID:2177834
 A/Accession: JH0190
 A/Molecule type: mRNA
 A/Residues: 1-450 <CHA>
 A/Experimental source: brain
 C/Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It medi
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein
 F/34-59/Domain: hydrophobic <HDI>
 F/71-96/Domain: hydrophobic <HII>
 F/106-131/Domain: hydrophobic <HII>
 F/150-175/Domain: hydrophobic <HIV>
 F/193-218/Domain: hydrophobic <HIV>
 F/375-400/Domain: hydrophobic <HVI>
 F/405-430/Domain: hydrophobic <VII>

Query Match 45.9%; Score 1091.5; DB 2; Length 450;
 Best Local Similarity 50.4%; Pred. No. 4.1e-67;
 Matches 237; Conservative 49; Mismatches 99; Indels 85; Gaps 12;

QY 6 PYSVQATAAIAAATFTLFTFGNALVTLAVTSRSLAPQNLFLVSLAADIIVATLI 65
 27 PYSVQVTLITLCLAGLMLFTVFGNALVTLAVTSRSLAPQNLFLVSLAADIIVATLI 65
 QY 66 IFFSLANELLGYWYRRRTWCCEVTLADLVFCSTSIYHLCALISDRYANVSRALFNKRT 125
 87 IFFSLANELLGYWYRRRTWCCEVTLADLVFCSTSIYHLCALISDRYANVSRALFNKRT 125
 QY 126 PRRKICILITWMLIAVLSLPLI---YKSGQGPGRPOCKNOEAWYTLASSISGFFP 182
 147 PRRKICILITWMLIAVLSLPLI---YKSGQGPGRPOCKNOEAWYTLASSISGFFP 182
 QY 163 APCLIMILYVRLIYLIAR-----SNRRGPRAGKGGPOGSGKOPR---PDHGAALASAKL 234
 207 APCLIMILYVRLIYLIAR-----SNRRGPRAGKGGPOGSGKOPR---PDHGAALASAKL 234
 QY 235 PALASVASAEVNGHSKSTGEKEGETPEDTGTALPSPMAALPNSGQGGKGVGASPE 294
 267 EPLPT-----QLNG---APGE-----PAPTRPR-----D 287
 QY 295 DAEEEEESEEECEPQAVPSPASCSPPLOQPGSRVATLR-----D 287
 288 GDALDESSSSSEHARPOG-----PGKPRGPRAGKTKASQVPRDLSLPRG 336
 QY 349 VGAIG-----GQWRR-----RAOLTEKRTYTLAVVIGVPLCMPEFFSYSL 393
 337 PGAAGFGASGSGQEEEAAGAKASRRGRONREKRTFTFLAVVIGVPLCMPEFFSYSL 393
 QY 394 GAICPKCKVPHGLPFPFWMIGYCNSSINPVTYITINODFRAPRILCR 443
 397 IAV---GCPVPIOLNFNFWMYCNSSINPVTYITINODFRAPRILCR 443

RESULT 12

Alpha-2-adrenergic receptor (clone RG10) - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 06-Dec-1991 #sequence revision 03-Apr-1992 #text change 13-Aug-1999
 A/Accession: A40392
 R/Linker: S.M. A40392
 A/Biot: Chem. S.; Downing, S.; Duzic, E.; Homcy, C.J.
 A>Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic receptor
 A/Reference number: A40392; MUID:9124423; PMID:1643550
 A/Accession: A40392
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-458 <LAN>
 A/Cross-references: GB:M62371; NID:9206612; PIDN:AAA42033.1; PID:9206613
 C/Superfamily: Vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match
 Best Local Similarity 45.5%; Score 1083; DB 2; Length 458;
 Matches 237; Conservative 46; Mismatches 108; Indels 60; Gaps 10;
 QY 7 YSVQATMAIAAATFTLFTFGNALVTLAVTSRSLAPQNLFLVSLAADIIVATLI 65
 46 YSVQATMAIAAATFTLFTFGNALVTLAVTSRSLAPQNLFLVSLAADIIVATLI 65
 QY 67 PPSLANELLGYWYRRRTWCCEVTLADLVFCSTSIYHLCALISDRYANVSRALFNKRT 125
 106 PPSLANELLGYWYRRRTWCCEVTLADLVFCSTSIYHLCALISDRYANVSRALFNKRT 125
 QY 126 PRRKICILITWMLIAVLSLPLI---YKSGQGPGRPOCKNOEAWYTLASSISGFFP 182
 147 PRRKICILITWMLIAVLSLPLI---YKSGQGPGRPOCKNOEAWYTLASSISGFFP 182
 QY 163 APCLIMILYVRLIYLIAR-----SNRRGPRAGKGGPOGSGKOPR---PDHGAALASAKL 234
 207 APCLIMILYVRLIYLIAR-----SNRRGPRAGKGGPOGSGKOPR---PDHGAALASAKL 234
 QY 235 PALASVASAEVNGHSKSTGEKEGETPEDTGTALPSPMAALPNSGQGGKGVGASPE 294
 267 EPLPT-----QLNG---APGE-----PAPTRPR-----D 287
 QY 295 DAEEEEESEEECEPQAVPSPASCSPPLOQPGSRVATLR-----D 287
 288 GDALDESSSSSEHARPOG-----PGKPRGPRAGKTKASQVPRDLSLPRG 336
 QY 349 VGAIG-----GQWRR-----RAOLTEKRTYTLAVVIGVPLCMPEFFSYSL 393
 337 PGAAGFGASGSGQEEEAAGAKASRRGRONREKRTFTFLAVVIGVPLCMPEFFSYSL 393
 QY 394 GAICPKCKVPHGLPFPFWMIGYCNSSINPVTYITINODFRAPRILCR 443
 397 IAV---GCPVPIOLNFNFWMYCNSSINPVTYITINODFRAPRILCR 443

QY 282 EPDESSAARRRRRAGVRRGRREG-ARGDTGS-----ADPGPGLAABQARTSR 333
 294 EPDESSAARRRRRAGVRRGRREG-ARGDTGS-----ADPGPGLAABQARTSR 333
 QY 334 -----SPG-----PGRLSRASSRSEFFLSRRRRR 360
 353 GQWWRRAOLTEKRTYTLAVVIGVPLCMPEFFSYSLCAICPGKCVPHGLPFPF 412
 361 SSVCRRKVAO-AREKRTFTFLAVVIGVPLCMPEFFSYSLCAICPGKCVPHGLPFPF 412
 QY 413 WIGYCNSSINPVTYITINODFRAPRILCR 443
 420 WIGYCNSSINPVTYITINODFRAPRILCR 443

RESULT 13

Alpha-2 adrenergic receptor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 13-Aug-1999
 A/Accession: U9480
 R/Linker: R.; Dauter, D.; Barsh, G.S.; Christakos, A.; Kobilka, B.
 A/Biot: Pharmacia. 42.16-27, 1992
 A>Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and 1st in antiserone binding.
 A/Reference number: U9480; MUID:9234231; PMID:1353249
 A/Accession: U9480
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-458 <RES>
 A/Cross-references: GB:M99376; NID:9191880; PIDN:AAA37222.1; PID:9191881
 C/Superfamily: Vertebrate rhodopsin
 C/Keywords: neurotransmitter receptor

Query Match
 Best Local Similarity 52.4%; Score 1082; DB 2; Length 458;
 Matches 239; Conservative 46; Mismatches 101; Indels 70; Gaps 12;
 QY 7 YSVQATMAIAAATFTLFTFGNALVTLAVTSRSLAPQNLFLVSLAADIIVATLI 65
 46 YSVQATMAIAAATFTLFTFGNALVTLAVTSRSLAPQNLFLVSLAADIIVATLI 65
 QY 67 PPSLANELLGYWYRRRTWCCEVTLADLVFCSTSIYHLCALISDRYANVSRALFNKRT 125
 106 PPSLANELLGYWYRRRTWCCEVTLADLVFCSTSIYHLCALISDRYANVSRALFNKRT 125
 QY 126 PRRKICILITWMLIAVLSLPLI---YKSGQGPGRPOCKNOEAWYTLASSISGFFP 182
 147 PRRKICILITWMLIAVLSLPLI---YKSGQGPGRPOCKNOEAWYTLASSISGFFP 182
 QY 163 APCLIMILYVRLIYLIAR-----SNRRGPRAGKGGPOGSGKOPR---PDHGAALASAKL 234
 207 APCLIMILYVRLIYLIAR-----SNRRGPRAGKGGPOGSGKOPR---PDHGAALASAKL 234
 QY 235 PALASVASAEVNGHSKSTGEKEGETPEDTGTALPSPMAALPNSGQGGKGVGASPE 294
 267 EPLPT-----QLNG---APGE-----PAPTRPR-----D 287
 QY 295 DAEEEEESEEECEPQAVPSPASCSPPLOQPGSRVATLR-----D 287
 288 GDALDESSSSSEHARPOG-----PGKPRGPRAGKTKASQVPRDLSLPRG 336
 QY 349 VGAIG-----GQWRR-----RAOLTEKRTYTLAVVIGVPLCMPEFFSYSL 393
 337 PGAAGFGASGSGQEEEAAGAKASRRGRONREKRTFTFLAVVIGVPLCMPEFFSYSL 393
 QY 394 GAICPKCKVPHGLPFPFWMIGYCNSSINPVTYITINODFRAPRILCR 443
 397 IAV---GCPVPIOLNFNFWMYCNSSINPVTYITINODFRAPRILCR 443

RESULT 14

Alpha-2 adrenergic receptor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 13-Aug-1999
 A/Accession: U9480
 R/Linker: R.; Dauter, D.; Barsh, G.S.; Christakos, A.; Kobilka, B.
 A/Biot: Pharmacia. 42.16-27, 1992
 A>Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and 1st in antiserone binding.
 A/Reference number: U9480; MUID:9234231; PMID:1353249
 A/Accession: U9480
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-458 <RES>
 A/Cross-references: GB:M99376; NID:9191880; PIDN:AAA37222.1; PID:9191881
 C/Superfamily: Vertebrate rhodopsin
 C/Keywords: neurotransmitter receptor

Query Match	45.4%;	Score 1079;	DB 2;	Length 458;
Beat Local Similarity	51.3%;	Pred. No. 3e-66;		
Matches 236;	Conservative 47;	Mismatches 99;	Indels 78;	Gaps 12

RESULT 15

A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic receptor

Query Match	45.4%;	Score 1078.5;	DB 2;	Length 461;
Best Local Similarity	52.2%;	Pred. No. 3.2e-66;		
Matches 240;	Conservative 41;	Mismatches 104;	Indels 75;	Gaps 12

Search completed: February 6, 2004, 18:20:08
Job time : 17.5552 secs

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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:52:15 ; Search time 10.0334 Seconds
(without alignments)
2109.148 Million cell updates/sec

Title: US-09-692-077d-7
Perfect score: 2378
Sequence: 1 MDHQDPYSVQATAIAAAT.....QDFRFRRLICRPWTQTAW 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2378	100.0	450	1 A2AB_HUMAN	P18089 homo sapien
2	2075	87.3	448	1 A2AB_CAVPO	Q60476 cavia porce
3	1981	83.3	453	1 A2AB_RAT	P19328 rattus norv
4	1940	81.6	455	1 A2AB_MOUSE	P30545 mus musculu
5	1803.5	75.8	394	1 A2AB_RABIT	O77830 corycolagus
6	1775.5	74.7	388	1 A2AB_ORYX	O19032 orycteropus
7	1775	74.6	389	1 A2AB_HORSE	O77721 equus cabal
8	1771	74.5	391	1 A2AB_ERIEU	O19012 erinaceus e
9	1748.5	73.5	384	1 A2AB_ELEMA	O19014 elephas max
10	1747.5	73.5	386	1 A2AB_AMBHO	O18935 amblysomus
11	1743.5	73.3	392	1 A2AB_BOVIN	O77700 bos taurus
12	1742	73.3	397	1 A2AB_TALEU	O19091 talpa europ
13	1739.5	72.1	390	1 A2AB_DUGDU	O77713 dugong dugo
14	1723	72.5	389	1 A2AB_PROHA	O19054 procavia ca
15	1696	71.3	387	1 A2AB_MACPR	O19025 macropscelid
16	1601.5	67.3	384	1 A2AB_ECHTE	O77723 echinops te
17	1451.5	61.0	382	1 A2AB_DIDMA	O77715 didelphis m
18	1141.5	48.0	450	1 A2AA_MOUSE	O01337 mus musculu
19	1139.5	47.9	450	1 A2AA_RAT	P22909 rattus norv
20	1134.5	47.7	452	1 A2AA_BOVIN	Q28838 bos taurus
21	1126.5	47.4	450	1 A2AA_CAVPO	Q60476 cavia porce
22	1124.5	47.3	450	1 A2AA_HUMAN	P08933 homo sapien
23	1118.5	47.0	450	1 A2AA_PIG	P18871 sus scrofa
24	1106.5	46.5	432	1 A2AR_LABOS	Q01081 labrus osbi
25	1085.5	45.6	455	1 A2AC_CAVPO	Q60476 cavia porce
26	1082	45.5	458	1 A2AC_MOUSE	O01337 mus musculu
27	1082	45.5	458	1 A2AC_RAT	P22066 rattus norv
28	1076	45.2	462	1 A2AC_HUMAN	P18828 homo sapien
29	1062	44.7	469	1 A2AC_DIDMA	P35405 didelphis m
30	980	41.2	484	1 A2AR_CARAU	P32522 carassius a
31	685	28.8	484	1 OAR1_LOCOMI	Q25322 locusta mig
32	685	28.8	484	1 OAR1_LOCOMI	Q25322 locusta mig
33	669	28.1	477	1 OAR_HELVY	Q25188 heliothis v

34	651	27.4	601	1 OAR_DROME	P22270 drosophila
35	645.5	27.1	379	1 GRE2_BALAM	Q93127 balanus amp
36	644	27.1	479	1 OAR_BOMMO	Q17232 bombyx mori
37	613.5	25.8	416	1 SH1B_FUGRU	Q42384 figu rubrip
38	604.5	25.4	638	1 OAR1_TYMST	O77408 tymnaea ste
39	598	25.1	476	1 GRE1_BALAM	Q93126 balanus amp
40	594.5	25.0	467	1 D4DR_HUMAN	P21917 homo sapien
41	592.5	24.9	463	1 D2DR_FUGRU	P53453 figu rubrip
42	589	24.8	422	1 SH1A_RAT	P19327 rattus norv
43	589	24.8	444	1 OAR_CAREL	O02213 caenorhabdi
44	585	24.6	444	1 D2DR_BOVIN	P20288 bos taurus
45	585	24.6	519	1 A1AB_HUMAN	P35368 homo sapien

ALIGNMENTS

RESULT 1
A2AB_HUMAN STANDARD; PRT; 450 AA.
ID A2AB_HUMAN
AC P18089; O9BZKO;
DT 01-NOV-1990 (Rel. 16, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Subtype C2).
GN ADRA2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90311349; PubMed=2164221;
RA Lomasney J.W., Lorenz W., Allen U.F., King K., Regan J.W.,
RA Yang-Feng T.L., Caron M.G., Leikowitz R.J.;
RT "Expansion of the alpha 2-adrenergic receptor family: cloning and
RT characterization of a human alpha 2-adrenergic receptor subtype, the
RT gene for which is located on chromosome 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5094-5098(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042469; PubMed=2172775;
RA Weinshank R.L., Zgonibek J.M., Macchi M., Adham N., Lichthau H.,
RA Branchek T.A., Hartig P.R.;
RT "Cloning, expression, and pharmacological characterization of a human
RT alpha 2B-adrenergic receptor.";
RL Mol. Pharmacol. 38:681-688(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX Cayla C., Schack S., Bouloumie A., Devédjian J.C., Paris H.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT 301-GLU--GLU-303.
RX MEDLINE=21265012; PubMed=11056163;
RA Small K.M., Brown K.M., Forbes S.L., Liggett S.B.;
RT "Polymorphic deletion of three intracellular acidic residues of the
RT alpha 2B-adrenergic receptor decreases G protein-coupled receptor
RT kinase-mediated phosphorylation and desensitization.";
RL J. Biol. Chem. 276:4917-4922(2001).
RN [5]
RP SEQUENCE OF 95-389 FROM N.A.
RX MEDLINE=91054503; PubMed=2173582;
RA Chang A.C., Ho T.F., Chang N.-C.A.;
RT "In vitro amplification by polymerase chain reaction of a partial
RT gene encoding the third subtype of alpha-2 adrenergic receptor in
RT humans.";
RL Biochem. Biophys. Res. Commun. 172:817-823(1990).
-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
IS CLONIDINE > NORPINEPRINE > EPINEPRINE = OXYMETAZOLINE >
DOPAMINE > P-TYRAMINE = PHENYLEPRINE > SEROTONIN > P-SYNEPRINE /
P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >

QY 1 MDHODPYSVATATAIAAATITELLFTI FGNALVILAVLTSRSRLAPQVL PVLSLAADIL 60

Dd 1 MDHODPYSVATATAIAAATITELLFTI FGNALVILAVLTSRSRLAPQVL PVLSLAADIL 60

QY 61 VALLIPFSLANELLGYWIFRRTWCVEVIALDVLFECTSIYHLCAISLDPRVAWSRALEY 120

Db 61 VATLLIPSIANELLGTYFFRTICEVYLLADVLFTCTSIYHLCALSIDRYWVSRALLEY 120

Qy 121 NSKRTPRIKICILLTWLILAAVISLPLLYKGDGPQPRGRPOCKLNQEMVLIASSIGS 180

Db 121 NSKRTPRIKICILLTWLILAAVISLPLLYKGDGPQPRGRPOCKLNQEMVLIASSIGS 180

Qy 181 FFAPCLIMILVYLYLRIYLIARSNRGRGARGGQGGSKQPRDRHGALASATLPAIASV 240

Db 181 FFAPCLIMILVYLYLRIYLIARSNRGRGARGGQGGSKQPRDRHGALASATLPAIASV 240

Qy 241 ASAEVNGHSHSTKEKEGETPEDTGTRALPSPWALPNSGGQKXGVCASPEDAAEE 300

Db 241 ASAEVNGHSHSTKEKEGETPEDTGTRALPSPWALPNSGGQKXGVCASPEDAAEE 300

Qy 301 EEEEEEECEPQAVPVPSPASACSPPLQDPQGSRYVATLRGVLLGRGICGALGGQWRRR 360

Db 301 EEEEEEECEPQAVPVPSPASACSPPLQDPQGSRYVATLRGVLLGRGICGALGGQWRRR 360

Qy 361 AQLTRERGFYVAVIGVFTLCWPFPPFSYSIGALCPHGKCVPHGLFQFPFWIGCNSS 420

Db 361 AQLTRERGFYVAVIGVFTLCWPFPPFSYSIGALCPHGKCVPHGLFQFPFWIGCNSS 420

Qy 421 LNPVIYTIENQDFRRAFRRLICSPMTQTM 450

Db 421 LNPVIYTIENQDFRRAFRRLICSPMTQTM 450

RESULT 2

A2AB_CAVPO

ID _A2AB_CAVPO STANDARD; PRT; 448 AA.

AC Q60475;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).

OS ADRA2B.

OS Cavia porcellus (Guinea pig).

OC Bakayota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.

OX NCBI_TaxId=10141;

RN [1]

RA SEQUENCE FROM N.A.

RC STRAIN=Hartley;

RX MEDLINE=96152573; PubMed=8573196;

RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;

RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,

RT and alpha 2C adrenoceptor subtypes. Radioligand binding and

RT functional coupling to a CAMP-responsive reporter gene.",

RL Biochem. Pharmacol. 51:291-300 (1996).

CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-

CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G

CC PROTEINS.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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DR EMBL; U25723; AAA67075.1; -

DR HSSP; P29274; IMMH.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHOPOPSN.

DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.

DR G-protein coupled receptor; Transmembrane; Multigene family;

DR Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 12 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 13 38 1 (POTENTIAL).
 FT DOMAIN 39 49 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 50 75 2 (POTENTIAL).
 FT DOMAIN 76 85 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 86 108 3 (POTENTIAL).
 FT DOMAIN 109 130 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 131 153 4 (POTENTIAL).
 FT DOMAIN 154 168 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 169 192 5 (POTENTIAL).
 FT DOMAIN 193 370 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 371 394 6 (POTENTIAL).
 FT DOMAIN 395 403 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 404 427 7 (POTENTIAL).
 FT DOMAIN 428 448 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 85 163 BY SIMILARITY.
 FT LIPID 440 440 PALMITATE (POTENTIAL).
 FT DOMAIN 294 309 ASP/Glu-RICH (ACIDIC).
 FT SITE 92 92 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
 FT SITE 175 175 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
 FT SITE 179 179 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
 FT SITE 179 179 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
 SQ SEQUENCE 448 AA; 49597 MW; 83848757E04777 CRC64;

Query Match 87.3%; Score 2075; DB 1; Length 448;
 Best Local Similarity 88.5%; Pred. No. 4.2e-111;
 Matches 399; Conservative 15; Mismatches 33; Indels 4; Gaps 3;

QY 1 MDHDPYVQNTAAIAAATPFLFTFGNALVILAVTSRSLAPONTPLVSLAADIL 60
 DB 1 MDHGPYVQNTAAIAAATPFLFTFGNALVILAVTSRSLAPONTPLVSLAADIL 60
 QY 61 VATLIIPFSLANELLGYWFRRTWCEVYALDVLCTSSIVHLCAISLDRYMAVSRLLEY 120
 DB 61 VATLIIPFSLANELLGYWFRRTWCEVYALDVLCTSSIVHLCAISLDRYMAVSRLLEY 120
 QY 121 NSKRTPRICILITLWLAIAVSLPLIYKDGQPPRRPOCKINOEMVYIASSIGS 180
 DB 121 NSKRTPRICILITLWLAIAVSLPLIYKDGQPPRRPOCKINOEMVYIASSIGS 180
 QY 181 FFAFCLIMILVLYLRIYIAKSNRRGRKAGPQSGSKOPRPHGALASAKLPALAS 239
 DB 181 FFAFCLIMILVLYLRIYIAKSNRRGRKAGPQSGSKOPRPHGALASAKLPALAS 239
 QY 239 180 FFAFCLIMILVLYLRIYIAKSNRRGRKAGPQSGSKOPRPHGALASAKLPALAS 239
 DB 239 180 FFAFCLIMILVLYLRIYIAKSNRRGRKAGPQSGSKOPRPHGALASAKLPALAS 239
 QY 240 VASAREVNGHSKSTGEKEGETPEDTGTALPSSWALPNSGQKQKGVCGASPEDEAE 299
 DB 240 VASAREVNGHSKSTGEKEGETPEDTGTALPSSWALPNSGQKQKGVCGASPEDEAE 299
 QY 299 240 VASAREVNGHSKSTGEKEGETPEDTGTALPSSWALPNSGQKQKGVCGASPEDEAE 299
 DB 299 240 VASAREVNGHSKSTGEKEGETPEDTGTALPSSWALPNSGQKQKGVCGASPEDEAE 299
 QY 300 EEEEEECEPQAVVSPASACSPLOQPOGSRVATLRGVLLRGVGAIGGQWRR 359
 DB 300 EEEEEECEPQAVVSPASACSPLOQPOGSRVATLRGVLLRGVGAIGGQWRR 359
 QY 359 300 EEEEEECEPQAVVSPASACSPLOQPOGSRVATLRGVLLRGVGAIGGQWRR 359
 DB 359 300 EEEEEECEPQAVVSPASACSPLOQPOGSRVATLRGVLLRGVGAIGGQWRR 359
 QY 360 RAQLTREKRTFLVAVVIGVLCWPPFPYSYLGALCPKCKVPHGLPOFFFIYICNS 419
 DB 360 RAQLTREKRTFLVAVVIGVLCWPPFPYSYLGALCPKCKVPHGLPOFFFIYICNS 419
 QY 419 360 RAQLTREKRTFLVAVVIGVLCWPPFPYSYLGALCPKCKVPHGLPOFFFIYICNS 419
 DB 419 360 RAQLTREKRTFLVAVVIGVLCWPPFPYSYLGALCPKCKVPHGLPOFFFIYICNS 419
 QY 420 SLNPVITYTFNODFRRAFRILCRPWTOTAM 450
 DB 420 SLNPVITYTFNODFRRAFRILCRPWTOTAM 450
 QY 450 420 SLNPVITYTFNODFRRAFRILCRPWTOTAM 450
 DB 450 420 SLNPVITYTFNODFRRAFRILCRPWTOTAM 450
 QY 418 SLNPVITYTFNODFRRAFRILCRPWTOTAM 448
 DB 418 SLNPVITYTFNODFRRAFRILCRPWTOTAM 448

RESULT 3
 A2AB RAT STANDARD; PRT; 453 AA.
 AC P19328; 063021;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
 GN ADRA2B.
 OS Rattus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA MEDLINE=90222177; PubMed=2158103;
 RX Zeng D., Harrison J.K., D'Angelo D.D., Barber C.M., Tucker A.L.,
 RA Lu Z., Lynch K.R.;
 RT "Molecular characterization of a rat alpha 2B-adrenergic receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3102-3106(1990).
 RN [2]
 RP SEQUENCE OF 6-453 FROM N.A.
 RC STRAIN=Sabra; TISSUE=Kidney;
 RX MEDLINE=95275492; PubMed=7755946;
 RA le Jossac M., Cloix J.F., Pecquery R., Giudicelli Y., Danuse J.P.;
 RT "Differential sodium regulation between salt-sensitive and salt-
 RT resistant Sabra rats is not due to any mutation in the renal alpha
 RT 2B-adrenoceptor gene.";
 RL Am. J. Hypertens. 8:177-182(1995).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIANE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@ebi.ac.uk).

CC EMBL; M32061; AAA40635.1; -;
 CC EMBL; X74400; CA52411.1; -;
 CC PIR; A35642; A35642.
 DR HSP; P29274; 1MMH.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR P1.1;
 DR PROSITE; PS50262; G PROTEIN RECEPTOR P2.1;
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 17
 FT TRANSSEM 18 42
 FT DOMAIN 43 54
 FT TRANSSEM 55 80
 FT DOMAIN 81 90
 FT TRANSSEM 91 113
 FT DOMAIN 114 135
 FT TRANSSEM 136 158
 FT DOMAIN 159 174
 FT TRANSSEM 175 198
 FT DOMAIN 199 375
 FT TRANSSEM 376 399
 FT DOMAIN 400 408
 FT TRANSSEM 409 432
 FT DOMAIN 433 453
 FT DISULFID 90 169
 FT LIPID 445 445
 FT DOMAIN 300 314
 FT SITE 97 97
 FT SITE 181 181
 FT SITE 185 185
 FT SITE 132 132
 FT CONFLICT 162 163
 FT CONFLICT 162 163
 SQ SEQUENCE 453 AA; 50276 MW; BCA040FF9A310EB CRC64;

Query Match 83.3%; Score 1981; DB 1; Length 453;
 Best Local Similarity 83.8%; Pred. No. 9e-106;
 Matches 378; Conservative 24; Mismatches 45; Indels 4; Gaps 2;

QY 1 MDHDPYVQATAAIAAATFTLLFTFGNALVITLTSGLRAPONTFLVSLAADIL 60
 DB 6 MDHDPYVQATAAIAAATFTLLFTFGNALVITLTSGLRAPONTFLVSLAADIL 60
 QY 61 VATTIIPFSLANELLGYWFRRTWCYVIALDVLTCTSSIVHLCAISIDRYMAVSRLEY 120
 DB 66 VATTIIPFSLANELLGYWFRRTWCYVIALDVLTCTSSIVHLCAISIDRYMAVSRLEY 120
 QY 121 NSKRTPRKICITLWMLIAAVISLPLLYKDGQPPRGRPOCKLNOEMWYIASSIGS 180
 DB 126 NSKRTPRKICITLWMLIAAVISLPLLYKDGQPPRGRPOCKLNOEMWYIASSIGS 180
 QY 181 FPAFLCITLWMLIYLRILYLAQRNRRGPRAGGPGQSGSKOPRPHGALASAKLPALA 238
 DB 186 FPAFLCITLWMLIYLRILYLAQRNRRGPRAGGPGQSGSKOPRPHGALASAKLPALA 238
 QY 240 VASAEVNGHSGKSGKEGETPEDTGTALPPSMALPNSGQKQGVGASPEDAE 297
 DB 246 LSVGANGHPKPREKEGETPEDTGTALPPSMALPNSGQKQGVGASPEDAE 297
 QY 300 EEEEEECEPQAVSPASACSPLOQSGRYALTLRGQVLAGRGVAGIAGQWWR 359
 DB 303 DEEDEEVECEPQTLPASASVCNPLQOPQTSVTLTLRGQVLAGRGVAGIAGQWWR 359
 QY 360 RAQLTREKRTFLAVAVIGVPLCMFPFPPSYSLGALCPKCKVPHGLPFPFWITGYS 419
 DB 363 RTQLSKERTVPLAVAVIGVPLCMFPFPPSYSLGALCPKCKVPHGLPFPFWITGYS 419
 QY 420 SLNPVYITFNQDFFRAFRRLICRPMTOTAM 450
 DB 423 SLNPVYITFNQDFFRAFRRLICRPMTOTAM 453

RESULT 4
 A2AB MOUSE STANDARD; PRT; 455 AA.
 ID A2AB MOUSE
 AC P30545;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
 GN ADRA2B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA/2; TISSUE=Liver;
 RC MEDLINE=93129625; PubMed=1336396;
 RA Chen W.-M., Chang A.C., Shie B.J., Chang Y.-H., Chang N.-C.A.,
 RT "Molecular cloning and characterization of a mouse alpha 2C2
 RT adrenoceptor subtype gene.";
 RL Biochim. Biophys. Acta 1171:219-223 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=92378586; PubMed=1354956;
 RA Chrusciel A.J., Link R.E., Daut D.A., Barsh G.S., Koblika B.K.,
 RT "Cloning and expression of the mouse homolog of the human alpha 2-C2
 RT adrenergic receptor.";
 RL Biochem. Biophys. Res. Commun. 186:1280-1287 (1992).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 or send an email to license@ebi.ac.uk).

DR EMBL; M94583; AAA73895.1;
 DR EMBL; L00978; AAA7131.1; ALT_INIT.
 DR PIR; S28221; S28221.
 DR HSSP; P28274; 1MMH.
 DR MCD; MG1:87935; Adra2b.
 DR GO; GO:0004938; F:alpha2-adrenergic receptor activity; IDA.
 DR GO; GO:0001525; P:angiogenesis; IMP.
 DR GO; GO:0000165; P:MAPKK cascade; IMP.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR P1.1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR P1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 FT DOMAIN 1 17
 FT TRANSSEM 18 42
 FT DOMAIN 43 54
 FT TRANSSEM 55 80
 FT DOMAIN 81 90
 FT TRANSSEM 91 113
 FT DOMAIN 114 135
 FT TRANSSEM 136 158
 FT DOMAIN 159 174
 FT TRANSSEM 175 198
 FT DOMAIN 199 377
 FT TRANSSEM 378 401
 FT DOMAIN 402 410
 FT TRANSSEM 411 434
 FT DOMAIN 435 455
 FT DISULFID 90 169
 FT LIPID 447 447
 FT DOMAIN 306 316
 FT SITE 97 97
 FT SITE 181 181
 FT SITE 185 185
 FT CONFLICT 202 202
 FT CONFLICT 229 230
 SQ SEQUENCE 455 AA; 50615 MW; A3954AD76E0B263 CRC64;

Query Match 81.6%; Score 1940; DB 1; Length 455;
 Best Local Similarity 83.0%; Pred. No. 1.9e-103;
 Matches 376; Conservative 22; Mismatches 49; Indels 6; Gaps 3;

QY 1 MDHDPYVQATAAIAAATFTLLFTFGNALVITLTSGLRAPONTFLVSLAADIL 60
 DB 6 MDHDPYVQATAAIAAATFTLLFTFGNALVITLTSGLRAPONTFLVSLAADIL 60
 QY 61 VATTIIPFSLANELLGYWFRRTWCYVIALDVLTCTSSIVHLCAISIDRYMAVSRLEY 120
 DB 66 VATTIIPFSLANELLGYWFRRTWCYVIALDVLTCTSSIVHLCAISIDRYMAVSRLEY 120
 QY 121 NSKRTPRKICITLWMLIAAVISLPLLYKDGQPPRGRPOCKLNOEMWYIASSIGS 180
 DB 126 NSKRTPRKICITLWMLIAAVISLPLLYKDGQPPRGRPOCKLNOEMWYIASSIGS 180
 QY 181 FPAFLCITLWMLIYLRILYLAQRNRRGPRAGGPGQSGSKOPRPHGALASAKLPALA 238
 DB 186 FPAFLCITLWMLIYLRILYLAQRNRRGPRAGGPGQSGSKOPRPHGALASAKLPALA 238
 QY 239 S-VASAEVNGHSGKSGKEGETPEDTGTALPPSMALPNSGQKQGVGASPEDAE 297
 DB 246 SPSVANGANGHPKPREKEGETPEDTGTALPPSMALPNSGQKQGVGASPEDAE 297

```

Oy 298 EEEEEEEBEECECPAIVSPASACSPLQOPQSGRVATLRGVYLAKRGVAGIGGQMW 35
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 306 --- EEDDEVEBCECFQTLASPAISVNPPLQOPQTSRVATLRGVYLAKRGVAGIGGQMW 362
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 358 RRRALQTRREKRTFVLAVVIGVFLCMFPFPFSYSIGAICPKHKCKVPHGLPFPFWMGYC 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 363 RRRQTLSREKRTFVLAVVIGVFLCMFPFPFSYSIGAICPKHKCKVPHGLPFPFWMGYC 422
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 418 NSSLNPIVYITTFNODFRFRFRILLCRPWTQTAM 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 423 NSSLNPIVYITTFNODFRFRFRILLCRPWTQTAM 455
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
A2AB_RABIT
ID _A2AB_RABIT STANDARD; PRT; 394 AA.
AC 077830;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Euryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanhope M.J., Madsen O.J., Wadell V.G., Cleven G.C., de Jong W.W.,
RA Springer M.S., Madsen O.O.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CAECOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -! SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y16189; CAAT76115.1; -
DR EMBL; Y15946; CAAT75899.2; -
DR HSSP; P29274; IMMH.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
FW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT NON_TER 1
FT TRANSMEM 1
FT DOMAIN <1 25 1 (POTENTIAL).
FT TRANSMEM 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 37 62 2 (POTENTIAL).
FT DOMAIN 73 72 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 118 140 4 (POTENTIAL).
FT TRANSMEM 141 156 5 (POTENTIAL).
FT TRANSMEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 358 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 359 382 6 (POTENTIAL).
FT DOMAIN 383 391 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 392 >394 7 (POTENTIAL).
FT DISULFID 72 151 BY SIMILARITY.
FT DOMAIN 282 297 ASP/GLU-RICH (ACIDIC).
FT NON_TER 394
SQ SEQUENCE 394 AA; 42906 MW; 5D520975ACA6916A CRC64;

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Query Match	Similarity	75.8%	Score 1803.5	DB 1	Length 394
Best Local	Similarity	88.6%	Pred No. 9.1e-96		
Matches	Conservative	14	Mismatches	28	Indels
				3	Gaps
				2	
Qy	14	ATAAATPELLFTTIGNALVTLAVLTSTRSLRAPONTFLVLSAADIIVATTLIPESLANE	73		
Db	1	ATAAATPELLFTTIGNALVTLAVLTSTRSLRAPQMLFVLSAADIIVATTLIPESLANE	60		
Qy	74	LIGVYFPERTCEVVALADVLCFSSIVYHCAISIDRWAAVSRALEVNSKXTPRRIKCI	133		
Db	61	LIGVYFPERTCEVVALADVLCFSSIVYHCAISIDRWAAVSRALEVNCKTPRRIKCI	120		
Qy	134	LTWVLIAAVISLPLIYKDGDPQPRGRPOCKLNOEANYIIASSIGSFAPCLIMILVYL	193		
Db	121	LTWVLIAAVISLPLIYKDGDPQPHGAPQCKLNOEANYIIASSIGSFVFCILMILVYL	180		
Qy	194	RIYLIJAKSNRRGPAPKAGPGQGSKQPRPHGALASAKIPLAAS-VASAREVNGHSKS	252		
Db	181	RIYLIJAKSHRRGPAPKAGPGEGESROACPYPGSPSASAKIPLTATPVASASEANGPSKP	240		
Qy	253	TGEKEGEGTPEDTGRALPPSWAALPNSGGQOKKEVCASPEDAEKEEEEEEEBCECP	312		
Db	241	AGEKEGEGTPEDTGRQALPPCGKATLPPNSGGQOKKEVSASALEEKEEEEEEEBCEED--EP	298		
Qy	313	QAVPVSPASACSPPIQOPQGSRVLTATLFGQVILGKGVALGQWRRRAOULTREKRFYV	372		
Db	299	QAVPVSPASVSPPIQOPQGSRVLTATLFGQVILGKGVAGMGQWRRRAOLSRERKRFYV	358		
Qy	373	LAVVIGVFLVLCMPPEFSYSIGALCPKXCVPHGIF	408		
Db	359	LAVVIGVFLVLCMPPEFSYSIALCLCPQCKRVPHGIF	394		

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      A2AB_ORYAE          RESULT 6
ID _A2AB_ORYAF          STANDARD; PRT; 388 AA.
AC O19032;
DT 15-JUL-1998 (Rel. 36, Created)
DR 15-JUL-1998 (Rel. 36, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
OS ADRA2B.
OC Orycteropus afer (Aardvark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Tubulidentata; Orycteropodidae; Orycteropus.
OX NCBT_taxonomy=9818;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97357151; PubMed=9214502;
RA Springer M.S., Clevon G.C., Madson O.J., de Jong W.W., Weddell V.G.,
RA Amrine H.M., Scanhope M.J.;
RT "Endemic African mammals shake the phylogenetic tree.";
RL Nature 388:61-64(1997).
CC -! FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATÉCHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcement/
CC or send an email to licenses@ebi.ac.uk).
CC -----
DR EMBL; Y12522; CAAT73122.2; ALT SEQ.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHOOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.

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KW G-protein coupled receptor; Transmembrane; Multigene family;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT NON TER 1
 FT TRANSMEM <1 25
 FT TRANSMEM 26 36
 FT TRANSMEM 37 62
 FT TRANSMEM 63 72
 FT TRANSMEM 73 95
 FT TRANSMEM 96 117
 FT TRANSMEM 118 140
 FT TRANSMEM 141 156
 FT TRANSMEM 157 180
 FT TRANSMEM 181 352
 FT TRANSMEM 353 376
 FT TRANSMEM 377 385
 FT TRANSMEM 386 >388
 FT DISULFID 72 151
 FT DOMAIN 280 291
 FT SITE 79
 FT SITE 163 163
 FT SITE 167 167
 FT NON TER 388 388
 FT SEQUENCE 388 AA; 42429 MW; 1810DC767E838897 CRC64;
 Query Match 74.7%; Score 1775.5; DB 1; Length 388;
 Best Local Similarity 87.1%; Pred. No. 3.5e-94;
 Matches 345; Conservative 15; Mismatches 27; Indels 9; Gaps 4;
 QY 14 AIAAAITFLIETFTFGNALVILAVLTSRSRAPONFLVLSLAADILVATLIIIPSLANE 73
 DB 1 AIAAVITFLIETFTFGNALVILAVLTSRSRAPONFLVLSLAADILVATLIIIPSLANE 60
 QY 74 LLGWTFRRTWCERYALDLVLCFTSSIVHCAISLDRYVAVRALRYNSKTRPRKICII 133
 DB 61 LLGWTFRRTWCERYALDLVLCFTSSIVHCAISLDRYVAVRALRYNSKTRPRKICII 120
 QY 134 LTVWLLAAVLSLPLLYKGDQGPGRPOCKLNOBAMWTLASISGSPAPCLIMLVYL 193
 DB 121 LTVWLLAAVLSLPLLYKGDQGPGRPOCKLNOBAMWTLASISGSPAPCLIMLVYL 180
 QY 194 RIVLAKRSNRPRRAKGGPQGESKOPRDHGALASAKI.PAL-ASVASARENGHSKS 252
 DB 181 RIVLAKRSNRPRRAKGGPQGESKOPRDHGALASAKI.PAL-ASVASARENGHSKS 239
 QY 253 TGEKEGETPEDTGTALPPSWAALPNGGQKQKGVCGASPEDDAEEEEESECEP 312
 DB 240 TGEK-EGKTPEDGTILTPSPWPAFNPNGEQKGI.CGTSPDEEA-----EESECEP 292
 QY 313 QAVPVSPACSPPIQQPQGSRTATLIRGOVLLRGVGAIGQWRRRAQLTREKFTTV 372
 DB 293 QAAAPSASACNPPIQQPQGSRTATLIRGOVLLRGVGAIGQWRRRAQLTREKFTTV 352
 QY 373 LAVVGVEFLCMFPFFFSYSGAICPKKCKVPHLFL 408
 DB 353 LAVVGVEFLCMFPFFFSYSGAICPKKCKVPHLFL 388
 RESULT 7
 A2AB_HORSE
 ID_A2AB_HORSE STANDARD; PRT; 389 AA.
 AC 077721;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADBA2B.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxId=9796;

RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=98334573; PubMed=9667998;
 RA Stanhope M.J., Madsen O.J., Maddehl V.G., Cleven G.C., de Jong W.W.,
 RA Springer M.S.,
 RT "Highly congruent molecular support for a diverse superordinal clade
 of endemic African mammals.";
 RL Mol. Phylogenet. Evol. 9:501-508 (1998).
 RN [2]
 REVISIONS.
 RA Madsen O.J.;
 RL Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; Y15945; CAA75898.2;
 DR HSBP; P29274; IMMH.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1.1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family.
 FT NON TER 1
 FT TRANSMEM <1 25
 FT TRANSMEM 26 36
 FT TRANSMEM 37 62
 FT TRANSMEM 63 72
 FT TRANSMEM 73 95
 FT TRANSMEM 96 117
 FT TRANSMEM 118 140
 FT TRANSMEM 141 156
 FT TRANSMEM 157 180
 FT TRANSMEM 181 363
 FT TRANSMEM 364 387
 FT TRANSMEM 388 >389
 FT DISULFID 72 151
 FT DOMAIN 281 302
 FT SITE 79
 FT SITE 163 163
 FT SITE 167 167
 FT NON TER 389 389
 FT SEQUENCE 389 AA; 42257 MW; 992179431679B0FD CRC64;
 Query Match 74.6%; Score 1775; DB 1; Length 389;
 Best Local Similarity 89.5%; Pred. No. 3.7e-94;
 Matches 349; Conservative 11; Mismatches 24; Indels 6; Gaps 3;
 QY 14 AIAAAITFLIETFTFGNALVILAVLTSRSRAPONFLVLSLAADILVATLIIIPSLANE 73
 DB 1 AIAAVITFLIETFTFGNALVILAVLTSRSRAPONFLVLSLAADILVATLIIIPSLANE 60
 QY 74 LLGWTFRRTWCERYALDLVLCFTSSIVHCAISLDRYVAVRALRYNSKTRPRKICII 133
 DB 61 LLGWTFRRTWCERYALDLVLCFTSSIVHCAISLDRYVAVRALRYNSKTRPRKICII 120
 QY 134 LTVWLLAAVLSLPLLYKGDQGPGRPOCKLNOBAMWTLASISGSPAPCLIMLVYL 193
 DB 121 LTVWLLAAVLSLPLLYKGDQGPGRPOCKLNOBAMWTLASISGSPAPCLIMLVYL 180

Qy	194	R1Y1IAKSNRGRPAKGPQGESEKQRPDHGALAAK1.PALAS	-VASAREVNGHSKS	252
Db	181	R1Y1IAKSHLRGPPAKGPGGGGSKQHPHVPAGASNAK1.PTVAS	CLAANGNGHSDP	240
Qy	253	TGKEBEGTPEBDTGTTRALPSPWALPNSGGQKQEGVCASPEDEA	EEEEEEEEEE	308
Db	241	TGKR-EAETPDSCTPALPSSWPALPSSGGQDKQEGVCASLEEA	EEEEEEEEEE	299
Qy	309	ECEPAVVSASACSPLOQPGSRVYATLRGVTLRGVGLGGQWRRPAQ	LTREKR	368
Db	300	ECEPAALPASPASASPPLOQPGSRVYATLRGVTLRGVATAGAQW	RRRAQLTREKR	359
Qy	369	FTFVLAVIGVFVLCWPPFPFSSYSALICP	398	
Db	360	FTFVLAVIGVFVLCWPPFPFSSYSALICP	389	
RESULT 8				
AZAB	ERIEU	STANDARD;	PRT;	391 AA.
ID	AZAB	ERIEU	019012;	
DT	15-JUL-1998	(Rel. 36, Created)		
DT	15-JUL-1998	(Rel. 36, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor)	(Fragment).		
GN	ADRA2B			
OS	Erinaceus europaeus (Western European hedgehog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.			
OX	NCBI_TaxID=9365;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97357151; PubMed=9214502;			
RA	Springer M.S., Clevon G.C., Madsen O.J., de Jong W.W., Waddell V.G.,			
RA	Aminde H.M., Scanhane M.J.;			
RT	"Endemic African mammals shake the phylogenetic tree.";			
RL	Nature 388:61-64(1997).			
CC	-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-			
CC	INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G			
CC	PROTEINS.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	OR SEND AN EMAIL TO license@sib-sib.ch).			
CC	-----			
DR	EMBL; Y12521; CAA73121.1; -.			
DR	HSSP; P29274; IMMH.			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHDOPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.			
DR	PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Multigene family;			
KW	Phosphorylation; Lipoprotein; Palmitate.			
FT	NON TER	1		
FT	TRANSMEM	<1	25	1 (POTENTIAL).
FT	TRANSMEM	26	36	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	37	62	2 (POTENTIAL).
FT	DOMAIN	63	72	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	73	95	3 (POTENTIAL).
FT	TRANSMEM	96	117	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	118	140	4 (POTENTIAL).
FT	DOMAIN	141	156	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	157	180	5 (POTENTIAL).
FT	DOMAIN	181	355	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	356	379	6 (POTENTIAL).

[illegible]

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DR EMBL: Y12525; CAA73125.1; -
 DR HSSP: P29274; IMM.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane; Multigene family;
 FT Phosphorylation; Lipoprotein; Palmitate.

FT NON_TER 1 1
 FT TRANSMEM 1 25
 FT DOMAIN 26 36
 FT TRANSMEM 37 62
 FT DOMAIN 63 72
 FT TRANSMEM 73 95
 FT DOMAIN 96 117
 FT TRANSMEM 118 140
 FT DOMAIN 141 156
 FT TRANSMEM 157 180
 FT DOMAIN 181 348
 FT TRANSMEM 349 372
 FT DOMAIN 373 381
 FT TRANSMEM 382 384
 FT DISULFID 72 151
 FT DOMAIN 281 285
 FT SITE 79 79
 FT SITE 163 163
 FT SITE 167 167
 FT NON_TER 384 384
 FT SEQUENCE 384 AA; 41911 MW; CFA1B56C355B94F CRC64;

Query Match Best Local Similarity 73.5%; Score 1748.5; DB 1; Length 384;
 Matches 341; Conservative 8; Mismatches 34; Indels 13; Gaps 3;

QY 14 AIAAATPFLITFTFGNALVILAVLTSSSLAPONLFLVSLAADIIVATIIIPPSLANE 73
 DB 1 AIAAATPFLITFTFGNALVILAVLTSSSLAPONLFLVSLAADIIVATIIIPPSLANE 60
 QY 74 LIGVWERTCEVIALDVLFCTSSIVHLCASIDRYMAVSRALEVNSKRTPRICII 133
 DB 61 LIGVWERTCEVIALDVLFCTSSIVHLCASIDRYMAVSRALEVNSKRTPRICII 120
 QY 134 LTVMLIAVLSLPLIYKGDOPORGRPOCKNOEMYLASSISGFAPCLIMILVYI 193
 DB 121 LTVMLIAVLSLPLIYKGDOPORGRPOCKNOEMYLASSISGFAPCLIMILVYI 180
 QY 194 RYILAKSNRGRPAKGGPGGSSKOPRDPHGALASAKLPALA-SVASAREVNGSHS 252
 DB 191 RYILAKSNRGRPAKGGPGGSSKOPRDPHGALASAKLPALA-SVASAREVNGSHS 240
 QY 253 TGEKEEGTPEPTDTTRALPESMALPNSGOGKEGVGASPEDEABEEEBEEBEECEP 312
 DB 241 TGEKEEGTPEPTDTTRALPESMALPNSGOGKEGVGASPEDEABEEEBEEBEECEP 288
 QY 313 QAVVSPASACSPYLOQPGSRVIALTARGVLLGRGVAGIGGOWRRRAQITREKRFIV 372
 DB 289 PAVPASALACSPYLOQPGSRVIALTARGVLLGRGVAGIGGOWRRRAQITREKRFIV 348
 QY 373 LAVVIGFVLCMPFFFSYSIGAIICPKGVPHGLP 408
 DB 349 LAVVIGFVLCMPFFFSYSIGAIICPKGVPHGLP 384

RESULT 10
 A2AB_AMBHO ID A2AB_AMBHO STANDARD; PRT; 386 AA.
 AC 018935;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 OS ADRA2B.
 OS Amblysomus hottentotus (Hottentot golden mole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Chrysochloridae; Amblysomus.
 OX NCBI_TaxID=9391;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97357151; PubMed=9214502;
 RA Springer M.S., Clevon G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
 RA Amrine H.M., Stanhope M.J.;
 RT "Endemic African mammals shake the phylogenetic tree.";
 RN Nature 388:61-64 (1997).
 RN [2]
 RP REVISION TO 121.
 RA Madsen O.J.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL: Y12526; CAA73126.2; -
 DR HSSP: P29274; IMM.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane; Multigene family;
 FT Phosphorylation; Lipoprotein; Palmitate.

FT NON_TER 1 1
 FT TRANSMEM 1 25
 FT DOMAIN 26 36
 FT TRANSMEM 37 62
 FT DOMAIN 63 72
 FT TRANSMEM 73 95
 FT DOMAIN 96 117
 FT TRANSMEM 118 140
 FT DOMAIN 141 156
 FT TRANSMEM 157 180
 FT DOMAIN 181 350
 FT TRANSMEM 351 374
 FT DOMAIN 375 383
 FT TRANSMEM 384 386
 FT DISULFID 72 151
 FT SITE 79 79
 FT SITE 163 163
 FT SITE 167 167
 FT NON_TER 386 386
 FT SEQUENCE 386 AA; 42157 MW; ECE11E0B7192D955 CRC64;

Query Match 73.5%; Score 1747.5; DB 1; Length 386;
 Best Local Similarity 87.1%; Pred. No. 1.3e-92;
 Matches 345; Conservative 7; Mismatches 33; Indels 11; Gaps 3;

QY 14 AIAAATFTLFTFGNALVTLAVLTSRSLAPQNLPLVSLAADIIVATLIPPSLANE 73
 DB 1 AIAAVITFLFTFGNALVTLAVLTSRSLAPQNLPLVSLAADIIVATLIPPSLANE 60
 QY 74 LAGYWRRTWCCEVYALADVLCFTSSIVHCAISLDYRWAVSRALRYNSKRTPRKICII 133
 DB 61 LAGYWRRTWCCEVYALADVLCFTSSIVHCAISLDYRWAVSRALRYNSKRTPRKICII 120
 QY 134 LTVWLIAAVISLPLIYKDGQPGQSRVLTATLRGVLTGRGVGALIGQWRRRAQLTREKRTFTV 193
 DB 121 LTVWLIAAVISLPLIYKDGQPGQSRVLTATLRGVLTGRGVGALIGQWRRRAQLTREKRTFTV 180
 QY 194 RIYLIARSRNRGRAGGPGQSGSKQPRPHGALASAKIPAL-ASVARSREYNGSKS 252
 DB 181 RIYLIARSRNRGRAGGPGQSGSKQPRPHGALASAKIPAL-ASVARSREYNGSKS 240
 QY 253 TGEKEGETPEDTGTALPPSMALPNSGQSGKEGVGASPEDAEDEEEDDEEEDCEP 312
 DB 241 TG--EEGETLEDPTSTLPSWPAIPNSDQSGKEGVGCTSP-----EEDDEEEDCEP 290
 QY 313 QAVVSPASACSPPLQPGQSRVLTATLRGVLTGRGVGALIGQWRRRAQLTREKRTFTV 372
 DB 291 QAVVSPASACSPPLQPGQSRVLTATLRGVLTGRGVGALIGQWRRRAQLTREKRTFTV 350
 QY 373 LAVVIGVFLVLCWPFPPFSYSLGAIICPKCKVPHGLF 408
 DB 351 LAVVIGVFLVLCWPFPPFSYSLGAIICPKCKVPHGLF 386

RESULT 11
 A2AB_BOVIN STANDARD; PRT; 392 AA.
 AC 077700;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADRAB2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_taxid=9913;
 RN [1]
 RP MEDLINE=98334573; PubMed=9667998;
 RA Stanhope M.J., Madsen O.J., Madsen V.G., Cleven G.C., de Jong W.W.,
 RA Springer M.S.;
 RT "Highly congruent molecular support for a diverse superordinal clade
 of endemic African mammals."
 RL Mol. Phylogenet. Evol. 9:501-508 (1998).
 CC -1- FUNCTION: ALPHA-2B ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: Y15944; CAAT5897.2; -.
 DR HSSP: P29274; IMMH.
 DR InterPro: IPR000276; GPCR_Rhodopn.
 DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_RHODOPN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family.

FT NON_TER 1
 FT TRANSMEM 1
 FT DOMAIN 26
 FT TRANSMEM 37
 FT DOMAIN 63
 FT TRANSMEM 72
 FT DOMAIN 73
 FT TRANSMEM 96
 FT TRANSMEM 118
 FT DOMAIN 141
 FT TRANSMEM 157
 FT DOMAIN 181
 FT TRANSMEM 357
 FT DOMAIN 381
 FT DISULFID 72
 FT DOMAIN 283
 FT SITE 79
 FT SITE 163
 FT SITE 167
 FT SITE 167
 FT NON_TER 392
 FT SEQUENCE 392 AA; 42839 MM; 471596A744647550 CRC64;

Query Match 73.3%; Score 1743.5; DB 1; Length 392;
 Best Local Similarity 86.4%; Pred. No. 2.3e-92;
 Matches 343; Conservative 12; Mismatches 35; Indels 7; Gaps 3;

QY 14 AIAAATFTLFTFGNALVTLAVLTSRSLAPQNLPLVSLAADIIVATLIPPSLANE 73
 DB 1 AIAAVITFLFTFGNALVTLAVLTSRSLAPQNLPLVSLAADIIVATLIPPSLANE 60
 QY 74 LAGYWRRTWCCEVYALADVLCFTSSIVHCAISLDYRWAVSRALRYNSKRTPRKICII 133
 DB 61 LAGYWRRTWCCEVYALADVLCFTSSIVHCAISLDYRWAVSRALRYNSKRTPRKICII 120
 QY 134 LTVWLIAAVISLPLIYKDGQPGQSRVLTATLRGVLTGRGVGALIGQWRRRAQLTREKRTFTV 193
 DB 121 LTVWLIAAVISLPLIYKDGQPGQSRVLTATLRGVLTGRGVGALIGQWRRRAQLTREKRTFTV 180
 QY 194 RIYLIARSRNRGRAGGPGQSGSKQPRPHGALASAKIPAL-ASVARSREYNGSKS- 251
 DB 121 RIYLIARSRNRGRAGGPGQSGSKQPRPHGALASAKIPAL-ASVARSREYNGSKS- 180
 QY 194 RIYLIARSRNRGRAGGPGQSGSKQPRPHGALASAKIPAL-ASVARSREYNGSKS- 251
 DB 181 RIYLIARSRNRGRAGGPGQSGSKQPRPHGALASAKIPAL-ASVARSREYNGSKS- 240
 QY 252 STGEKEGETPEDTGTALPPSMALPNSGQSGKEGVGASPEDAEDEEEDDEEEDCEP 311
 DB 241 STGEKEGETPEDTGTALPPSMALPNSGQSGKEGVGASPEDAEDEEEDDEEEDCEP 295
 QY 312 QAVVSPASACSPPLQPGQSRVLTATLRGVLTGRGVGALIGQWRRRAQLTREKRTFTV 371
 DB 296 QAVVSPASACSPPLQPGQSRVLTATLRGVLTGRGVGALIGQWRRRAQLTREKRTFTV 355
 QY 372 LAVVIGVFLVLCWPFPPFSYSLGAIICPKCKVPHGLF 408
 DB 356 LAVVIGVFLVLCWPFPPFSYSLGAIICPKCKVPHGLF 392

RESULT 12
 A2AB_TALEU STANDARD; PRT; 397 AA.
 AC 019091;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADRAB2.
 OS Talpa europaea (European mole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.

NCBI_TaxID=29082;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=97357151; PubMed=9214502;
 RA Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
 RA Amrine H.M., Stachope W.J.;
 RT "Endemic African mammals shake the phylogenetic tree.";
 RL Nature 388:61-64(1997).
 [2]
 RP REVISIONS TO 148 AND 255.
 RA Springer M.S., Cleven G.C., Madsen O., de Jong W.W., Waddell V.G.,
 RA Amrine H.M., Stachope W.J.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, Y12524; CAA73124.2; -.
 DR HSPB, P29274; 1MMH.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT NON_TER 1 1
 FT TRANSMEM 1 25
 FT DOMAIN 26 36 1 (POTENTIAL).
 FT TRANSMEM 37 62 2 (POTENTIAL).
 FT DOMAIN 63 72 3 (POTENTIAL).
 FT TRANSMEM 73 95 3 (POTENTIAL).
 FT DOMAIN 96 117 4 (POTENTIAL).
 FT TRANSMEM 118 140 4 (POTENTIAL).
 FT DOMAIN 141 156 5 (POTENTIAL).
 FT TRANSMEM 157 180 5 (POTENTIAL).
 FT DOMAIN 181 351 6 (POTENTIAL).
 FT TRANSMEM 352 375 6 (POTENTIAL).
 FT DOMAIN 376 384 7 (POTENTIAL).
 FT TRANSMEM 385 387 7 (POTENTIAL).
 FT DOMAIN 388 288 ASP/GLU-RICH (ACIDIC).
 FT DISULFD 72 151 BY SIMILARITY.
 FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
 SIMILARITY).
 FT SITE 163 163 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT NON_TER 387 387
 FT SEQUENCE 387 AA; 42587 MM; B74AD5F0EE23BD5A CRC64;
 Query Match 71.3%; Score 1696; DA 1; Length 387;
 Best Local Similarity 84.4%; Pred. No. 1,le-89;
 Matches 335; Conservative 13; Mismatches 37; Indels 12; Gaps 4;
 QY 14 AIAAATFLIFLFTFGNALVTLAVLTSSRLAPQNLFLVSLAADIIVATLIIIPSLANE 73
 DB 1 AIAAVITFLIFLFTFGNALVTLAVLTSSRLAPQNLFLVSLAADIIVATLIIIPSLANE 60
 QY 74 LIGTWYFRRTWCEVYLAADVLFCTISSIVHLCAISLDRYWAVSRALFNKSKTPRIKCTI 133
 DB 61 LIGTWYFRRTWCEVYLAADVLFCTISSIVHLCAISLDRYWAVSRALFNKSKTPRIKCTI 120

QY 134 LTVWLIAAVISLPLEIYKGDQGPQPRGRPOCKLNQEAWYLIASSIGSPFAPCLIMILVYL 193
 DB 121 LTVWLIAAAISLPLEIYKGDQDPQPRGRPOCKLNQEAWYLISSIGSPFAPCLIMILVYL 180
 QY 194 RIYLIAR-SNRGPRAKGPGGEGSKQPRPDHCGALASAKLPPLAS-VASAREVNGHSK 251
 DB 181 RIYLIARSSSRKPRKGPREGESKQPRPVGVTSVARPPALTSPLAVTANGHSK 240
 QY 252 STGEKEGETPEDTGTALPPSMALPNSSGQKEGVCGASPEDEAESEEESECE 311
 DB 241 PTGER---ETPEDLVSPASFPSPWPAIPISSGQKREGVCGTSPDEEA-----EESEECG 290
 QY 312 PQAVVSPASACSPPLQPGQSRVATLRQVILRGVGAIGQWRRRAQLTEKRTF 371
 DB 291 PEAVPASPALACSPSLQPPQGSRLVATLRQVILRGVGTARCGWRRRAQLTREKRTF 350
 QY 372 VLAVVIGVFLCWPFFFSYSLGAIKPKKVPKGLF 408
 DB 351 VLAVVIGVFLCWPFFFSYSLGAIKPKKVPKGLF 387

Search completed: February 6, 2004, 18:18:03
 Job time : 11.0334 secs

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OM protein - protein search, using sw model

Run on: February 6, 2004, 18:11:25 / Search time 33.1104 Seconds
(without alignments)
3507.169 Million cell updates/sec

Title: US-09-692-077D-7
Perfect score: 2378
Sequence: 1 MDHODPYSVQATAIAAAT.....QDFRARPRLICRPWTQTAW 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteria:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2139.5	90.0	451	6	Q8HY8 tupaii
2	1999	84.1	453	11	Q925E4 ratu
3	1950	82.0	448	11	Q925K7 mus
4	1945	81.8	448	11	Q925K6 mus
5	1885	79.3	401	6	Q8MK45 cap
6	1856	78.0	397	11	Q8K1W6 cas
7	1855	78.0	393	6	Q9GL11 myc
8	1855	78.0	399	6	Q8M1D0 myc
9	1844	77.5	395	6	Q9GL12 man
10	1842	77.5	395	11	Q8K1U9 ere
11	1842	77.5	391	6	Q9GL06 sus
12	1841	77.4	387	6	Q9GL17 fel
13	1833	77.1	389	6	Q9GL07 pho
14	1828	76.9	399	6	Q8MK51 lama
15	1824.5	76.7	390	6	Q9GL19 cyn
16	1814	76.3	399	6	Q8M1E3 lep

17	1811	76.2	389	6	Q9GK25	Q9GK25 tupaii tana
18	1808	76.0	395	6	Q95N91	Q95N91 tonatia bid
19	1807.5	76.0	398	6	Q8SQ92	Q8SQ92 natalis str
20	1807	76.0	392	6	Q8M1E1	Q8M1E1 lama guanic
21	1806.5	76.0	392	11	Q8K1U3	Q8K1U3 marmota mon
22	1806	75.9	395	11	Q8K1R6	Q8K1R6 anomalous
23	1798.5	75.6	390	6	Q95N89	Q95N89 tapozous s
24	1798	75.6	393	6	Q9GL16	Q9GL16 hippopotamu
25	1795	75.5	389	11	Q8K1V1	Q8K1V1 echinus chr
26	1792.5	75.4	388	6	Q8SQ93	Q8SQ93 mycteris gr
27	1791	75.3	389	11	Q8CG78	Q8CG78 chinilla
28	1790.5	75.3	388	6	Q8SQ91	Q8SQ91 mycteris th
29	1789	75.2	393	11	Q8K1P2	Q8K1P2 tichys fas
30	1787	75.1	393	11	Q9JTW2	Q9JTW2 cavia porce
31	1786	75.0	395	6	Q8SQ94	Q8SQ94 noctilio al
32	1783.5	75.0	388	6	Q9GL18	Q9GL18 diceros bic
33	1782	74.9	389	6	Q95N94	Q95N94 hipposidero
34	1779	74.8	391	6	Q8SQ90	Q8SQ90 emballonura
35	1778.5	74.8	406	11	Q8K1N6	Q8K1N6 thomomys ta
36	1776.5	74.7	392	6	Q9GL35	Q9GL35 balaenopter
37	1776	74.7	389	11	Q8K1W8	Q8K1W8 bathyergus
38	1776	74.7	395	11	Q8K1U7	Q8K1U7 myoxus glis
39	1774.5	74.6	394	6	Q8SQ91	Q8SQ91 desmodus ro
40	1772	74.5	391	6	Q8HY23	Q8HY23 physeter ca
41	1772	74.5	391	11	Q8K1R1	Q8K1R1 massoutiera
42	1771.5	74.5	392	11	Q8K4Y3	Q8K4Y3 sciurus vul
43	1769.5	74.4	392	6	Q95N90	Q95N90 tadarda br
44	1769	74.4	391	6	Q8M1E5	Q8M1E5 hyalomys sui
45	1760.5	74.0	400	6	Q8HXW4	Q8HXW4 galenys pyr

ALIGNMENTS

RESULT 1	
Q8HY8	PRELIMINARY; PRT; 451 AA.
ID	Q8HY8
AC	Q8HY8
DT	01-MAR-2003 (TREMREL. 23, Created)
DT	01-MAR-2003 (TREMREL. 23, Last sequence update)
DT	01-MAR-2003 (TREMREL. 23, Last annotation update)
DE	Alpha-2B adrenoceptor.
OS	Tupaia belangeri (Northern tree shrew).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX	NCBI_TaxID=37347;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Heilbronner U., Van Kampen M., Isovich E., Fluegge G.;
RT	"Thalamic alpha-2B adrenoceptors under chronic stress: persistent
RT	upregulation in the paraventricular nucleus."
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY150333; ANAN2436.1; -
SQ	SEQUENCE 451 AA; 50356 MW; 3172403011F3BC60 CRC64;

Query Match	90.0%; Score 2139.5; DB 6; Length 451;
Best Local Similarity	91.1%; Pred. No. 2.7e-163;
Matches	411; Conservative 8; Mismatches 31; Indels 1; Gaps 1;
Qy	1 MDHODPYSVQATAIAAATFTPLIFTEFGNALVTILAVTSRSLRAPONTPLVSLAADI 60
Db	1 MHOEPYSVQATAIAAATFTPLIFTEFGNALVTILAVTSRSLRAPONTPLVSLAADI 60
Qy	61 VATLIIPFSLANELLGWYFRRTWCYVLAADVLCFTSSIVHLCALSIDRYAVASALEY 120
Db	61 VATLIIPFSLANELLGWYFRRTWCYVLAADVLCFTSSIVHLCALSIDRYAVASALEY 120
Qy	121 NSKRTPRKICITITWVLAIAVISLPLIYKGDGPPQPRGRPOCKNOEMAYTIASSIGS 180
Db	121 NSKRTPRKICITITWVLAIAVISLPLIYKGDGPPQPRGRPOCKNOEMAYTIASSIGS 180
Qy	181 FFAFCLIMLVIAIRIYIAKSRNRRGPRAGKGPQGGSKQPRPHGALSAKLPALA-S 239
Db	181 FFAFCLIMLVIAIRIYIAKSRNRRGPRAGKGPQGGSKQPRPHGALSAKLPALA-S 239

Db 181 FFAPCLIMILVLRILYIAKSNRGRPVKRGPGWQSGKQPRFVGRASAKLPPLTAS 240
QY 240 VASAREVNGSHKSGEKEGETPEDTGTALPFSMAALPNSGGQKEGVCASPDEABE 299
Db 241 LATGANGSHKSPGNNEDEDEPDGTATLPPSMAALASSGQGGQEGREMSABE 300
QY 300 EEEEEEECEPQAVSPASACSPPLQOPQSGRYLATLRGVLLRGVGAIGGQWRR 359
Db 301 EEEEEEECEPQAVSPASACSPPLQOPQSGRYLATLRGVLLRGVGAIGGQWRR 360
QY 360 RAOLREKRTFTFLAVVIGVULCWPFFFSYSGALCPKXCKVPHGLPQFFMIGYCN 419
Db 361 RAOLREKRTFTFLAVVIGVULCWPFFFSYSGALCPKXCKVPHGLPQFFMIGYCN 420
QY 420 SINPIYITIFNODFRAPRRLICRPMTOTAM 450
Db 421 SINPIYITIFNODFRAPRRLICRPMTOTAM 451

RESULT 2
Q925E4 PRELIMINARY; PRT; 453 AA.
AC 0925E4; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
GN Alpha2B-adrenergic receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Schaak S., Cusack D., Paris H.,
RT "Cloning and characterization of the rat alpha2B-adrenergic receptor
gene promoter."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AF366899; AAK53388.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 453 AA; 50369 MW; CBA69CE23BACB511 CRC64;

Query Match 84.1%; Score 1999; DB 11; Length 453;
Best Local Similarity 84.3%; Pred. No. 4.9e-152;
Matches 380; Conservative 25; Mismatches 42; Indels 4; Gaps 2;
QY 1 MDHODPVSQVATAAIAAATFLILFTIFGNALVILAVLTSRSIRAPONLFLVSLAADIL 60
Db 6 MDHODPVSQVATAAIAAATFLILFTIFGNALVILAVLTSRSIRAPONLFLVSLAADIL 65
QY 61 VATTIIPFSLANELGYWYFRTWCEVYALDVLCTSSIVHLCAISLDRYMAVSRALEY 120
Db 66 VATTIIPFSLANELGYWYFRTWCEVYALDVLCTSSIVHLCAISLDRYMAVSRALEY 125
QY 121 NSKRTPRRIKCIILTWLIAAVISLPPLIYKDGQOPGRPOCKLNOEAWYIIASSIGS 180
Db 126 NSKRTPRRIKCIILTWLIAAVISLPPLIYKDGQOPGRPOCKLNOEAWYIIASSIGS 185
QY 181 FFAPCLIMILVLRILYIAKSNRGRPVKRGPGWQSGKQPRFVGRASAKLPPLTAS 240
Db 186 FFAPCLIMILVLRILYIAKSNRGRPVKRGPGWQSGKQPRFVGRASAKLPPLTAS 245
QY 240 VASAREVNGSHKSGEKEGETPEDTGTALPFSMAALPNSGGQKEGVCASPDEABE 299
Db 246 LSSVGEANGHPRPREKEGETPEDTGTALPFSMAALPNSGGQKEGVCASPDEABE 302

QY 300 EEEEEEECEPQAVSPASACSPPLQOPQSGRYLATLRGVLLRGVGAIGGQWRR 359
Db 303 DEEDEVEVECEPQAVSPASACSPPLQOPQSGRYLATLRGVLLRGVGAIGGQWRR 362
QY 360 RAOLREKRTFTFLAVVIGVULCWPFFFSYSGALCPKXCKVPHGLPQFFMIGYCN 419
Db 361 RAOLREKRTFTFLAVVIGVULCWPFFFSYSGALCPKXCKVPHGLPQFFMIGYCN 422
QY 420 SINPIYITIFNODFRAPRRLICRPMTOTAM 450
Db 423 SINPIYITIFNODFRAPRRLICRPMTOTAM 451

RESULT 3
Q925K7 PRELIMINARY; PRT; 448 AA.
AC 0925K7; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
GN Adrenergic receptor alpha 2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Cammiff J.,
RT "High-throughput sequence identification of Gene Coding Variants
within Alcohol-Related QTLs."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AF330493; AAK56078.1; -
DR MGI; MGI:879303; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 448 AA; 50018 MW; 1B5BD9456C0B2873 CRC64;

Query Match 82.0%; Score 1950; DB 11; Length 448;
Best Local Similarity 83.4%; Pred. No. 4.1e-148;
Matches 376; Conservative 22; Mismatches 49; Indels 4; Gaps 2;
QY 1 MDHODPVSQVATAAIAAATFLILFTIFGNALVILAVLTSRSIRAPONLFLVSLAADIL 60
Db 1 MDHODPVSQVATAAIAAATFLILFTIFGNALVILAVLTSRSIRAPONLFLVSLAADIL 65
QY 61 VATTIIPFSLANELGYWYFRTWCEVYALDVLCTSSIVHLCAISLDRYMAVSRALEY 120
Db 61 VATTIIPFSLANELGYWYFRTWCEVYALDVLCTSSIVHLCAISLDRYMAVSRALEY 125
QY 121 NSKRTPRRIKCIILTWLIAAVISLPPLIYKDGQOPGRPOCKLNOEAWYIIASSIGS 180
Db 122 NSKRTPRRIKCIILTWLIAAVISLPPLIYKDGQOPGRPOCKLNOEAWYIIASSIGS 185
QY 181 FFAPCLIMILVLRILYIAKSNRGRPVKRGPGWQSGKQPRFVGRASAKLPPLTAS 240
Db 181 FFAPCLIMILVLRILYIAKSNRGRPVKRGPGWQSGKQPRFVGRASAKLPPLTAS 245
QY 240 VASAREVNGSHKSGEKEGETPEDTGTALPFSMAALPNSGGQKEGVCASPDEABE 299
Db 241 LSSVGEANGHPRPREKEGETPEDTGTALPFSMAALPNSGGQKEGVCASPDEABE 302
QY 300 EEEEEEECEPQAVSPASACSPPLQOPQSGRYLATLRGVLLRGVGAIGGQWRR 359

Db 299 - EEDDEEECEPQTLPASPASVENPQOQTSRVATLRLGCVLLSKNGVAGQWRR 357
 QY 360 RAQTRERKFTFLAVAVIGVFLCMPPFFFSYSGAICPKKCKVPHGLFOFFFWIGYCN 419
 Db 358 RTQLSRKRFVFLAVAVIGVFLCMPPFFFSYSGAICPKKCKVPHGLFOFFFWIGYCN 417
 QY 420 SLNPVIYITINODFRRAFRILCRPMTOTAW 450
 Db 418 SLNPVIYITINODFRRAFRILCRPMTOTAW 448

RESULT 4

Q925K6 PRELIMINARY; PRT: 448 AA.
 AC 0925K6
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Adrenergic receptor alpha 2B.
 GN ADRA2B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=ILS;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikea J.M.,
 RT "High-Throughput Sequence Identification of Gene Coding Variants
 RT within Alcohol-Related QTLs";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF332050; AAKS6079.1; -.
 DR MGI: MGI:87935; Adra2b.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 448 AA; 49998 MW; B37BEB21B0EC4625 CRC64;

Query Match 81.8%; Score 1945; DB 11; Length 448;
 Best Local Similarity 83.1%; Pred. No. 1e-147;

Matches 375; Conservative 22; Mismatches 50; Indels 4; Gaps 2;

QY 1 MDHODPVSQVATAIAAIFLFTIFGNALVTLAVLTSRSLRAPONLFLVSLAADIL 60
 Db 1 MHOEPISVQNTAIAIAAIFLFTIFGNALVTLAVLTSRSLRAPONLFLVSLAADIL 60
 QY 61 VATLIIFPSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCATSLDRYMAVSRL 120
 Db 61 VATLIIFPSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCATSLDRYMAVSRL 120
 QY 121 NSKTRPRIRKIIITLWVLAIVSLPLIYKGGQPOPRGRPOCKLNOEAMYLIIASSIG 180
 Db 121 NSKTRPRIRKIIITLWVLAIVSLPLIYKGGQPOPRGRPOCKLNOEAMYLIIASSIG 180
 QY 121 NSKTRPRIRKIIITLWVLAIVSLPLIYKGGQPOPRGRPOCKLNOEAMYLIIASSIG 180
 Db 121 NSKTRPRIRKIIITLWVLAIVSLPLIYKGGQPOPRGRPOCKLNOEAMYLIIASSIG 180
 QY 181 FPAFLCLMILVLYLIIYIAKSNRGRPRAGKGGPOGSGKOPRPHGALASAKLPALAS 239
 Db 181 FPAFLCLMILVLYLIIYIAKSNRGRPRAGKGGPOGSGKOPRPHGALASAKLPALAS 239
 QY 240 VASAREVNGHSKSTGKEBETPEDTGTALPSSMAALPNSGQKQGVGASPEDBAE 299
 Db 240 VASAREVNGHSKSTGKEBETPEDTGTALPSSMAALPNSGQKQGVGASPEDBAE 299
 QY 241 LSSVGEANGHPKPREKEBETPEDPARALPFWMSALPNSVDQKXGTSATKKA-- 298
 Db 241 LSSVGEANGHPKPREKEBETPEDPARALPFWMSALPNSVDQKXGTSATKKA-- 298
 QY 300 EEEEEECEBPAPVSPASACSPPLQOQSGRVATLRLGCVLLGRGVALIGQWRR 359
 Db 300 EEEEEECEBPAPVSPASACSPPLQOQSGRVATLRLGCVLLGRGVALIGQWRR 359
 QY 299 -EEDDEEECEPQTLPASPASVENPQOQTSRVATLRLGCVLLSKNGVAGQWRR 357
 Db 299 -EEDDEEECEPQTLPASPASVENPQOQTSRVATLRLGCVLLSKNGVAGQWRR 357
 QY 360 RAQTRERKFTFLAVAVIGVFLCMPPFFFSYSGAICPKKCKVPHGLFOFFFWIGYCN 419
 Db 360 RAQTRERKFTFLAVAVIGVFLCMPPFFFSYSGAICPKKCKVPHGLFOFFFWIGYCN 419

Db 358 RTQLSRKRFVFLAVAVIGVFLCMPPFFFSYSGAICPKKCKVPHGLFOFFFWIGYCN 417
 QY 420 SLNPVIYITINODFRRAFRILCRPMTOTAW 450
 Db 418 SLNPVIYITINODFRRAFRILCRPMTOTAW 448

RESULT 5

Q8MK45 PRELIMINARY; PRT: 401 AA.
 AC 08MK45
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha 2B adrenergic receptor (Fragment).
 GN ADRA2B.
 OS Tapirus terrestris (Lowland tapir) (Brazilian tapir).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
 OX NCBI_TaxID=9801;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=21608557; PubMed=11743200;
 RA Murphy W.J., Eizirik E., O'Brien S.J., Madsen O., Scally M.,
 RA Douady C.J., Teeling E., Ryder O.A., Stanhope M.J., de Jong W.W.,
 RA Springer M.S.;
 RT "Resolution of the early placental mammal radiation using Bayesian
 RT phylogenetics";
 RL Science 294:2348-2351 (2001).
 DR EMBL: AJ15939; CAC87003.1; -.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KM Receptor.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 401 AA; 43635 MW; 8D01F4C2548BFEB6 CRC64;

Query Match 79.3%; Score 1885; DB 6; Length 401;
 Best Local Similarity 90.5%; Pred. No. 5.8e-143;

Matches 363; Conservative 12; Mismatches 20; Indels 6; Gaps 2;

QY 14 AIAAATFLILFTIFGNALVTLAVLTSRSLRAPONLFLVSLAADILVATLIIFPSLANE 73
 Db 1 AIAAATFLILFTIFGNALVTLAVLTSRSLRAPONLFLVSLAADILVATLIIFPSLANE 73
 QY 74 LIGWYFRRTWCEVYALDVLFCTSSIVHLCATSLDRYMAVSRLAYNSKTRPRIRKII 133
 Db 74 LIGWYFRRTWCEVYALDVLFCTSSIVHLCATSLDRYMAVSRLAYNSKTRPRIRKII 133
 QY 134 LTVWLAIVSLPLIYKGGQPOPRGRPOCKLNOEAMYLIIASSIGSFPAFLMILVYL 193
 Db 134 LTVWLAIVSLPLIYKGGQPOPRGRPOCKLNOEAMYLIIASSIGSFPAFLMILVYL 193
 QY 121 LTVWLAIVSLPLIYKGGQPOPRGRPOCKLNOEAMYLIIASSIGSFPAFLMILVYL 180
 Db 121 LTVWLAIVSLPLIYKGGQPOPRGRPOCKLNOEAMYLIIASSIGSFPAFLMILVYL 180
 QY 194 RIYLIARSNRGRPRAGKGGPOGSGKOPRPHGALASAKLPALAS-VASAREVNGHSK 252
 Db 194 RIYLIARSNRGRPRAGKGGPOGSGKOPRPHGALASAKLPALAS-VASAREVNGHSK 252
 QY 181 RIYLIARSNRGRPRAGKGGPOGSGKOPRPHGALASAKLPALAS-VASAREVNGHSK 240
 Db 181 RIYLIARSNRGRPRAGKGGPOGSGKOPRPHGALASAKLPALAS-VASAREVNGHSK 240
 QY 253 TGEKEBETPEDTGTALPSSMAALPNSGQKQGVGASPEDBAE-----EEDDEEE 307
 Db 253 TGEKEBETPEDTGTALPSSMAALPNSGQKQGVGASPEDBAE-----EEDDEEE 307
 QY 241 TGEKEBETPEDTGTALPSSMAALPNSGQKQGVGASPEDBAE-----EEDDEEE 300
 Db 241 TGEKEBETPEDTGTALPSSMAALPNSGQKQGVGASPEDBAE-----EEDDEEE 300
 QY 308 EEECPQAVPSPASACSPPLQOQSGRVATLRLGCVLLGRGVALIGQWRRRAQLTRK 367
 Db 308 EEECPQAVPSPASACSPPLQOQSGRVATLRLGCVLLGRGVALIGQWRRRAQLTRK 367
 QY 301 EEECPQAVPSPASACSPPLQOQSGRVATLRLGCVLLGRGVALIGQWRRRAQLTRK 360
 Db 301 EEECPQAVPSPASACSPPLQOQSGRVATLRLGCVLLGRGVALIGQWRRRAQLTRK 360
 QY 368 RFTFLAVAVIGVFLCMPPFFFSYSGAICPKKCKVPHGLF 408
 Db 368 RFTFLAVAVIGVFLCMPPFFFSYSGAICPKKCKVPHGLF 408
 QY 361 RFTFLAVAVIGVFLCMPPFFFSYSGAICPKKCKVPHGLF 401
 Db 361 RFTFLAVAVIGVFLCMPPFFFSYSGAICPKKCKVPHGLF 401

RESULT 6

O8K1W6

ID O8K1W6 PRELIMINARY; PRT; 397 AA.

AC O8K1W6; 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

DN Alpha 2B adrenergic receptor (Fragment).

OS Caenor. canadensis (Beaver).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Castoridae; Castor.

NCBI_Taxid=51338;

[1]

SEQUENCE FROM N.A.

RA Huchon D., Maden O., Sibbald M.J.J.B., Ament K., Stanhope M.,

RT "Rodent phylogeny and a timescale for the evolution of Glires:

RL evidence from an extensive taxon sampling using three nuclear genes."

Mol. Biol. Evol. 0:0-0(2002).

DR EMBL; AJ427260; CAD20298.1;

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm1; 1.0; GPCR.

DR PRINTS; PR00237; GPCR_RHODOPSIN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER

FT NON_TER

SQ SEQUENCE 397 AA; 43571 MW; BEAF239E4236A128 CRC64;

Query Match

Best Local Similarity 78.0%; Score 1856; DB 11; Length 397;

Matches 359; Conservative 10; Mismatches 26; Indels 2; Gaps 2;

14 A1AAATFTLFTIFGNALVILAVLTSRSLAPQNLFLVSLAADILVATLIIIPSLANE 73

1 A1AAATFTLFTIFGNALVILAVLTSRSLAPQNLFLVSLAADILVATLIIIPSLANE 60

74 LGGVYFRTCEVYALDVLFCSTSVHLCAISLDRYAVASRALEVNSKTPRIKII 133

61 LGGVYFRTCEVYALDVLFCSTSVHLCAISLDRYAVASRALEVNSKTPRIKII 120

121 LTVWLIAAVISLPLIYKDGQPPRGRPOCKLNDQAWYIIASSIGSFAPCLIMILVYL 193

121 LTVWLIAAVISLPLIYKDGQPPRGRPOCKLNDQAWYIIASSIGSFAPCLIMILVYL 180

194 RYLIARSRNRGRPRKAGPGESEKQPPD-HGGALASAKLPAL-ASVAREVNSKTP 251

181 RYLIARSRNRGRPRKAGPGESEKQPPD-HGGALASAKLPAL-ASVAREVNSKTP 240

252 STGEKEGETPEDTGRALPPSWALPNSGGQKQGVGASPEDEAESEEESECE 311

241 PPEKEEGETPEDPGARALTSPWVALPNSGGQKQGVGASPEDEAESEEESECE 300

312 POAVPSPASACSPPLQOPQSGRYLATLRGOVLLGRGVGAIIGQWRRRAQLTREKRTFV 371

301 POAVPSPASACSPPLQOPQSGRYLATLRGOVLLGRGVGAIIGQWRRRAQLTREKRTFV 360

372 VLAIVIGVFLCWFPPFFSYSLGAIICPKCKVPHGLF 408

361 VLAIVIGVFLCWFPPFFSYSLGAIICPKCKVPHGLF 397

RESULT 7

O8GL11

ID O8GL11 PRELIMINARY; PRT; 393 AA.

AC O8GL11; 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)

DN Alpha adrenergic receptor 2B (Fragment).

GN

AAR2B.

OS Nycticebus coucang (Slow loris).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Strepsirrhini; Loridae; Nycticebus.

NCBI_Taxid=9470;

[1]

SEQUENCE FROM N.A.

RA Maden O., Scally M., Douady C., Kao D., DeBry R., Adkins R.,

RT "Parallels adaptive radiations in two major clades of placental

mammals."

Nature 409:610-614(2001).

DR EMBL; AJ251186; CAC16695.1;

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm1; 1.0; GPCR.

DR PRINTS; PR00237; GPCR_RHODOPSIN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Receptor; Transmembrane.

FT NON_TER

FT NON_TER

SQ SEQUENCE 393 AA; 42990 MW; 713D3D10EE08714A CRC64;

Query Match

Best Local Similarity 78.0%; Score 1855; DB 6; Length 393;

Matches 361; Conservative 11; Mismatches 20; Indels 4; Gaps 2;

14 A1AAATFTLFTIFGNALVILAVLTSRSLAPQNLFLVSLAADILVATLIIIPSLANE 73

1 A1AAATFTLFTIFGNALVILAVLTSRSLAPQNLFLVSLAADILVATLIIIPSLANE 60

74 LGGVYFRTCEVYALDVLFCSTSVHLCAISLDRYAVASRALEVNSKTPRIKII 133

61 LGGVYFRTCEVYALDVLFCSTSVHLCAISLDRYAVASRALEVNSKTPRIKII 120

121 LTVWLIAAVISLPLIYKDGQPPRGRPOCKLNDQAWYIIASSIGSFAPCLIMILVYL 193

121 LTVWLIAAVISLPLIYKDGQPPRGRPOCKLNDQAWYIIASSIGSFAPCLIMILVYL 180

194 RYLIARSRNRGRPRKAGPGESEKQPPD-HGGALASAKLPAL-ASVAREVNSKTP 252

181 RYLIARSRNRGRPRKAGPGESEKQPPD-HGGALASAKLPAL-ASVAREVNSKTP 240

253 TGEKEGETPEDTGRALPPSWALPNSGGQKQGVGASPEDEAESEEESECE 312

241 PPEKEEGETPEDPGARALTSPWVALPNSGGQKQGVGASPEDEAESEEESECE 300

313 QAVPSPASACSPPLQOPQSGRYLATLRGOVLLGRGVGAIIGQWRRRAQLTREKRTFV 372

298 KAVPSPASACSPPLQOPQSGRYLATLRGOVLLGRGVGAIIGQWRRRAQLTREKRTFV 357

373 LAVVIGVFLCWFPPFFSYSLGAIICPKCKVPHGLF 408

358 LAVVIGVFLCWFPPFFSYSLGAIICPKCKVPHGLF 393

RESULT 8

O8M1D0

ID O8M1D0 PRELIMINARY; PRT; 399 AA.

AC O8M1D0; 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

DN Alpha 2B adrenergic receptor (Fragment).

OS Manis tetradactyla (Long-tailed pangolin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Pholidota; Manidae; Manis.

NCBI_Taxid=73815;

[1]

RP SEQUENCE FROM N.A.
RA Madsen O., Williamsen D., Ursing B.M., Arnaeson U., de Jong W.W.;
RT "Molecular evolution of the alpha 2B adrenergic receptor";
RL Submitted (Aug-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL, AJ505820; CAD4321.1; -
DR InterPro; IPR002761; GPCR_Rhodpn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM Receptor.
FT NON_TER
SQ SEQUENCE 399 AA; 43888 MW; 910ECAFBI0659EDD CRC64;
Query Match 78.0%; Score 1855; DB 6; Length 399;
Best Local Similarity 90.3%; Pred. No. 1,5e-140;
Matches 362; Conservative 10; Mismatches 21; Indels 8; Gaps 3;
QY 14 AIAAAIFLLIFFTFGNALVTLAVLTSRLAPONLFLVSLAADIIVATLIIPFSLANE 73
DB 1 AIAAVITFLIFFTFGNALVTLAVLTSRLAPONLFLVSLAADIIVATLIIPFSLANE 60
QY 74 LAGYFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRALEYNKRPRIKII 133
DB 61 LAGYFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRALEYNKRPRIKII 120
QY 134 LTVWLIAAVISLPLIYKGDGQPPRGRPOCKLNOEMAYILASSISGFPAFLIMILVYL 193
DB 121 LTVWLIAAVISLPLIYKGDGQPPRGRPOCKLNOEMAYILASSISGFPAFLIMILVYL 180
QY 194 RIYLIARSNRGRGPRAGKPGQGESKOPRPHGALSAKLPAASVARSAREVNGHSKST 253
DB 181 RIYLIARSHRGRRAKRGREGSKOPRWPGG--ASATLPTLASLAASEANGHSKPT 238
QY 254 GEKEGETPEDTGTRALPPSWAALPNSGQGEKGVCGASPEDEA-----EEEEEEEEEE 309
DB 239 GEKKGDNPEDPGTRPALPPSWPALPNSGQGEKGVCGASPEDEAEEEEEEEEEEEDHPQ 298
QY 310 CEPAPVSPASACSPPLIQOQSGSVLTLRGVTLGRGVAT--GGQWRRRAQLTREK 367
DB 299 HEPPALPASPASVCSPLRQPGSGRVTLTLRGVTLGIGVGAAGVSGQWRRRAQLTREK 358
QY 368 RFTFVLAVIGFVLCWPFPPFSYSLGALCPHCKVPHGLF 408
DB 359 RFTFVLAVIGFVLCWPFPPFSYSLGALCPHCKVPHGLF 399
RESULT 9
ID Q9GLI2 PRELIMINARY; PRT; 395 AA.
AC Q9GLI2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Manis sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Pholidota; Manidae; Manis.
OX NCBI_TaxID=49127;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082081; PubMed=11214318;
RA Madsen O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer M.;
RT "Parallel adaptive radiations in two major clades of placental
mammals";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ511185; CAC6694.1; -
DR InterPro; IPR000276; GPCR_Rhodpn.

DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER
SQ SEQUENCE 395 AA; 43427 MW; 2663DA564356DD84 CRC64;
Query Match 77.5%; Score 1844; DB 6; Length 395;
Best Local Similarity 90.4%; Pred. No. 1.1e-139;
Matches 359; Conservative 11; Mismatches 23; Indels 4; Gaps 2;
QY 14 AIAAAIFLLIFFTFGNALVTLAVLTSRLAPONLFLVSLAADIIVATLIIPFSLANE 73
DB 1 AIAAVITFLIFFTFGNALVTLAVLTSRLAPONLFLVSLAADIIVATLIIPFSLANE 60
QY 74 LAGYFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRALEYNKRPRIKII 133
DB 61 LAGYFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRALEYNKRPRIKII 120
QY 134 LTVWLIAAVISLPLIYKGDGQPPRGRPOCKLNOEMAYILASSISGFPAFLIMILVYL 193
DB 121 LTVWLIAAVISLPLIYKGDGQPPRGRPOCKLNOEMAYILASSISGFPAFLIMILVYL 180
QY 194 RIYLIARSNRGRGPRAGKPGQGESKOPRPHGALSAKLPAASVARSAREVNGHSKST 253
DB 181 RIYLIARSHRGRRAKRGREGSKOPRWPGG--ASATLPTLASLAASEANGHSKPT 238
QY 254 GEKEGETPEDTGTRALPPSWAALPNSGQGEKGVCGASPEDEAEEEEEEEEEECEPQ 313
DB 239 GEKKGDNPEDPGTRPALPPSWPALPNSGQGEKGVCGASPEDEAEEEEEEEEEDHPQ 298
QY 314 AVPSPASACSPPLIQOQSGSVLTLRGVTLGRGVAT--GGQWRRRAQLTREKPTF 371
DB 299 ALPASPASVCSPLRQPGSGRVLTLRGVTLGIGVGAAGVSGQWRRRAQLTREKPTF 358
QY 372 VLAIVIGFVLCWPFPPFSYSLGALCPHCKVPHGLF 408
DB 359 VLAIVIGFVLCWPFPPFSYSLGALCPHCKVPHGLF 395
RESULT 10
ID Q8KIU9 PRELIMINARY; PRT; 395 AA.
AC Q8KIU9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN A2AB.
OS Erethizon dorsatum (North American porcupine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Erethizontidae;
OC Erethizon.
OX NCBI_TaxID=34844;
RN [1]
RP SEQUENCE FROM N.A.
RA Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., Stanhope M.,
RA Catzeflis F., de Jong W.W., Douzery E.J.P.;
RT "Rodent phylogeny and a timescale for the evolution of Glires:
evidence from an extensive taxon sampling using three nuclear genes";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL; AJ427270; CAD20308.1; -
DR InterPro; IPR002761; GPCR_Rhodpn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM Receptor.
FT NON_TER
SQ SEQUENCE 395 AA; 43157 MW; 9E46A1E10EBD41FB CRC64;


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QY 134 LTWLLAAVLSLPLLYKGDGPPRGRPOCKLNOEAMWYLIASSIGSFPAACLMILVYL 193
DB 121 LTWLLAAVLSLPLLYKGDGPPRGRPOCKLNOEAMWYLIASSIGSFPAACLMILVYL 180
QY 194 RYLIARSNRGRGKAGGQESKOPRDPHGALASAKLPALASVASAREVNGHSKT 253
DB 181 RYLIARSNRGRGKAGGQESKOPRDPHGALASAKLPALASVASAREVNGHSKT 238
QY 254 GKEEGEPEDTGTALPSPWALPNSGQCKEVCASPEDAESEEESEEESEEPQ 313
DB 239 GKEEGEPEDTGTALPSPWALPNSGQCKEVCASPEDAESEEESEEESEEPQ 292
QY 314 AVPSPASACSPPLQOQGSRLVATLRGQVLLRGVGAIGQWRRRAQLTRERKFTFVL 373
DB 293 ALPASPASACSPPLQOQGSRLVATLRGQVLLRGVGTSSQWRRRAQLTRERKFTFVL 352
QY 374 AVVIGVFVLCMPFFFSYSLGALICPKKCKVPHGLF 408
DB 353 AVVIGVFVLCMPFFFSYSLGALICPKKCKVPHGLF 387

RESULT 13
Q9GL07 PRELIMINARY; PRT; 389 AA.
ID 09GL07
AC 09GL07;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082081; PubMed=11214318;
RA Madsen O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
RA Amrine H., Stanhope W., de Jong W., Springer M.;
RT "Parallel adaptive radiations in two major clades of placental
RT mammal";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ251176; CAC16696.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 389
SQ SEQUENCE 389 AA; 42278 MW; 842F17673FE47FF CRC64;

Query Match 77.1%; Score 1833; DB 6; Length 389;
Best Local Similarity 90.1%; Pred. No. 8.3e-119;
Matches 356; Conservative 10; Mismatches 23; Indels 6; Gaps 3;

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DB 181 RYLIARSNRGRGKAGGQESKOPRDPHGALASAKLPALASVASAREVNGHSKT 238
QY 254 GKEEGEPEDTGTALPSPWALPNSGQCKEVCASPEDAESEEESEEESEEPQ 313
DB 239 GKEEGEPEDTGTALPSPWALPNSGQCKEVCASPEDAESEEESEEESEEPQ 294
QY 314 AVPSPASACSPPLQOQGSRLVATLRGQVLLRGVGAIGQWRRRAQLTRERKFTFVL 373
DB 295 ALPASPASACSPPLQOQGSRLVATLRGQVLLRGVGTSSQWRRRAQLTRERKFTFVL 354
QY 374 AVVIGVFVLCMPFFFSYSLGALICPKKCKVPHGLF 408
DB 355 AVVIGVFVLCMPFFFSYSLGALICPKKCKVPHGLF 389

RESULT 14
Q8MK51 PRELIMINARY; PRT; 399 AA.
ID Q8MK51
AC Q8MK51;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN ADRA2B.
OS Lama guanicoe paco (Alpaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=30538;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608557; PubMed=11743200;
RA Murphy W.J., Elzirik E., O'Brien S.J., Madsen O., Scally M.,
RA Douady C.J., Teeling E., Ryder O.A., Stanhope M.J., de Jong W.W.,
RA Springer M.S.;
RT "Resolution of the early placental mammal radiation using Bayesian
RT phylogenetics";
RL Science 294:2348-2351(2001).
CC EMBL: AJ15941; CAC87005.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 399
SQ SEQUENCE 399 AA; 43887 MW; 19391AB652F42F23 CRC64;

Query Match 76.9%; Score 1828; DB 6; Length 399;
Best Local Similarity 89.2%; Pred. No. 2.1e-118;
Matches 356; Conservative 10; Mismatches 29; Indels 4; Gaps 2;

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QY 310 CEPQAVPVSASACSPPLQOPQSGSRVLTATRGVLLGRGVGAIGQWRRRAQLTREKRF 369
 DB 301 CEPQALPASPSASCSPLQOPQISRVLTATRGVLLGRGVGTSRGQWRRRAQLTREKRF 360
 QY 370 TFWLAIVIGVFLCMFPFFFSYSIGAIQPCPKCVPHGLF 408
 DB 361 TFWLAIVIGVFLCMFPFFFSYSIGAIQPCPKCVPHGLF 399

DB 355 LAVVIGAFVLCMFPFFFSYSIGAIQPCPKCVPHGLF 390
 Search completed: February 6, 2004, 18:19:23
 Job time : 35.1104 secs

RESULT 15

O9GL19 PRELIMINARY; PRT; 390 AA.
 AC O9GL19;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Alpha adrenergic receptor 2b (Fragment).
 GN AAR2B.
 OS Cynocephalus variegatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus;
 OX NCBI_TaxId=9457;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082081; PubMed=11214318;
 RA Maden O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
 RA Amrine H., Stanhope M., de Jong W., Springer M.,
 RT "Parallel adaptive radiations in two major clades of placental
 RT mammals.",
 RL Nature 409:610-614(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ251182; CAC16685.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS02624; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON_TER 1
 FT 390
 SQ SEQUENCE 390 AA; 42428 MM; C99055D3EC60E2C6 CRC64;

Query Match 76.7%; Score 1824.5; DB 6; Length 390;
 Best Local Similarity 89.4%; Pred. No. 4e-138;
 Matches 354; Conservative 10; Mismatches 25; Indels 7; Gaps 2;

QY 14 AIAAATFLILFTIFGNALVLAIVLTSRSLAPQNLFLVSLAADIIVATLIIIPSLANE 73
 DB 1 AIAAVITFLILFTIRGNVVIILAVLSRSLAPQNLFLVSLAADIIVATLIIIPSLANE 60
 QY 74 LIGYWFRTNCEVYIALDVLTCTSSIVHLCASIDRYMAVSRALFENSKRTPRIKCII 133
 DB 61 LIGYWFRTNCEVYIALDVLTCTSSIVHLCASIDRYMAVSRALFENSKRTPRIKCII 120
 QY 114 LTVMLIAVLSLPLIYKGDGPOPRGRPOCKLQEAAYTLASSISGFAPCLIMILVYL 193
 DB 121 LTVMLIAVLSLPLIYKGDGPOPRGRPOCKLQEAAYTLASSISGFAPCLIMILVYL 180
 QY 194 RIYLIARSNRGRPAKGGPQSGSKQRPDPHGALASAKLPALAS-VASAREVNHGSKS 252
 DB 181 RIYLIARSNRGRPAKGGPQSGSKQRPDPHGALASAKLPALAS-VASAREVNHGSKS 240
 QY 253 TGEKEGETPEDTGTALPPSMALPNSGQGEKVCASPEDAEHEEEHEEEHEECPEP 312
 DB 241 TGEKEGETPEDTGTALPPSMALPNSGQGEKVCASPEDAEHEEEHEEEHEECPEP 294
 QY 313 QAVPVSPASACSPPLQOPQSGSRVLTATRGVLLGRGVGAIGQWRRRAQLTREKRF 372
 DB 295 QAVPVSPASACSPPLQOPQSGSRVLTATRGVLLGRGVGAIGQWRRRAQLTREKRF 354
 QY 373 LAVVIGFVLCMFPFFFSYSIGAIQPCPKCVPHGLF 408

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 18:18:11 ; Search time 37.3746 Seconds

(without alignments)
1898.370 Million cell updates/sec

Title: US-09-692-077D-8

Perfect score: 447

Sequence: 1 MDHQDPYSVQATAAIAAAT.....QDFRRAFRRLICRPMTQTAW 447

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 20

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	447	100.0	447	22	AAAS2118 Human alpha-2BAR t
2	447	100.0	447	22	AAE00989 Human alpha2B-adre
3	447	100.0	447	23	AAE26633 Human alpha-2B-adr
4	306	68.5	450	22	AAAS2117 Human alpha-2BAR t
5	306	68.5	450	22	AAE00990 Human alpha2B-adre
6	306	68.5	450	23	AAE26634 Human alpha-2B-adr
7	306	68.5	450	24	ABP81780 Human alpha 2B-adr
8	179	40.0	487	12	AAAR1419 Human alpha 2 beta
9	179	40.0	487	18	AAW1804 Human alpha-2b adr

10	120	26.8	330	15	AAAR48699	G-protein coupled
11	120	26.8	330	17	AAW02671	G-protein coupled
12	29	6.5	29	23	ABU67205	G-protein coupled
13	29	6.5	29	24	ABP53986	Human alpha 2B adr
14	26	5.8	457	22	AAAS2126	Human alpha-2CAR v
15	26	5.8	458	15	AAAS4834	Human derived adre
16	26	5.8	461	22	AAAS2124	Human alpha-2CAR p
17	26	5.8	461	24	ABP81781	Human alpha 2c-adr
18	25	5.6	330	15	AAAR48700	G-protein coupled
19	25	5.6	330	17	AAW02672	G-protein coupled
20	25	5.6	450	22	AAAS2122	Human alpha-2BAR p
21	25	5.6	450	25	AAAS2123	Human alpha-2BAR v
22	25	5.6	450	24	ABP81779	Human alpha 2a-adr
23	23	5.1	26	19	AAW39955	Peptide effecting
24	23	5.1	26	19	AAW39948	Peptide effecting
25	23	5.1	99	15	AAAS0781	G-protein coupled
26	23	5.1	99	17	AAW02983	G-protein coupled
27	21	4.7	330	15	AAAR48698	G-protein coupled
28	21	4.7	330	17	AAW02670	G-protein coupled
29	21	4.7	334	15	AAAR48701	G-protein coupled
30	21	4.7	307	17	AAW02673	G-protein coupled
31	20	4.5	307	22	AAU08334	Human alpha 2 adre
32	20	4.5	307	24	ABG73538	Human alpha2-adren

ALIGNMENTS

```
RESULT 1
AAAS2118
ID AAAS2118 standard; Protein; 447 AA.
AC
XX
AC AAAS2118;
DT
XX 18-FEB-2002 (first entry)
DE
XX Human alpha-2BAR third intracellular loop variant.
XX
XX Human, genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX polymorphic site; allelic variant; cardiovascular disease;
XX central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX phosphorylation; inositol phosphate; alpha-2BAR.
XX
XX Homo sapiens.
OS
XX
XX Key
XX Location/Qualifiers
XX Domain
XX 170..193
XX /label=transmembrane_domain
XX Region
XX 307..309
XX /label=polymorphic_site
XX FT Domain
XX 370..393
XX /label=transmembrane_domain
XX
XX WO200179561-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12575.
XX
XX 17-APR-2000; 2000US-0551744.
XX 10-AUG-2000; 2000US-0636259.
XX 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
XX (SMAL/) SMALL K M.
XX
XX LIGGETT SB, Small KM;
XX
XX WPI; 2001-611728/70.
XX N-PSDB; AA199906.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
```


PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 20; Page 147-149; 163pp; English.

CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC or (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (999GCG999CG) or (B) (999GCG999CG) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlates to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC rauvolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to the site to a
 CC level). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR variant protein, the sequence is deleted for the 3
 CC amino acid polymorphic site at residues 301-303 (EEB) of the wildtype
 CC protein (AA052117).
 XX
 XX Sequence 447 AA;

Query Match 100.0%; Score 447; DB 22; Length 447;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDHODPSVQATAAIAATFTLFTFGNALVTLVTSRSLAPQNLFLVSLAADI 60
 DB 1 MDHODPSVQATAAIAATFTLFTFGNALVTLVTSRSLAPQNLFLVSLAADI 60
 QY 61 VATTIIPFSLANELGWTYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYAVASRALEY 60
 DB 61 VATTIIPFSLANELGWTYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYAVASRALEY 60
 QY 121 NSKRTPRRIKCIITLWTLIAVSLPPLIYKGDQGPORGRPOCKLNOAMWYTLASSTGS 180
 DB 121 NSKRTPRRIKCIITLWTLIAVSLPPLIYKGDQGPORGRPOCKLNOAMWYTLASSTGS 180
 QY 181 FFAPCLIMILVYRIYLLAKRSNRGPRAKGPGQGESKOPRPHGALASATLPLASV 240
 DB 181 FFAPCLIMILVYRIYLLAKRSNRGPRAKGPGQGESKOPRPHGALASATLPLASV 240
 QY 241 ASAREVNGSKSTGKEGETPEDTGTALPPSNAALPNSGQCKGVCASPEDEAEE 300
 DB 241 ASAREVNGSKSTGKEGETPEDTGTALPPSNAALPNSGQCKGVCASPEDEAEE 300
 QY 301 EEEBEECEPQAVPSPASACSPPIQOQSGRVATLARGVLLGRGVALGQGMARRAOL 360
 DB 301 EEEBEECEPQAVPSPASACSPPIQOQSGRVATLARGVLLGRGVALGQGMARRAOL 360
 QY 361 TREKRTFTVLAIVGVFLCMFPFFSYSLGATCPHGCVHGLTQFFFWTGYCNSSILNP 420
 DB 361 TREKRTFTVLAIVGVFLCMFPFFSYSLGATCPHGCVHGLTQFFFWTGYCNSSILNP 420
 QY 421 VIYTIFFQDPRRAFRRIICRPWTQZAW 447
 DB 421 VIYTIFFQDPRRAFRRIICRPWTQZAW 447
 QY 421 VIYTIFFQDPRRAFRRIICRPWTQZAW 447
 DB 421 VIYTIFFQDPRRAFRRIICRPWTQZAW 447

RESULT 2
 AA000989
 ID AA000989 standard; Protein; 447 AA.

XX
 AC AA000989;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human alpha2B-adrenoceptor (alpha2B-AR) variant protein.
 XX
 KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Prinzmetal's variant.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Location/Qualifiers
 FT Region
 FT 298..306
 FT /note="Glutamic acid repeat"
 XX
 PN MO200129082-A1.
 XX
 PD 26-APR-2001.
 XX
 PF 20-OCT-2000; 2000MO-F100913.
 XX
 PF 22-OCT-1999; 99US-0422985.
 XX
 PR (JUVVA-) JUVANTIA PHARMA LTD OY.
 PA
 XX
 PI Snajir A, Heinonen P, Alhopuro P, Kartonen M, Koulou M, Pesonen U;
 PI Scheinin M, Salonen JT, Tuomala T, Lakka TA, Nyssönen K;
 PI Salonen R, Kauhainen J, Valkonen V,
 DR MPI; 2001-300318/31.
 DR N-PSDB; AAD04761.
 XX
 PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -
 XX
 PS Claim 8; Page 26-27; 37pp; English.

CC The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) variant
 CC protein. Alpha2B-AR has a glutamic acid repeat element (amino acids
 CC 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino
 CC acids 294-311), located in the third intracellular loop of the receptor
 CC the Glu repeat. The variant is obtained by deletion of three glutamates from
 CC chromosome 2. Alpha2-AR mediate many of the physiological effects of the
 CC catecholamines, norepinephrine and epinephrine. An antagonist of
 CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
 CC vascular contraction of coronary arteries and a disease involving
 CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
 CC clinically expressed as Prinzmetal's variant form or acute myocardial
 CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
 CC
 XX
 XX Sequence 447 AA;

Query Match 100.0%; Score 447; DB 22; Length 447;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDHODPSVQATAAIAATFTLFTFGNALVTLVTSRSLAPQNLFLVSLAADI 60
 DB 1 MDHODPSVQATAAIAATFTLFTFGNALVTLVTSRSLAPQNLFLVSLAADI 60
 QY 61 VATTIIPFSLANELGWTYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYAVASRALEY 120
 DB 61 VATTIIPFSLANELGWTYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYAVASRALEY 120
 QY 121 NSKRTPRRIKCIITLWTLIAVSLPPLIYKGDQGPORGRPOCKLNOAMWYTLASSTGS 180
 DB 121 NSKRTPRRIKCIITLWTLIAVSLPPLIYKGDQGPORGRPOCKLNOAMWYTLASSTGS 180


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Db 121 NSKRTPRRRCIIILTWLIAAVISLPLIYKDGQPPRGRPOCKLNOEAMYLASSIGS 180
Qy 181 FPAACLMIILVYRIYLIARSNRGRAGKGPQGGSKOPRPHGALASAKLPALASV 240
Db 181 FPAACLMIILVYRIYLIARSNRGRAGKGPQGGSKOPRPHGALASAKLPALASV 240
Qy 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWALPNSGQOGKEGVCGASPEDAEAE 300
Db 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWALPNSGQOGKEGVCGASPEDAEAE 300
Qy 301 EEEBEECEPQAVVSPASACSPPLQOPQGSRLVATLGRGVLAGRGVAGIGQWRRRAQL 360
Db 301 EEEBEECEPQAVVSPASACSPPLQOPQGSRLVATLGRGVLAGRGVAGIGQWRRRAQL 360
Qy 361 TREKRFTFVLAVVIGVFLVCMFPFFFSYSIGAIQPKKCKVPHGLFOFFWIGYCNSSLNP 420
Db 361 TREKRFTFVLAVVIGVFLVCMFPFFFSYSIGAIQPKKCKVPHGLFOFFWIGYCNSSLNP 420
Qy 421 VIYTIQNPDRRAFRRLICRPMTOTAM 447
Db 421 VIYTIQNPDRRAFRRLICRPMTOTAM 447
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RESULT 3
AAE26633 standard; Protein; 447 AA.

AC AAE26633;

DT 13-DEC-2002 (first entry)

DE Human alpha-2B-adrenoceptor variant.

KM Human; hypertension; alpha-2B-adrenoceptor; AE; antihypertensive;
KW hypertension; hypotensive; variant.

OS Homo sapiens.
OS Synthetic.

PN WO200266617-A1.

PD 29-AUG-2002.

PF 13-FEB-2002; 2002WO-FI00113.

PR 20-FEB-2001; 2001FI-0000323.

PA (JURI-) JURILAB LTD OY.

PI Salonen J;

DR MPI; 2002-667063/71.

DR N-PSDB; AAD44388.

PT Detecting a risk of hypertension and targeting treatment in a subject
by determining the pattern of alleles encoding a variant
alpha-2-adrenoceptor

PS Disclosure; Page 26-27; 35pp; English.

XX The invention relates to a method for detecting a risk of hypertension
by determining the pattern of alleles encoding a variant alpha-2B-
adrenoceptor (AR) protein. The methods and compositions of the invention
are useful for detecting risks and targeting treatment for hypertension.
XX The kit is also useful for selecting for clinical drug trials testing
CC the antihypertensive effect of compounds. The present sequence is human
CC alpha-2B-adrenoceptor variant.

XX Sequence 447 AA;

Query Match 100.0%; Score 447; DB 23; Length 447;
Best Local Similarity 100.0%; Pred. No. 0;

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Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDHODPYSVOATTAIAAATFTLLFTFGNALVIAVTSRSRAPONLFLVSLAADIL 60
Db 1 MDHODPYSVOATTAIAAATFTLLFTFGNALVIAVTSRSRAPONLFLVSLAADIL 60
Qy 61 VATLIIFPSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRLAEY 120
Db 61 VATLIIFPSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRLAEY 120
Qy 121 NSKRTPRRRCIIILTWLIAAVISLPLIYKDGQPPRGRPOCKLNOEAMYLASSIGS 180
Db 121 NSKRTPRRRCIIILTWLIAAVISLPLIYKDGQPPRGRPOCKLNOEAMYLASSIGS 180
Qy 181 FPAACLMIILVYRIYLIARSNRGRAGKGPQGGSKOPRPHGALASAKLPALASV 240
Db 181 FPAACLMIILVYRIYLIARSNRGRAGKGPQGGSKOPRPHGALASAKLPALASV 240
Qy 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWALPNSGQOGKEGVCGASPEDAEAE 300
Db 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWALPNSGQOGKEGVCGASPEDAEAE 300
Qy 301 EEEBEECEPQAVVSPASACSPPLQOPQGSRLVATLGRGVLAGRGVAGIGQWRRRAQL 360
Db 301 EEEBEECEPQAVVSPASACSPPLQOPQGSRLVATLGRGVLAGRGVAGIGQWRRRAQL 360
Qy 361 TREKRFTFVLAVVIGVFLVCMFPFFFSYSIGAIQPKKCKVPHGLFOFFWIGYCNSSLNP 420
Db 361 TREKRFTFVLAVVIGVFLVCMFPFFFSYSIGAIQPKKCKVPHGLFOFFWIGYCNSSLNP 420
Qy 421 VIYTIQNPDRRAFRRLICRPMTOTAM 447
Db 421 VIYTIQNPDRRAFRRLICRPMTOTAM 447
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RESULT 4
AAM52117 standard; Protein; 450 AA.

AC AAM52117;

DT 18-FEB-2002 (first entry)

DE Human alpha-2BAR third intracellular loop.

XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;

KM polymorphic site; allelic variant; cardiovascular disease;

KW central nervous system disease; adenylyl cyclase; MAP kinase activity;

KW phosphorylation; inositol phosphate; alpha-2BAR.

XX Homo sapiens.

OS Location/Qualifiers

FH Key 167..399

FT /note= "Featured in figure 2"

FT Domain 170..193

FT /label= transmembrane_domain

FT Region 301..303

FT /label= polymorphic site

FT /note= "Polymorphic site absent in the variant protein
(AAM52118)"

FT Region 310..312

FT /label= polymorphic_site

FT Domain 373..396

FT /label= transmembrane_domain

PN WO200179561-A2.

PD 25-OCT-2001.

PF 17-APR-2001; 2001WO-US12575.

XX 17-APR-2000; 2000US-0551744.

1 MDHDDPYSVQATTAIAAATFLLFTTIGNALVILAVLTSRSLAPQNLFLVSLAAADIL 6

61 VATLIIPSLANELGYMYFRFTWCEVYLLADVLFCYSSIVHLCAISLDRYNAVSRALEY 120

```

Db 61 VATTIIPFSLANELGTYWFRRTWCEVYLAADVLFCTSSIVHLCAISLDRYMAVSRALEY 120
Qy 121 NSKRTPRRIKCIITITWMLIAAVISLPLIYKGDGPPGRGRPOCKLNOEAWYIIASSIGS 180
Db 121 NSKRTPRRIKCIITITWMLIAAVISLPLIYKGDGPPGRGRPOCKLNOEAWYIIASSIGS 180
Qy 181 FFAPCLIMILVYLAITVLIARSNRGRPRAGGPGQGSCKOPRPHGALASAKLPALASV 240
Db 181 FFAPCLIMILVYLAITVLIARSNRGRPRAGGPGQGSCKOPRPHGALASAKLPALASV 240
Qy 241 ASAREVNGHSKSTGEKEGETPEBDTGTRALPPSWAALPNSGQGQKEGVCGASPEDAEAE 300
Db 241 ASAREVNGHSKSTGEKEGETPEBDTGTRALPPSWAALPNSGQGQKEGVCGASPEDAEAE 300
Qy 301 EEEEE 306
Db 301 EEEEE 306

```

RESULT 6

```

AAE26634
ID AAE26634 standard; Protein; 450 AA.
XX
AC AAE26634;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human alpha-2B-adrenoceptor protein.
XX
KM Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KW hypertension; hypotensive.
XX
OS Homo sapiens.
XX
PN MO200266617-A1.
XX
PD 29-AUG-2002.
XX
PF 13-FEB-2002; 2002WO-FI00113.
XX
PR 20-FEB-2001; 2001FI-0000323.
XX
PA (JURI-) JURILAB LTD OY.
XX
PI Salonen J;
XX
PI Salonen J;
XX
DR WPI; 2002-667063/71.
DR N-PSDB; AAD26634.
XX
PT Detecting a risk of hypertension and targeting treatment in a subject
PT by determining the pattern of alleles encoding a variant
PT alpha-2-adrenoceptor -
XX
PS Disclosure; Page 30-31; 35pp; English.
XX
CC The invention relates to a method for detecting a risk of hypertension
CC by determining the pattern of alleles encoding a variant alpha-2B-
CC adrenoceptor (AR) protein. The methods and compositions of the invention
CC are useful for detecting risks and targeting treatment for hypertension.
CC The kit is also useful for selecting for clinical drug trials testing
CC the antihypertensive effect of compounds. The present sequence is human
CC alpha-2B-adrenoceptor protein.
XX
SQ Sequence 450 AA;

```

Query Match 68.5%; Score 306; DB 23; Length 450;

Best Local Similarity 100.0%; Pred. No. 1.6e-271; Indels 0; Gaps 0;

Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDHDDPYSVQATAIAAATFLITFTFGNALVILAVLTSRSLRAPONTFLVSLAADI 60

Db 1 MDHDDPYSVQATAIAAATFLITFTFGNALVILAVLTSRSLRAPONTFLVSLAADI 60

```

Qy 61 VATTIIPFSLANELGTYWFRRTWCEVYLAADVLFCTSSIVHLCAISLDRYMAVSRALEY 120
Db 61 VATTIIPFSLANELGTYWFRRTWCEVYLAADVLFCTSSIVHLCAISLDRYMAVSRALEY 120
Qy 121 NSKRTPRRIKCIITITWMLIAAVISLPLIYKGDGPPGRGRPOCKLNOEAWYIIASSIGS 180
Db 121 NSKRTPRRIKCIITITWMLIAAVISLPLIYKGDGPPGRGRPOCKLNOEAWYIIASSIGS 180
Qy 181 FFAPCLIMILVYLAITVLIARSNRGRPRAGGPGQGSCKOPRPHGALASAKLPALASV 240
Db 181 FFAPCLIMILVYLAITVLIARSNRGRPRAGGPGQGSCKOPRPHGALASAKLPALASV 240
Qy 241 ASAREVNGHSKSTGEKEGETPEBDTGTRALPPSWAALPNSGQGQKEGVCGASPEDAEAE 300
Db 241 ASAREVNGHSKSTGEKEGETPEBDTGTRALPPSWAALPNSGQGQKEGVCGASPEDAEAE 300
Qy 301 EEEEE 306
Db 301 EEEEE 306

```

RESULT 7

```

ABP81780
ID ABP81780 standard; Protein; 450 AA.
XX
AC ABP81780;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human alpha 2b-adrenoceptor protein SEQ ID NO:42.
XX
KM G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM G protein-coupled receptor modulator; antibody; immune-related disease;
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM immunological-related cell proliferative disease; autoimmune disease;
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KM ulcer.
XX
OS Homo sapiens.
XX
PN MO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US50107.
XX
PR 19-DEC-2000; 2000US-257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burner GC; Roush CL; Brown JP;
XX
PI Burner GC; Roush CL; Brown JP;
XX
DR WPI; 2003-046718/04.
DR N-PSDB; ABZ42624.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (1) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity

```

CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides may be
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC regenerative immune-related diseases, growth-related diseases, cell
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, nausea, hypertension, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, mental retardation,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in AB241675 to AB242018, which are used in the
 CC exemplification of the present invention.

SQ Sequence 450 AA;

Query Match 68.5%; Score 306; DB 24; Length 450;
 Best Local Similarity 100.0%; Pred. No. 1.6e-271;
 Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHDDPYSVQATAIAAATFTLFTFGNALVLAITSRLAPQNLFLVSLAAADL 60
 Db 1 MDHDDPYSVQATAIAAATFTLFTFGNALVLAITSRLAPQNLFLVSLAAADL 60
 QY 61 VATLIIPFSLANELLGWYFRRTWCVEVYLAIDLFTGSSIVHLCAISLDRYVAASRALEY 120
 Db 61 VATLIIPFSLANELLGWYFRRTWCVEVYLAIDLFTGSSIVHLCAISLDRYVAASRALEY 120
 QY 121 NSKRTPRRIKICILITWVLAAVISLPLLYKGDQGPQPRPOCKLNDEAWYTLASSTGS 180
 Db 121 NSKRTPRRIKICILITWVLAAVISLPLLYKGDQGPQPRPOCKLNDEAWYTLASSTGS 180
 QY 181 FFAPCLIMILVYRIYLAKRSNRGPRKAGPGGSGSKOPRDPHGALASAKLPALASV 240
 Db 181 FFAPCLIMILVYRIYLAKRSNRGPRKAGPGGSGSKOPRDPHGALASAKLPALASV 240
 QY 241 ASAREVNGHSKSTGKEBEGTETDGTALPPSWAALPNSGGQKGVCASPEDEAEE 300
 Db 241 ASAREVNGHSKSTGKEBEGTETDGTALPPSWAALPNSGGQKGVCASPEDEAEE 300
 QY 301 EEEEEE 306
 Db 301 EEEEEE 306

RESULT 8
 AARI1419
 ID AARI1419 standard; Protein; 487 AA.

AC AARI1419;

DT 06-JAN-1992 (first entry)

DE Human alpha 2 beta adrenergic receptor.

KW Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta.

OS Homo sapiens.

XX US053337-A.

XX 01-OCT-1991.

XX 30-OCT-1989; 89US-0428856.

XX 30-OCT-1989; 89US-0428856.

XX (NEUR-) NEUROGENETIC CORP.
 PA Weinshank RL, Hartig PR;
 PI WPI; 1991-310087/42.
 DR N-PSDB; AA014151.
 XX
 PT Isolated DNA encoding human adrenergic receptor - for detecting
 PT nucleic acids encoding alpha, 2-beta adrenergic receptor, for
 PT screening drugs.
 XX Disclosure; Fig 2; 15pp; English.
 XX
 CC Clone NGC-alpha2beta was isolated from a human spleen genomic
 CC library by screening with a fragment of the human 5-HT1A receptor
 CC gene. The gene was used to express recombinant receptor protein
 CC which can be used to produce antibodies for inhibition of receptor
 CC function.

SQ Sequence 487 AA;

Query Match 40.0%; Score 179; DB 12; Length 487;
 Best Local Similarity 100.0%; Pred. No. 3.5e-155;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 RIKCIILTWVLAAVISLPLLYKGDQGPQPRPOCKLNDEAWYTLASSTGSFFAPCLI 187
 Db 165 RIKCIILTWVLAAVISLPLLYKGDQGPQPRPOCKLNDEAWYTLASSTGSFFAPCLI 224
 QY 188 MIIIVYRIYLAKRSNRGPRKAGPGGSGSKOPRDPHGALASAKLPALASVASAREVN 247
 Db 225 MIIIVYRIYLAKRSNRGPRKAGPGGSGSKOPRDPHGALASAKLPALASVASAREVN 284
 QY 248 GHSKSTGKEBEGTETDGTALPPSWAALPNSGGQKGVCASPEDEAEE 306
 Db 285 GHSKSTGKEBEGTETDGTALPPSWAALPNSGGQKGVCASPEDEAEE 343

RESULT 9
 AAM11804
 ID AAM11804 standard; Protein; 487 AA.

XX AAM11804;

DT 25-MAR-2003 (updated)

DT 06-MAY-1997 (first entry)

DE Human alpha-2b adrenergic receptor.

KW Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
 KW epinephrine; signal transduction; neurotransmitter; ligand.

OS Homo sapiens.

XX US5595880-A.

XX 21-JAN-1997.

XX 22-OCT-1992; 92US-0965040.

XX 30-OCT-1989; 89US-0428856.

XX 30-MAY-1991; 91US-0707604.

XX 22-OCT-1992; 92US-0965040.

XX (SYNA-) SYNAPTIC PHARM CORP.

XX Hartig PR, Weinshank RL;

XX WPI; 1997-107576/10.

XX N-PSDB; AAT59499.

PT Assay for alpha-2b adrenergic receptor ligands - using membranes of

PT cells expressing recombinant receptor
XX
PS Disclousure; Fig 2A-E; 16pp; English.
XX
CC Human alpha-2B adrenergic receptor (AA011804) is a member of the
CC rhodopsin-like signal transducer family. Its amino acid sequence
CC was deduced from a genomic DNA clone (AA059499) obt. from a human
CC spleen DNA library. Vectors have been adapted to allow produ. of
CC alpha-2B adrenoceptor in bacterial, yeast or mammalian cells;
CC transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as
CC ATCC CRL 10275. Membranes of transfected mammalian cells can used
CC in novel methods to identify drugs which specifically interact
CC with, and bind to, the alpha-2B adrenergic receptor.
CC (Updated on 25-MAR-2003 to correct pr field.)
XX
SQ Sequence 487 AA;
Query Match 40.0%; Score 179; DB 18; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.5e-155;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 128 RIKCIIITVWLIAAVISLPLIYKDGQPOPRGRPOCKLNGEAWYILASSIGSFAPCLI 187
DB 165 RIKCIIITVWLIAAVISLPLIYKDGQPOPRGRPOCKLNGEAWYILASSIGSFAPCLI 224
QY 188 MILVYLRIVLIAKSNRRGPRAKGGPGGSEKOPRPDHGALASAKLPALASVASAREVN 247
DB 225 MILVYLRIVLIAKSNRRGPRAKGGPGGSEKOPRPDHGALASAKLPALASVASAREVN 284
QY 248 GHSKSTGEKEGEPEDTGTALPPSWALPNSGQGGQKGVCGASPEDEABEEEEEE 306
DB 285 GHSKSTGEKEGEPEDTGTALPPSWALPNSGQGGQKGVCGASPEDEABEEEEEE 343
RESULT 10
AA048699
ID AA048699 standard; Protein; 330 AA.
XX
AC AA048699;
XX
DT 05-JUN-1996 (first entry)
XX
DE G-protein coupled human alpha-2 C2 adrenergic receptor protein.
XX
KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW psychotic disorder; schizophrenia; dopamine; AMP; adenosine; thrombin;
KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
KW rhodopsin; opsin; odorant; cytomagalovirus.
XX
OS Homo sapiens.
XX
PN W09405695-A1.
XX
PD 17-MAR-1994.
XX
PF 09-SEP-1993; 93WO-US08528.
XX
PR 10-SEP-1992; 92US-0943236.
XX
PA (UTNY) UNIV NEW YORK STATE.
XX
PI Murphy RB, Schuster DI;
XX
DR WPI; 1994-101120/12.
XX
PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for
PT binding GPR ligands or modulating GPR binding
XX
PS Disclousure; Page 72-73; 160pp; English.
XX
CC Proteins AA048695-R48758 represent a range of G-protein coupled receptor
CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,

CC odorant, cytomagaloviral and other G-protein coupled receptors. The
CC receptor proteins were used to design polypeptides, pref. based on the
CC transmembrane domains, for use in G-protein coupled receptor ligand
CC binding assays. The polypeptide fragments retain biological activity
CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
CC (see AA048759-R48758, AA050569-R50807 and AA09189-R89195 for examples
CC of polypeptide fragments). The polypeptide fragments can be used in
CC compositions for treating subjects suffering from a pathology related to
CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
XX
SQ Sequence 330 AA;
Query Match 26.8%; Score 120; DB 15; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.7e-101;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 55 AAADIVATLIPPSLANELIGYFRRTWCEVTLADVLFCTSIYHLCAISDRYAV 114
DB 44 AAADIVATLIPPSLANELIGYFRRTWCEVTLADVLFCTSIYHLCAISDRYAV 103
QY 115 SRALFVNSKRPRIKICIIITVWLIAAVISLPLIYKDGQPOPRGRPOCKLNGEAWYIL 174
DB 104 SRALFVNSKRPRIKICIIITVWLIAAVISLPLIYKDGQPOPRGRPOCKLNGEAWYIL 163
RESULT 11
AA02671
ID AA02671 standard; peptide; 330 AA.
XX
AC AA02671;
XX
DT 25-MAR-2003 (updated)
DT 12-NOV-1996 (first entry)
XX
DE G-protein coupled human alpha-2 C2 adrenergic receptor.
XX
KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW schizophrenia; dopamine; AMP; adenosine; thrombin; adrenergic; opsin;
KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
KW odorant; cytomagalovirus; serotonergic.
XX
OS Homo sapiens.
XX
PN US5508384-A.
XX
PD 16-APR-1996.
XX
PF 09-SEP-1993; 93US-0118270.
XX
PR 09-SEP-1993; 93US-0118270.
XX
PR 10-SEP-1992; 92US-0943236.
XX
PA (UTNY) UNIV NEW YORK STATE.
XX
PI Murphy RB, Schuster DI;
XX
DR WPI; 1996-208785/21.
XX
PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
PT for treating schizophrenia
XX
PS Disclousure; Column 69-72; 184pp; English.
XX
CC Proteins AA02657-W02720 represent a range of G-protein coupled receptor
CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
CC odorant, cytomagaloviral and other GPR proteins. The receptor proteins
CC were used to design polypeptides, pref. based on the transmembrane
CC domains, for use in G-protein coupled receptor ligand binding assays.
CC The polypeptide fragments retain biological activity such as binding a
CC GPR ligand or modulating GPR ligand binding to a GPR (see
CC AA02747-W02999 for examples of polypeptide fragments). The polypeptide
CC fragments can be used in compositions for treating subjects suffering

CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
CC such as schizophrenia.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 330 AA:
Query Match 26.8%; Score 120; DB 17; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.7e-101;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 55 AAADILVATLIPPSLANELLGYFRRWCEVYALDVLEFCTSSIVHCAISLDRYMAY 114
DB 44 AAADILVATLIPPSLANELLGYFRRWCEVYALDVLEFCTSSIVHCAISLDRYMAY 103
OY 115 SRALEYSKRTPRRIKCIITLVWLIAMVSLPPLIKGDPGQPRGRPOCKLQEMAYTL 174
DB 104 SRALEYSKRTPRRIKCIITLVWLIAMVSLPPLIKGDPGQPRGRPOCKLQEMAYTL 163
RESULT 12
ABU67205 standard; Peptide; 29 AA.
XX
AC ABU67205;
XX
DT 28-MAY-2003 (first entry)
XX
DE G-protein coupled receptor (GPCR) fragment #.
XX
DE Human; G-protein coupled receptor; receptor; GPCR; palmitoylation site;
KM phosphorylation cluster; arrestin; endosome; angina pectoris; rhinitis;
KM atherosclerosis; asthma; emphysema; inflammatory disease; glaucoma; pain;
XX rheumatoid arthritis; obesity; Parkinson's disease; rat.
XX
OS Homo sapiens.
XX
PN US2002106739-A1.
XX
PD 08-AUG-2002.
XX
PF 05-NOV-2001; 2001US-0993844.
XX
PR 03-NOV-2000; 2000US-245772P.
PR 08-JAN-2001; 2001US-260363P.
XX
PA (OAKLEY) OAKLEY R. H.
PA (BARAK) BARAK L. S.
PA (LAPORTE) LAPORTE S. A.
PA (CARO) CARON M. G.
XX
PI Oakley RH, Barak LS, Laporte SA, Caron MG;
XX
DR WPI; 2002-690758/74.
XX
PT Modified G-protein coupled receptor useful for identifying an agonist,
PT inverse agonist or antagonist of the receptor, comprises a carboxyl
PT terminal having one or more clusters of phosphorylation.
XX
PS Disclosure; Fig 2; 57pp; English.
XX
CC The invention relates to a modified G-protein coupled receptor (GPCR)
CC comprising an NPXY motif, and a carboxyl terminal tail which comprises a
CC putative site of palmitoylation and clusters of phosphorylation, and a
CC retained portion of a carboxyl terminal region of a GPCR portion fused to
CC a portion of the carboxyl terminal from a second GPCR, that comprises
CC phosphorylation clusters and a putative palmitoylation site 10-25 amino
CC acid residues downstream of a second NPXY motif. The modified GPCR is
CC useful for screening compounds for GPCR activity which comprises
CC providing a cell that expresses at least one modified GPCR, where the
CC cell further comprises arrestin conjugated to a detectable molecule,
CC exposing the cell to the compound, detecting the location of the arrestin
CC within the cell, comparing the location of the arrestin within the cell
CC in the presence of the compound to the location of the arrestin within

CC the cell in the absence of the compound and correlating a difference
CC between the location of arrestin within the cell in the presence of the
CC compound and the presence of the location of the arrestin within the cell
CC in the absence of the compound. Preferably, the arrestin is detected in
CC endosomes. The GPCR and a nucleic acid encoding the modified GPCR are
CC useful for preventing and/or treating a disease associated with GPCR in
CC mammals, such as angina pectoris, atherosclerosis, asthma, emphysema,
CC rhinitis, inflammatory disease, rheumatoid arthritis, glaucoma, pain,
CC obesity or Parkinson's disease, by modulating GPCR activity and affinity
CC for arrestin. Sequences ABU67202-ABU67240 represent GPCR polypeptide
CC fragments used in the scope of the invention.
XX
SQ Sequence 29 AA:
Query Match 6.5%; Score 29; DB 23; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.2e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 419 NPVYTFNDFRRAPRRLICRPWTOTAW 447
DB 1 NPVYTFNDFRRAPRRLICRPWTOTAW 29
RESULT 13
ABP53986 standard; peptide; 29 AA.
XX
ID ABP53986
XX
AC ABP53986;
XX
DT 10-JAN-2003 (first entry)
XX
DE Human alpha 2B adrenergic receptor class A GPCR.
XX
KM G-protein-coupled receptor; GPCR; detection; receptor; olfaction;
KM photo-transduction; neurotransmission; vascular tone; cardiac output;
KM digestion; pain; fluid electrolyte balance.
XX
OS Homo sapiens.
XX
PN WO200273199-A1.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US07434.
XX
PR 13-MAR-2001; 2001US-275339P.
PR 12-MAR-2002; 2002US-0095620.
XX
PA (UYDU-) UYDU DUKE.
XX
PI Barak LS, Oakley RH;
XX
DR WPI; 2003-018747/01.
XX
PT Detecting G-protein-coupled receptor pathway activity comprises
PT treating a cell having G-protein-coupled receptor activity with a test
PT compound, obtaining a digital image of the cell and detecting position
PT of conjugated proteins.
XX
PS Disclosure; Page 24; 42pp; English.
XX
CC The present invention describes a method for detecting G protein-coupled
CC receptor (GPCR) pathway activity. The method comprises: (1) providing at
CC least one cell expressing GPCR and conjugated proteins; (2) treating the
CC cell with a test compound; (3) obtaining a digital image of the cell by
CC detecting and measuring energy emitted from the detectable molecules; and
CC (4) detecting the localization of some of the conjugated proteins at one
CC of endocytic vesicles and endosomes. The method can be used for detecting
CC compounds that activate GPCR-activity in vivo and in vitro, where the
CC compound is useful for regulating various physiological functions
CC including photo-transduction, olfaction, neurotransmission, vascular
CC tone, cardiac output, digestion, pain and fluid electrolyte balance.
CC The present sequence represents a GPCR amino acid sequence which is given

CC In the exemplification of the present invention.
XX
SQ Sequence 29 AA;

Query Match 6.5%; Score 29; DB 24; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.2e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 419 NPVITTFNODFRFRFRILCRPMTQTAM 447
DB 1 NPVITTFNODFRFRFRILCRPMTQTAM 29

RESULT 14

AAMS2126
ID AAMS2126 standard; Protein; 457 AA.

AC AAMS2126;

DT 18-FEB-2002 (first entry)

DE Human alpha-2CAR variant protein.

XX Human; genotyping: alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2CAR.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 208..231

FT Domain /label= transmembrane_domain

FT Domain 379..402

FT Domain /label= transmembrane_domain

XX MO200179561-A2.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-US12575.

XX 17-APR-2000; 2000US-0551744.

XX 10-AUG-2000; 2000US-0636259.

XX 19-OCT-2000; 2000US-0692077.

XX (LIGG/) LIGGETT S B.

XX (SMAL/) SMALL K M.

XX LIGGETT SB, Small KM;

XX WPI; 2001-611728/70.

XX N-PSDB; AA199933.

XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for

XX determining whether an individual is at increased risk of developing a

XX disease associated with the corresponding receptor comprises detecting

XX a polymorphic site -

XX Claim 78; Page 160-162; 163pp; English.

XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising;
XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX alpha2A or alpha2C or fragment or complement of; and
XX (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
XX or a site comprising (A) (ggggcgggcg) or (B) (ggggcgggcg) at
XX positions 961-972 of (IIIV). The method may be used for genotyping an
XX alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX whether an individual is at increased risk of developing a disease
XX associated with alpha2B, alpha2A or alpha2, comprising detecting a
XX polymorphic site which correlate to disease selected from cardiovascular

CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idaroxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2CAR variant
CC protein, deleted for a 4 amino acid polymorphic site at residues 321-324
CC of the wildtype protein (AAMS2124).

SQ Sequence 457 AA;

Query Match 5.8%; Score 26; DB 22; Length 457;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 VYLAADVLFCTSSIVHLCAISLDRYW 112
DB 126 VYLAADVLFCTSSIVHLCAISLDRYW 151

RESULT 15

AARS4834
ID AARS4834 standard; Protein; 458 AA.

AC AARS4834;

DT 01-FEB-1995 (first entry)

DE Human derived adrenaline alpha 2CII receptor.

XX adrenaline receptor; alpha CII; screening; detection; pharmacology;
XX drugs.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "may or may not be present, but is only

FT present if amino acid residues 2-17 are

FT Peptide 2..17 /label= N-terminal peptide

FT /note= "may or may not be present"

XX JP06121686-A.

XX 06-MAY-1994.

XX 12-OCT-1992; 92JP-0272744.

XX 12-OCT-1992; 92JP-0272744.

XX (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 1994-185923/23.

XX N-PSDB; AA064890.

XX Adrenaline receptor gene encoding alpha 2CII receptor - for

XX screening drugs reactive to the alpha 2CII receptor

XX Claim 1; Page 9-11; 13pp; Japanese.

XX AA064890 encodes the amino acid sequence of a polypeptide

XX (AARS4834) that constitutes human derived adrenaline alpha 2CII

XX receptor. The DNA can be used for the study of the pharmacological

XX importance of the gene expression in humans.

XX Sequence 458 AA;

Mon Feb 9 08:28:45 2004

us-09-692-077d-8.011go.rag

Page 10

[illegible]

Search completed: February 6, 2004, 18:23:32
Job time : 38.3746 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 6, 2004, 18:22:12 ; Search time 14.9498 Seconds
(without alignments)
1265.095 Million cell updates/sec

Title: US-09-692-077D-8

Perfect score: 447
Sequence: 1 MDHQDPYSVQATAAIAAAT.....QDFRAFRILCRPWTQTAW 447

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 20

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfill.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	26.8	330	1 US-08-118-270-20	Sequence 20, Appl
2	120	26.8	330	5 PCT-US93-08528-20	Sequence 20, Appl
3	26	5.8	461	1 US-08-194-338-4	Sequence 4, Appl
4	25	5.6	27	2 US-08-103-170-17	Sequence 17, Appl
5	25	5.6	56	3 US-07-741-453A-46	Sequence 46, Appl
6	25	5.6	330	1 US-08-118-270-21	Sequence 21, Appl
7	25	5.6	330	5 PCT-US93-08528-21	Sequence 21, Appl
8	25	5.6	358	2 US-08-465-971B-4	Sequence 4, Appl
9	25	5.6	450	1 US-08-194-338-5	Sequence 5, Appl
10	25	5.6	450	1 US-08-196-989B-11	Sequence 11, Appl
11	25	5.6	450	1 US-08-444-734A-8	Sequence 8, Appl
12	25	5.6	450	2 US-08-760-936-11	Sequence 11, Appl
13	25	5.6	450	4 US-09-225-024-11	Sequence 11, Appl
14	23	5.1	99	5 US-08-118-270-332	Sequence 332, App
15	23	5.1	99	5 PCT-US93-08528-332	Sequence 332, App
16	21	4.7	330	1 US-08-118-270-19	Sequence 19, Appl
17	21	4.7	330	5 PCT-US93-08528-19	Sequence 19, Appl
18	21	4.7	334	1 US-08-118-270-22	Sequence 22, Appl
19	21	4.7	334	5 PCT-US93-08528-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-118-270-20
; Sequence 20, Application US/08118270

Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-20

Query Match 26.8%; Score 120; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 3.3e-91;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 AAADIVATLIIIPPSLANELLGWPFRRTWCEVYALDVIFCTSSIVHLCAISIDRYAV 114
Db 44 AAADIVATLIIIPPSLANELLGWPFRRTWCEVYALDVIFCTSSIVHLCAISIDRYAV 103
Qy 115 SRALEVNSKRTPRRIKIIITWMLIAVLSLPLIYKGDGPGPGRGPOCKNOEANYIL 174
Db 104 SRALEVNSKRTPRRIKIIITWMLIAVLSLPLIYKGDGPGPGRGPOCKNOEANYIL 163

RESULT 2
PCT-US93-08528-20
; Sequence 20, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-20

Query Match 26.8%; Score 120; DB 5; Length 330;
Best Local Similarity 100.0%; Pred. No. 3.3e-91;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 AAADLVATLIPESLANELLGYWFRFTWCEVLAIDVFCSSIVHCAISLDRYAV 114
Db 44 AAADLVATLIPESLANELLGYWFRFTWCEVLAIDVFCSSIVHCAISLDRYAV 103
Qy 115 SRALEYSKRTPTRRKICILTWVLAIVISLPILYKGDGQPPRRGPOCKINQEWATL 174
Db 104 SRALEYSKRTPTRRKICILTWVLAIVISLPILYKGDGQPPRRGPOCKINQEWATL 163

RESULT 3

US-08-194-338-4
Sequence 4, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McComb, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NITH101.001DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-194-338-4

Query Match 5.8%; Score 26; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 VYALADVFCCTSSIVHCAISLDRYW 112
Db 126 VYALADVFCCTSSIVHCAISLDRYW 151

RESULT 4
US-08-103-170-17
Sequence 17, Application US/08103170
Patent No. 5885824
GENERAL INFORMATION:
APPLICANT: Yamada, Tadataka
APPLICANT: Gantz, Ira
TITLE OF INVENTION: Recombinant Genomic Clones Encoding
TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, Methods For Production
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/633,060
FILING DATE: 24-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-017-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-4500
TELEFAX: (703) 486-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-103-170-17

Query Match

5.6%; Score 25; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 87 YLADVLCTSSIVHLCAISIDRY 111
Db 3 YLADVLCTSSIVHLCAISIDRY 27

RESULT 5
US-07-741-453A-46
Sequence 46, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASARAT, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-741-453A-46
Query Match 5.6%; Score 25; DB 3; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 88 YLADVLCTSSIVHLCAISIDRY 112
Db 4 YLADVLCTSSIVHLCAISIDRY 28

RESULT 6
US-08-118-270-21
Sequence 21, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-21

Query Match 5.6%; Score 25; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 6.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 YLADVLCTSSIVHLCAISIDRY 112
Db 74 YLADVLCTSSIVHLCAISIDRY 98

RESULT 7
PCT-US93-08528-21
Sequence 21, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-21

Query Match 5.6%; Score 25; DB 5; Length 330;
Best Local Similarity 100.0%; Pred. No. 6.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLFCTSSIVHLCALSLDRYW 112
DB 74 YLALDVLFCTSSIVHLCALSLDRYW 98

RESULT 8
US-08-465-971B-4
Sequence 4, Application US/08465971B
Patent No. 5942414
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEP51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MILLINS, J G
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-465-971B-4

Query Match 5.6%; Score 25; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 7.4e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLFCTSSIVHLCALSLDRYW 112
DB 112 YLALDVLFCTSSIVHLCALSLDRYW 136

RESULT 9

US-08-194-338-5
Sequence 5, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-194-338-5

Query Match 5.6%; Score 25; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLFCTSSIVHLCALSLDRYW 112
DB 109 YLALDVLFCTSSIVHLCALSLDRYW 133

RESULT 10
US-08-196-989B-11
Sequence 11, Application US/08196989B
Patent No. 5585476
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,9898
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-196-9898-11

Query Match 5.6%; Score 25; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 YLADVLFCTSSIVHLCASISDRYW 112
Db 109 YLADVLFCTSSIVHLCASISDRYW 133

RESULT 11
US-08-444-734A-8
Sequence 8, Application US/08444734A
Patent No. 5610282
GENERAL INFORMATION:
APPLICANT: Sibley, David R.
APPLICANT: Monama, Frederick J.
APPLICANT: Mahan, Lawrence C.
APPLICANT: McVittie, Louis D.
TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and
TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
TITLE OF INVENTION: cell lines
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,734A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,917
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/548,714
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH065,001FW1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-444-734A-8

Query Match 5.6%; Score 25; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 YLADVLFCTSSIVHLCASISDRYW 112
Db 109 YLADVLFCTSSIVHLCASISDRYW 133

RESULT 12
US-08-760-936-11
Sequence 11, Application US/08760936
Patent No. 5656443
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936
FILING DATE: December 6, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-760-936-11

Query Match 5.6%; Score 25; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 YLADVLFCTSSIVHLCASISDRYW 112
Db 109 YLADVLFCTSSIVHLCASISDRYW 133

RESULT 13
US-09-225-024-11
Sequence 11, Application US/09225024
Patent No. 6518414
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,024
FILING DATE: 04-JAN-1999
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/760,936
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/196,989
FILING DATE: 15-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-225-024-11

Query Match 5.6%; Score 25; DB 4; Length 450;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLADVLFTSTSIIVLCAISIDRYW 112
DB 109 YLADVLFTSTSIIVLCAISIDRYW 133

RESULT 14
US-08-118-270-332
Sequence 332, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 332:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-332

Query Match 5.1%; Score 23; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TAAIAATFLIIFITFGNALVI 34
DB 1 TAAIAATFLIIFITFGNALVI 23

RESULT 15
PCT-US93-08528-332
Sequence 332, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 332:

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: SEQUENCE CHARACTERISTICS:
:   LENGTH: 99 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: MOLECULE TYPE: peptide
: PCT-US93-08528-332

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Query Match      5.1%; Score 23; DB 5; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      12 TAAIAAAITFLILFTIFGNALVI 34
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Db       1 TAAIAAAITFLILFTIFGNALVI 23

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 Job time : 15.9498 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 6, 2004, 18:23:37 ; Search time 29.4013 Seconds
(without alignments)
3183.320 Million cell updates/sec

Title: US-09-692-077D-8

Perfect score: 447
Sequence: 1 MDHDPYSVQATAIAAAT.....QDFRRARILCPWTOTAW 447

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 801455 seqs, 209382283 residues

Word size : 20

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:*
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14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	447	100.0	447	9	US-09-825-923-2
2	447	100.0	447	15	US-10-077-870-2
3	447	100.0	447	15	US-10-001-073-8
4	306	68.5	450	9	US-09-825-973-4
5	306	68.5	450	15	US-10-077-870-4
6	306	68.5	450	15	US-10-001-073-7
7	306	68.5	450	15	US-10-225-567A-42
8	29	6.5	29	10	US-09-393-844-18
9	26	5.8	451	15	US-10-001-073-46
10	26	5.8	451	15	US-10-325-567A-44
11	26	5.8	462	15	US-10-001-073-44
12	25	5.6	450	15	US-10-001-073-26
13	25	5.6	450	15	US-10-001-073-27
14	25	5.6	450	15	US-10-225-567A-40
15	21	4.7	307	15	US-10-060-795B-4

ALIGNMENTS

RESULT 1	
US-09-825-923-2	
Sequence 2, Application US/09825923	
Patent No. US20010016338A1	
GENERAL INFORMATION:	
APPLICANT: Snapir, Amir	
APPLICANT: Heinonen, Paula	
APPLICANT: Alhopuro, Pia	
APPLICANT: Karvonen, Martti	
APPLICANT: Koulu, Markku	
APPLICANT: Pesonen, Ullamari	
APPLICANT: Scheinin, Mika T	
APPLICANT: Salonen, Jukka T	
APPLICANT: Tuomainen, Tomi-Pekka	
APPLICANT: Lakka, Timo A	
APPLICANT: Nyysanen, Kristina	
APPLICANT: Salonen, Riitta	
APPLICANT: Kaunonen, Jussi	
APPLICANT: Valkonen, Veli-Pekka	
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor	
FILE REFERENCE: Alpha-2B-AR variant	
CURRENT FILING DATE: 2001-04-05	
PRIORITY FILING DATE: 2000-05-25	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO: 2	
LENGTH: 447	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-09-825-923-2	
Query Match	100.0%; Score 447; DB 9; Length 447;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MDHDPYSVQATAIAAATFTLFTFGNALVLAIVTSRLAPONLPLVSLAADIL 60
DB	1 MDHDPYSVQATAIAAATFTLFTFGNALVLAIVTSRLAPONLPLVSLAADIL 60
QY	61 VATLIIPFSLANBELGYWFRRTWCEVYALDVLECTSSIVHLCAISLDRYMAVSRLLEY 120
DB	61 VATLIIPFSLANBELGYWFRRTWCEVYALDVLECTSSIVHLCAISLDRYMAVSRLLEY 120
QY	121 NSKRTPRRIKIIITWVLAIVISLPLIYKDGQPPRRGPCKLNOEAMVYIASSIGS 180
DB	121 NSKRTPRRIKIIITWVLAIVISLPLIYKDGQPPRRGPCKLNOEAMVYIASSIGS 180
QY	181 FPAAPCLMIITVYRIYVLIARSNRGRKAGGPGQGSXKPPRHGALASAKLPALASV 240
DB	181 FPAAPCLMIITVYRIYVLIARSNRGRKAGGPGQGSXKPPRHGALASAKLPALASV 240
QY	241 ASAREVNGHSGKSTGEKEGETPEDTGTALPPSWAALPNSGQGGKEGVCGASPEDEAEE 300
DB	241 ASAREVNGHSGKSTGEKEGETPEDTGTALPPSWAALPNSGQGGKEGVCGASPEDEAEE 300
QY	301 EEEEEECEPAVPVSPASCPPIQOPQGSRVATLIRGQVILRGVAILGGQWRRRAQL 360
DB	301 EEEEEECEPAVPVSPASCPPIQOPQGSRVATLIRGQVILRGVAILGGQWRRRAQL 360
QY	361 TRERRFFVLAIVYGVLVCMPPFPFSYSGALCPKCKXYPHGLFQFPFMTGYNSSINP 420
DB	361 TRERRFFVLAIVYGVLVCMPPFPFSYSGALCPKCKXYPHGLFQFPFMTGYNSSINP 420
QY	421 VIYTFNQDFRRAFRILCPWTOTAW 447

Db 421 VIYTIENODFRRAFRRIICRPWTOTAW 447

RESULT 2

US-10-077-870-2
; Sequence 2, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077, 870
; PRIOR FILING DATE: 2002-05-21
; PRIORITY APPLICATION NUMBER: FI 20010323
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-2

Query Match 100.0%; Score 447; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHODPSVQATAIAAATFTLLFTFGNALVILAVTSRSIRAPQNLFLVSLAAADTL 60
Db 1 MDHODPSVQATAIAAATFTLLFTFGNALVILAVTSRSIRAPQNLFLVSLAAADTL 60
QY 61 VATLIIPFSLANELLGYWYFRRTWCEVYIALDVLFCCTSSIVHLCALSLDRYMAVSRALEY 120
Db 61 VATLIIPFSLANELLGYWYFRRTWCEVYIALDVLFCCTSSIVHLCALSLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIITLTVWLIAAVISLPLLYKDGQGPGRGRPOCKLNOEAMWYTLASSIGS 180
Db 121 NSKRTPRRIKCIITLTVWLIAAVISLPLLYKDGQGPGRGRPOCKLNOEAMWYTLASSIGS 180
QY 121 NSKRTPRRIKCIITLTVWLIAAVISLPLLYKDGQGPGRGRPOCKLNOEAMWYTLASSIGS 180
Db 121 NSKRTPRRIKCIITLTVWLIAAVISLPLLYKDGQGPGRGRPOCKLNOEAMWYTLASSIGS 180
QY 181 FPAFCLIMILVYRIYLIARSNRRGPRAKGSGGQESKOPRPHDGALASAKLPALASV 240
Db 181 FPAFCLIMILVYRIYLIARSNRRGPRAKGSGGQESKOPRPHDGALASAKLPALASV 240
QY 241 ASAREVNGHSKSTGEKEBETPEDTGTALPESWALPNSGQGQKGVCGASPEDAESEE 300
Db 241 ASAREVNGHSKSTGEKEBETPEDTGTALPESWALPNSGQGQKGVCGASPEDAESEE 300
QY 301 EEEBEECEPOAVVPSPASCSPLLOPQGSRYLATLRGCVLLGRGVGAIIGQWRRRAQL 360
Db 301 EEEBEECEPOAVVPSPASCSPLLOPQGSRYLATLRGCVLLGRGVGAIIGQWRRRAQL 360
QY 361 TREKFTFVLAVVIGVFLCWPFPPFSYSLGAIICPHCKVPHGLQFFFWIGYCNSSINLP 420
Db 361 TREKFTFVLAVVIGVFLCWPFPPFSYSLGAIICPHCKVPHGLQFFFWIGYCNSSINLP 420
QY 421 VIYTIENODFRRAFRRIICRPWTOTAW 447
Db 421 VIYTIENODFRRAFRRIICRPWTOTAW 447

RESULT 3
US-10-001-073-8

; Sequence 8, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCF
; CURRENT APPLICATION NUMBER: US/10/001, 073
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-073-8

Query Match 100.0%; Score 447; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHODPSVQATAIAAATFTLLFTFGNALVILAVTSRSIRAPQNLFLVSLAAADTL 60
Db 1 MDHODPSVQATAIAAATFTLLFTFGNALVILAVTSRSIRAPQNLFLVSLAAADTL 60
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Db 61 VATLIIPFSLANELLGYWYFRRTWCEVYIALDVLFCCTSSIVHLCALSLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIITLTVWLIAAVISLPLLYKDGQGPGRGRPOCKLNOEAMWYTLASSIGS 180
Db 121 NSKRTPRRIKCIITLTVWLIAAVISLPLLYKDGQGPGRGRPOCKLNOEAMWYTLASSIGS 180
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Db 181 FPAFCLIMILVYRIYLIARSNRRGPRAKGSGGQESKOPRPHDGALASAKLPALASV 240
QY 241 ASAREVNGHSKSTGEKEBETPEDTGTALPESWALPNSGQGQKGVCGASPEDAESEE 300
Db 241 ASAREVNGHSKSTGEKEBETPEDTGTALPESWALPNSGQGQKGVCGASPEDAESEE 300
QY 301 EEEBEECEPOAVVPSPASCSPLLOPQGSRYLATLRGCVLLGRGVGAIIGQWRRRAQL 360
Db 301 EEEBEECEPOAVVPSPASCSPLLOPQGSRYLATLRGCVLLGRGVGAIIGQWRRRAQL 360
QY 361 TREKFTFVLAVVIGVFLCWPFPPFSYSLGAIICPHCKVPHGLQFFFWIGYCNSSINLP 420
Db 361 TREKFTFVLAVVIGVFLCWPFPPFSYSLGAIICPHCKVPHGLQFFFWIGYCNSSINLP 420
QY 421 VIYTIENODFRRAFRRIICRPWTOTAW 447
Db 421 VIYTIENODFRRAFRRIICRPWTOTAW 447

RESULT 4

US-09-825-923-4
; Sequence 4, Application US/09825923
; Patent No. US2001001638A1
; GENERAL INFORMATION:
; APPLICANT: Snapit, Amir
; APPLICANT: Heimonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyysanen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kaunonen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: protein, and uses thereof
; CURRENT APPLICATION NUMBER: US/09/825, 923
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422, 985
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 450

TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-923-4

Query Match 68.5%; Score 306; DB 9; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.6e-252;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHODPYSVQATAIAAATFTLFTFGNALVILAVITSRSLRAPONLFLVSLAAADIL 60
DB 1 MDHODPYSVQATAIAAATFTLFTFGNALVILAVITSRSLRAPONLFLVSLAAADIL 60
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DB 61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKIIITWVLAIAVISLPLIYKGDGPQGRGPRGCKLQNEAWYIIASSIGS 180
DB 121 NSKRTPRRIKIIITWVLAIAVISLPLIYKGDGPQGRGPRGCKLQNEAWYIIASSIGS 180
QY 181 PFAPCLIMILVYLRILYIAKRSNRGPRAGKGPQGESKOPRPHGALASAKLPALASV 240
DB 181 PFAPCLIMILVYLRILYIAKRSNRGPRAGKGPQGESKOPRPHGALASAKLPALASV 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTTRALPPSWAALPNSGQKQEGVCGASPEDEAEE 300
DB 241 ASAREVNGHSKSTGEKEGETPEDTGTTRALPPSWAALPNSGQKQEGVCGASPEDEAEE 300
QY 301 EEEEEE 306
DB 301 EEEEEE 306

RESULT 5

US-10-077-870-4
Sequence 4, Application US/10077870
Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077, 870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 4
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-077-870-4

Query Match 68.5%; Score 306; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.6e-252;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKIIITWVLAIAVISLPLIYKGDGPQGRGPRGCKLQNEAWYIIASSIGS 180
DB 121 NSKRTPRRIKIIITWVLAIAVISLPLIYKGDGPQGRGPRGCKLQNEAWYIIASSIGS 180
QY 181 PFAPCLIMILVYLRILYIAKRSNRGPRAGKGPQGESKOPRPHGALASAKLPALASV 240
DB 181 PFAPCLIMILVYLRILYIAKRSNRGPRAGKGPQGESKOPRPHGALASAKLPALASV 240

QY 241 ASAREVNGHSKSTGEKEGETPEDTGTTRALPPSWAALPNSGQKQEGVCGASPEDEAEE 300
DB 241 ASAREVNGHSKSTGEKEGETPEDTGTTRALPPSWAALPNSGQKQEGVCGASPEDEAEE 300
QY 301 EEEEEE 306
DB 301 EEEEEE 306

RESULT 6

US-10-001-073-7
Sequence 7, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-073-7

Query Match 68.5%; Score 306; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.6e-252;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDHODPYSVQATAIAAATFTLFTFGNALVILAVITSRSLRAPONLFLVSLAAADIL 60
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DB 61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKIIITWVLAIAVISLPLIYKGDGPQGRGPRGCKLQNEAWYIIASSIGS 180
DB 121 NSKRTPRRIKIIITWVLAIAVISLPLIYKGDGPQGRGPRGCKLQNEAWYIIASSIGS 180
QY 181 PFAPCLIMILVYLRILYIAKRSNRGPRAGKGPQGESKOPRPHGALASAKLPALASV 240
DB 181 PFAPCLIMILVYLRILYIAKRSNRGPRAGKGPQGESKOPRPHGALASAKLPALASV 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTTRALPPSWAALPNSGQKQEGVCGASPEDEAEE 300
DB 241 ASAREVNGHSKSTGEKEGETPEDTGTTRALPPSWAALPNSGQKQEGVCGASPEDEAEE 300
QY 301 EEEEEE 306
DB 301 EEEEEE 306

RESULT 7

US-10-225-567A-42
Sequence 42, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292

Qy	MBHODPYSVOATAAIAAAITFLILFTTFGNALVITLAVLSRSRLAPQNLFLVSLAAADIL	60
Db	1 MBHODPYSVOATAIAAAITFLILFTTFGNALVITLAVLSRSRLAPQNLFLVSLAAADIL	60
Qy	61 VATLIIPESLANELLGYWYFRRTWCVEVYALADVLFCTSGSIYHLCASISLDRWAAVSRALEY	120
Db	61 VATLIIPESLANELLGYWYFRRTWCVEVYALADVLFCTSGSIYHLCASISDRWAAVSRALEY	120
Qy	121 NSKRTPRRIRKCIITLVTWVLIAAVITSLPRLITYKDGQOPGRGRPOCKLNDZAAWYILIASISIGS	180
Db	121 NSKRTPRRIRKCIITLVTWVLIAAVITSLPRLITYKDGQOPGRGRPOCKLNDZAAWYILIASISIGS	180
Qy	181 PFAPCCLIMLVYLRITYLIAKRSNRRGPRPAKGQGGEGSEKORPRPHGALMSAKIIPALASV	240
Db	181 PFAPCCLIMLVYLRITYLIAKRSNRRGPRPAKGSPQGESKORPRPHGALMSAKIIPALASV	240
Qy	241 ASAREVNGHSGKSTGKEKEGETPEDTGTAALPPSWAALPNSGQGGKEGVCGASPEDEAEE	300
Db	241 ASAREVNGHSGKSTGKEKEGETPEDTGTAALPPSWAALPNSGQGGKEGVCGASPEDEAEE	300
Qy	301 EEEEEE 306	
Db	301 EEEEEE 306	

```

SEQUENCE 8
US-09-993-844-18
Sequence 18, Application US/09993844
Patent No. US20020106739A1
GENERAL INFORMATION:
APPLICANT: Oakley, Robert H.
APPLICANT: Barak, Lawrence S.
APPLICANT: Laporte, Stephanie A.
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Modified G-Protein Coupled Receptors
FILE REFERENCE: 033072-026
CURRENT APPLICATION NUMBER: US/09/993,844
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,772
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/260,363
PRIOR FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FASTSBQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 29
TYPE: PRT
ORGANISM: Human
US-09-993-844-18

```

```

Query Match      100.5%; Score 29; DB 10; Length 29;
Best Local Similarity 100.0%; Fred. No. 2.6e-17;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY      419 NPVIYITFNODPRARFRRLICRPMQTAM 447
      |||||
Db       1 NPVIYITFNODPRARFRRLICRPMQTAM 29

```

RESULT 9
US-10-001-073-46
; Sequence 46, Application US/10001073

```

/ Publication No. US20030113725A1
/ GENERAL INFORMATION:
/ APPLICANT: Liggett, Stephen
/ APPLICANT: Small, Kirsten
/ TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
/ FILE REFERENCE: 13073-PCT
/ CURRENT APPLICATION NUMBER: US/10/001,073
/ CURRENT FILING DATE: 2001-11-01
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 46
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-001-073-46

```

	Query Match	5.8%	Score 26;	DB 15;	Length 458;
	Best Local Similarity	100.0%;	Pred. NO. 9e-14;		
	Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	87	VYIADVVFCTSSIVHLCALISDRW	112		
Dd	126	VYIADVVFCTSSIVHLCALISDRW	151		

```

RESULT 10
US-10-225-567A-44
; Sequence 44, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-44

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	Query Match	5.8%;	Score 26;	DB 15;	Length 461;
	Best Local Similarity	100.0%;	Pred. No. 9e-14;		
	Matches	26;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
Oy	87	VYIADVIFCTSSIVHLCALISDRYW		112	
Dd	126	VYIADVIFCTSSIVHLCALISDRYW		151	

```

RESULT 11
US-10-001-073-44
; Sequence 44, Application US/10001073
; Publication NO. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; INVENTOR: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCIT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 44
; LENGTH: 462
; TYPE: PRT

```

```
; ORGANISM: Homo sapiens
; US-10-001-073-44
Query Match      5.8%; Score 26; DB 15; Length 462;
Best Local Similarity 100.0%; Pred. No. 9.1e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      87 YLALDVLFCCTSSIVHLCAISLDRYW 112
Db      126 YLALDVLFCCTSSIVHLCAISLDRYW 151

RESULT 12
US-10-001-073-26
; Sequence 26, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCF
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 26
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-001-073-26

Query Match      5.6%; Score 25; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.3e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      88 YLALDVLFCCTSSIVHLCAISLDRYW 112
Db      109 YLALDVLFCCTSSIVHLCAISLDRYW 133

RESULT 13
US-10-001-073-27
; Sequence 27, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCF
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 27
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-001-073-27

Query Match      5.6%; Score 25; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.3e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      88 YLALDVLFCCTSSIVHLCAISLDRYW 112
Db      109 YLALDVLFCCTSSIVHLCAISLDRYW 133

RESULT 14
US-10-225-567A-40
; Sequence 40, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 40
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-40

Query Match      5.6%; Score 25; DB 15; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.3e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      88 YLALDVLFCCTSSIVHLCAISLDRYW 112
Db      109 YLALDVLFCCTSSIVHLCAISLDRYW 133
```

```
RESULT 15
US-10-060-795B-4
; Sequence 4, Application US/10060795B
; Publication No. US20030040022A1
; GENERAL INFORMATION:
; APPLICANT: Civelelli, Olivier
; APPLICANT: Bunzow, James R.
; APPLICANT: Grandy, David K.
; APPLICANT: Machida, Curtis A.
; TITLE OF INVENTION: Dopamine Receptors and Genes
; FILE REFERENCE: 90-1092-CCC
; CURRENT APPLICATION NUMBER: US/10/060,795B
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/238977
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 08/474892
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/973588
; PRIOR FILING DATE: 1992-11-09
; PRIOR APPLICATION NUMBER: 07/438544
; PRIOR FILING DATE: 1989-11-20
; PRIOR APPLICATION NUMBER: 07/273373
; PRIOR FILING DATE: 1988-11-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-060-795B-4
```

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Query Match      4.7%; Score 21; DB 15; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      88 YLALDVLFCCTSSIVHLCAISL 108
Db      109 YLALDVLFCCTSSIVHLCAISL 129
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Job time : 30.4013 secs

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OM protein - protein search, using sw model

Run on: February 6, 2004, 18:20:56 ; Search time 16.448 Seconds
(without alignments)
2614.040 Million cell updates/sec

Title: US-09-692-077D-8
447
Perfect score: 1 MDHODPYSVQATAIAAIAIT.....QDFRRAPRRLICRPWTQTAW 447
Sequence:

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 20

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	306	68.5	450	2 A37223	alpha-2B-adrenergic
2	176	39.4	276	2 I53161	alpha-2-adrenergic
3	71	15.9	448	2 I51883	alpha-2B-adrenergic
4	71	15.9	455	2 S28221	alpha-2-C2 adrenergic
5	63	14.1	453	2 A35642	alpha-2B-adrenergic
6	26	5.8	458	2 A48392	alpha-2C4 adrenergic
7	26	5.8	458	2 A40392	alpha-2-adrenergic
8	26	5.8	458	2 A37869	alpha-2B-adrenergic
9	26	5.8	458	2 I49480	alpha-2C-adrenergic
10	26	5.8	461	2 A31237	alpha-2-adrenergic
11	25	5.6	432	2 I50829	alpha-2-adrenoceptor
12	25	5.6	450	2 A38316	alpha-2-adrenergic
13	25	5.6	450	2 B40392	alpha-2-adrenergic
14	25	5.6	450	2 JH0190	alpha-2-adrenergic
15	25	5.6	450	2 A34169	alpha-2A-adrenergic
16	25	5.6	450	2 I49481	alpha-2-adrenergic

ALIGNMENTS

RESULT 1
A37223

alpha-2B-adrenergic receptor - human
N/Alternate names: alpha-2C2-adrenergic receptor
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 29-Oct-1999
C/Accession: A37223; I39407; S14308; A36158
R/Weinshank, R.L.; Zgombick, J.M.; Macchi, M.; Adham, N.; Lichtblau, H.; Branchek, T.A.

Mol. Pharmacol. 38, 681-688, 1990
A/Title: Cloning, expression, and pharmacological characterization of a human alpha-2B-adrenergic receptor
A/Reference number: A37223; MUID:91042469; PMID:2172775
A/Accession: A37223
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-450 <WEI>
R/Lomasney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, T.L.; Caron, M.G.; Nairn, A.C.; Nemeroff, C.B.; U.S.S. 87, 5094-5098, 1990
A/Title: Expansion of the alpha-2-adrenergic receptor family: cloning and characterization of the alpha-2A-adrenergic receptor
A/Reference number: I39407; MUID:90311345; PMID:2164221
A/Accession: I39407
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-450 <LOM>
A/Cross-references: GB:M34041; NID:9178197; PIDN:AAA51666.1; PID:9178198
R/Chen, J.; V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic receptor family
A/Reference number: S14308; MUID:91192139; PMID:1849485
A/Accession: S14308
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 56-185 <CHH>
A/Cross-references: GB:X59684; NID:928635
A/Note: this translation is not annotated in GenBank entry HSALPH216, release 111.0
R/Chang, A.C.; Ho, T.F.; Chang, N.C.
Biochem. Biophys. Res. Commun. 172, 817-823, 1990
A/Title: In vitro amplification by polymerase chain reaction of a partial gene encoding the alpha-2-adrenergic receptor
A/Reference number: A36158; MUID:91054503; PMID:2173582
A/Accession: A36158
A/Molecule type: DNA
A/Residues: 95-361, 364-389 <CHA>
A/Cross-references: GB:M38742; NID:9177867; PIDN:AAA62823.1; PID:9177868
C/Genetics:
A/Gene: GDB:ADRA2B; ADRA2L1; ADRA2R1
A/Cross-references: GDB:120539; OMIM:104260
A/Map position: 2p13-2q13
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 68.5%; Score 306; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 3.2e-289;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDHODPYSVQATAIAAIAITFLIIFTFGNALVTLAVTSLSLAPQNLFLVSLAADI	60
DB	1	MDHODPYSVQATAIAAIAITFLIIFTFGNALVTLAVTSLSLAPQNLFLVSLAADI	60
QY	61	VATLIIPPSLANELLGYWPFRTWCCEVYLAADVYFCTSSIVHLCAISIDRYWAVSRALEY	120
DB	61	VATLIIPPSLANELLGYWPFRTWCCEVYLAADVYFCTSSIVHLCAISIDRYWAVSRALEY	120
QY	121	NSKTPRRIKIIITLWLAIAVISLPLIYKGDGQPPGRGPOCKLNOEAYIILASSIGS	180
DB	121	NSKTPRRIKIIITLWLAIAVISLPLIYKGDGQPPGRGPOCKLNOEAYIILASSIGS	180
QY	181	FFAPCLIMILVYLIYLIYLAISNRGPRKAGPGQGSQKPRPHGALASAKLPALASV	240
DB	181	FFAPCLIMILVYLIYLIYLAISNRGPRKAGPGQGSQKPRPHGALASAKLPALASV	240
QY	241	ASAREVNGHSHSTGEKRGEPEDTGTALPPSMAALPNSGQGEVCGASPEDAEER	300
DB	241	ASAREVNGHSHSTGEKRGEPEDTGTALPPSMAALPNSGQGEVCGASPEDAEER	300
QY	301	EEEEEE 306	
DB	301	EEEEEE 306	

RESULT 2
I53161
alpha-2-adrenergic receptor, isolets of Langerhans - rat (fragment)

C:Species: Rattus sp. (rat)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 30-May-1997
C:Accession: I53161
R:Wang, S.Y., Pilkey, D.T.
Diabetes 43, 127-136, 1994
A:Title: Identification in islets of Langerhans of a new rat alpha 2-adrenergic receptor
A:Reference number: I53161; MUID:94085695; PMID:8262309
A:Accession: I53161
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-276 <RES>
A:Cross-references: GB:S67316; NID:g456949
A:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 39.4%; Score 176; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 5,8e-163;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 CTSSIVHCAISIDRYWAVSRALVNSKRTPRRIKCIITVWLIATVSLPILYKGDG 155
DB 1 CTSSIVHCAISIDRYWAVSRALVNSKRTPRRIKCIITVWLIATVSLPILYKGDG 60
QY 156 PQRGRPOCKLNEAWYIIASSIGSFAPCLITVILYINILYIAKSNRGRGAPGPG 215
DB 61 PQRGRPOCKLNEAWYIIASSIGSFAPCLITVILYINILYIAKSNRGRGAPGPG 120
QY 216 GESKOPRPHGALASAKLPALASVARSVNSKSTGEKEGETPEPTGRALP 271
DB 121 GESKOPRPHGALASAKLPALASVARSVNSKSTGEKEGETPEPTGRALP 176

RESULT 3

151883
alpha-2B-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C:Accession: I51883
R:Le Joesec, M.; Cloix, J.F.; Pecquery, R.; Giudicelli, Y.; Dausse, J.P.
Am. J. Hypertens. 8, 177-182, 1995
A:Title: Differential sodium regulation between salt-sensitive and salt-resistant Sabra
A:Reference number: I51883; MUID:95275492; PMID:7755946
A:Accession: I51883
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-448 <RES>
A:Cross-references: EMBL:X74400; NID:g940862; PIDN:CAA52411.1; PID:g940816
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 15.9%; Score 71; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.2e-60;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 WCEVTLADLVFCTSSIVHCAISIDRYWAVSRALVNSKRTPRRIKCIITVWLIATV 143
DB 84 WCEVTLADLVFCTSSIVHCAISIDRYWAVSRALVNSKRTPRRIKCIITVWLIATV 143

QY 144 SLPLIYKGDQ 154
DB 144 SLPLIYKGDQ 154

RESULT 4

528221
alpha-2-C2 adrenergic receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
C:Accession: S28221; JH0693
R:Chen, W.M.; Chang, A.C.; Shie, B.J.; Chang, Y.H.; Chang, N.C.A.
Biochim. Biophys. Acta 1171, 219-223, 1992
A:Title: Molecular cloning and characterization of a mouse alpha(2)C2 adrenoceptor subty
A:Reference number: S28221; MUID:93129625; PMID:1336396

A:Accession: S28221
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-455 <CHR>
A:Cross-references: EMBL:M94583
A:Note: The authors translated the codon CCA for residue 161 as Phe, ACT for residue 33,
R:Chruschanski, A.D.; Link, R.E.; Daunt, D.A.; Bersh, G.S.; Kobilka, B.K.
Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992
A:Title: Cloning and expression of the mouse homolog of the human alpha2-C2 adrenergic
A:Reference number: JH0693; MUID:92378586; PMID:1354956
A:Accession: JH0693
A:Molecule type: DNA
A:Residues: 6-228,231-455 <CHR>
A:Cross-references: GB:L00979; NID:g191547; PIDN:AAA37131.1; PID:g191548
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:18-43/Domain: transmembrane #status predicted <TM1>
F:150-81/Domain: transmembrane #status predicted <TM2>
F:190-116/Domain: transmembrane #status predicted <TM3>
F:134-158/Domain: transmembrane #status predicted <TM4>
F:173-199/Domain: transmembrane #status predicted <TM5>
F:377-402/Domain: transmembrane #status predicted <TM6>
F:410-435/Domain: transmembrane #status predicted <TM7>

Query Match 15.9%; Score 71; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-60;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 WCEVTLADLVFCTSSIVHCAISIDRYWAVSRALVNSKRTPRRIKCIITVWLIATV 143
DB 89 WCEVTLADLVFCTSSIVHCAISIDRYWAVSRALVNSKRTPRRIKCIITVWLIATV 148
QY 144 SLPLIYKGDQ 154
DB 149 SLPLIYKGDQ 159

RESULT 5

A35642
alpha-2B-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C:Accession: A35642
R:Zeng, D.; Harrison, J.K.; D'Angelo, D.D.; Barber, C.M.; Tucker, A.L.; Lu, Z.; Lynch, K
Proc. Natl. Acad. Sci. U.S.A. 87, 3102-3106, 1990
A:Title: Molecular characterization of a rat alpha-2B-adrenergic receptor.
A:Reference number: A35642; MUID:90222177; PMID:2158103
A:Accession: A35642
A:Molecule type: mRNA
A:Residues: 1-453 <ZEN>
A:Cross-references: GB:M32061; NID:g202589; PIDN:AAA40635.1; PID:g202590
A:Note: 169-Phe was also found
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 14.1%; Score 63; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 7.1e-53;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AITPLIFETFGNALVILAVITSRSLAPQNLPLVSLAADIIVATLIIPFSLANELLG 77
DB 23 AITPLIFETFGNALVILAVITSRSLAPQNLPLVSLAADIIVATLIIPFSLANELLG 82
QY 78 WYF 80
DB 83 WYF 85

RESULT 6

A48392
alpha 2C4 adrenoceptor subtype - mouse
N:Alternate names: alpha 2C4 isoceptor
C:Species: Mus musculus (house mouse)

C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C/Accession: A48392
R/Chang, Y.H.; Chang, N.C.; Chen, W.M.; Chang, A.C.
Biochem. Mol. Biol. Int. 29, 467-474, 1993
A/Title: Molecular characterization of a murine homologue of alpha 2C4 adrenoceptor sub
A/Reference number: A48392; MUID:93250567; PMID:8387367
A/Accession: A48392
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-458 <CH>
A/Cross-references: GB:M97516; NID:g191728; PIDN:AAA37183.1; PID:g191729
A/Experimental source: DBA/2, liver
A/Note: Sequence extracted from NCBI backbone (NCBIN:131475, NCBIPI:131476)
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor

Query Match 5.8%; Score 26; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 VYALDVLFCSTSIIVHLCALSLDRYW 112
Db 126 VYALDVLFCSTSIIVHLCALSLDRYW 151

RESULT 7
A40392
alpha-2-adrenergic receptor (clone RG10) - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C/Accession: A40392
R/Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A/Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic rec
A/Reference number: A40392; MUID:91244823; PMID:1645350
A/Accession: A40392
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-458 <LAN>
A/Cross-references: GB:M62371; NID:g206612; PIDN:AAA42033.1; PID:g206613
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 5.8%; Score 26; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 VYALDVLFCSTSIIVHLCALSLDRYW 112
Db 126 VYALDVLFCSTSIIVHLCALSLDRYW 151

RESULT 8
A37869
alpha-2B-adrenergic receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C/Accession: A37869; S13023
R/Floriell, C.S.; Handy, D.E.; Bresnahan, M.R.; Zannis, V.I.; Gavras, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 1019-1023, 1991
A/Title: Cloning and expression of a rat brain alpha-2B-adrenergic receptor.
A/Reference number: A37869; MUID:91126047; PMID:11704126
A/Accession: A37869
A/Molecule type: mRNA
A/Residues: 1-458 <FLIO>
A/Cross-references: GB:M58316; NID:g202585; PIDN:AAA40634.1; PID:g202586
A/Note: The authors translated the codon ACC for residue 69 as Asn and GCG for residue 8
R/Voigt, M.M.; McCune, S.K.; Kenteman, R.Y.; Felder, C.C.
FEBS Lett. 278, 45-50, 1991
A/Title: The rat alpha(2)-C4 adrenergic receptor gene encodes a novel pharmacological su
A/Reference number: S13023; MUID:91130596; PMID:11704314
A/Accession: S13023
A/Molecule type: DNA

A/Residues: 1-39, 'G', '41-68', 'N', '70-154', 'E', '156-244', 'S', '246-458 <VOI>
A/Cross-references: GB:X57659; NID:g288044; PIDN:CAA40861.1; PID:g288045
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 5.8%; Score 26; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 VYALDVLFCSTSIIVHLCALSLDRYW 112
Db 126 VYALDVLFCSTSIIVHLCALSLDRYW 151

RESULT 9
I49480
alpha-2 adrenergic receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C/Accession: I49480
R/Link, R.; Daut, D.; Barsh, G.S.; Chrusciel, A.; Koblika, B.
Mol. Pharmacol. 42, 16-27, 1992
A/Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and id
in antagonist binding.
A/Reference number: I49480; MUID:92342131; PMID:1353249
A/Accession: I49480
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-458 <RES>
A/Cross-references: GB:M93976; NID:g191880; PIDN:AAA37212.1; PID:g191881
C/Superfamily: vertebrate rhodopsin
C/Keywords: neurotransmitter receptor

Query Match 5.8%; Score 26; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 VYALDVLFCSTSIIVHLCALSLDRYW 112
Db 126 VYALDVLFCSTSIIVHLCALSLDRYW 151

RESULT 10
A31237
alpha-2C-adrenergic receptor - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999
C/Accession: A31237; S14309; S14310
R/Regan, J.W.; Koblika, T.S.; Yang-Feng, T.L.; Caron, M.G.; Lefkowitz, R.J.; Koblika, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 6301-6305, 1988
A/Title: Cloning and expression of a human kidney cDNA for an alpha-2-adrenergic recepto
A/Reference number: A31237; MUID:88320430; PMID:2842764
A/Accession: A31237
A/Molecule type: mRNA
A/Residues: 1-461 <REG>
A/Cross-references: GB:J03853; NID:g178193; PIDN:AAA35513.1; PID:g178194
R/Chajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept
A/Reference number: S14308; MUID:91192139; PMID:1849485
A/Accession: S14309
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 95-223 <CH2>
A/Molecule type: DNA
A/Residues: 95-223 <CH2>
A/Accession: S14310
A/Molecule type: DNA
A/Residues: 95-223 <CH2>
C/Genetics:
A/Gene: GDB:ADRA2C; ADRA2L2; ADRA2RL2
A/Cross-references: GDB:120540; OMIM:104250
A/Map position: 4p16.3-qp15
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 5.6%; Score 26; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 YLALDVLFCTSSIVHLCALISLDRYW 112
DB 126 YLALDVLFCTSSIVHLCALISLDRYW 151

RESULT 11

alpha-2-adrenoceptor - cuckoo wrasse
C:Species: Labrus ocellatus (cuckoo wrasse)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
R:Accession: 150829
R:SVenson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom, N.; Ala-Uocila, S.; Scheinin, B.; J. Pharmacol. 110, 54-60, 1993
A:Title: Cloning and expression of a fish alpha-2-adrenoceptor.
A:Reference number: 150829; MUID:94035926; PMID:7693288
A:Accession: 150829
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-432 <SVR>
A:Cross-references: EMBL:U07743; NID:9467287; PIDN:AA17386.1; PID:9467288
C:Superfamily: vertebrate rhodopsin

Query Match 5.6%; Score 25; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 6.2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLFCTSSIVHLCALISLDRYW 112
DB 108 YLALDVLFCTSSIVHLCALISLDRYW 132

RESULT 12

alpha-2-adrenergic receptor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
R:Accession: A38316
R:Guyl, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., E.J.; Limbird, L.E.
A:Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2-ad
A:Reference number: A38316; MUID:91009167; PMID:2170371
A:Accession: A38316
A:Molecule type: DNA
A:Residues: 1-450 <GVY>
A:Cross-references: GB:J05652; NID:9164303; PIDN:AAA30984.1; PID:9164304
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 5.6%; Score 25; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLFCTSSIVHLCALISLDRYW 112
DB 109 YLALDVLFCTSSIVHLCALISLDRYW 133

RESULT 13

alpha-2-adrenergic receptor (clone R010) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
R:Accession: B40392
R:Janter, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A:Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic rec
A:Reference number: A40392; MUID:91244823; PMID:1645350
A:Accession: B40392

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <LAN>
A:Cross-references: GB:M62372; NID:9206615; PIDN:AAA42034.1; PID:9206616
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 5.6%; Score 25; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLFCTSSIVHLCALISLDRYW 112
DB 109 YLALDVLFCTSSIVHLCALISLDRYW 133

RESULT 14

alpha-2-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
R:Accession: JH0190
R:Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.
Mol. Cell. Biochem. 97, 161-172, 1990
A:Title: Molecular cloning, sequencing and expression of an alpha-2-adrenergic receptor
A:Reference number: JH0190; MUID:91125329; PMID:2177834
A:Accession: JH0190
A:Molecule type: mRNA
A:Residues: 1-450 <CHA>
A:Experimental source: brain
C:Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It medi
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:71-96/Domain: hydrophobic <HDI>
F:106-131/Domain: hydrophobic <HII>
F:150-175/Domain: hydrophobic <HIV>
F:193-218/Domain: hydrophobic <HDV>
F:375-400/Domain: hydrophobic <HVI>
F:405-430/Domain: hydrophobic <HVI>

Query Match 5.6%; Score 25; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 YLALDVLFCTSSIVHLCALISLDRYW 112
DB 109 YLALDVLFCTSSIVHLCALISLDRYW 133

RESULT 15

alpha-2A-adrenergic receptor - human
N:Alternate names: alpha-2C10-adrenergic receptor
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 29-Oct-1999
R:Accession: A34169; A40132; S14311
R:Fraser, C.M.; Arakawa, S.; McCombie, W.R.; Venter, J.C.
J. Biol. Chem. 264, 11754-11761, 1989
A:Title: Cloning, sequence analysis, and permanent expression of a human alpha2-adrenergic
cycloase attenuation and activation.
A:Reference number: A34169; MUID:89308571; PMID:2568356
A:Accession: A34169
A:Molecule type: DNA
A:Residues: 1-450 <FRA>
A:Cross-references: GB:M23533; NID:9178195; PIDN:AAA51665.1; PID:9178196
R:Koblika, B.K.; Matsui, H.; Koblika, T.S.; Yang-Feng, T.L.; Francke, U.; Caron, M.G.; Le
Science 238, 650-656, 1987
A:Title: Cloning, sequencing, and expression of the gene coding for the human platelet a)
A:Reference number: A40132; MUID:88042789; PMID:2823383
A:Accession: A40132
A:Molecule type: DNA
A:Residues: 1-103, 'T', 105-156, 'C', 158-367, 'L', 369-450 <KOB>

A/Cross-references: GB:M18415; NID:G178191; PID:AAA5164.1; PID:G178192
 A/Note: the authors translated the codon TGT for residue 157 as Val, and CTC for residue
 R:Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
 FEBS Lett. 280, 241-244, 1991
 A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep
 A/Reference number: S14308; MUID:91192139; PMID:1849485
 A/Accession: S14311
 A/Molecule type: DNA
 A/Residues: 77-123, 'P', 125-209 <CHH>
 C/Genetics:
 A/Gene: GDB:ADRA2A; ADRA2; ADRA2R
 A/Cross-references: GDB:120538; OMIM:104210
 A/Map position: 10q25-10q25
 A/Intons: #status absent
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 5.6%; Score 25; DB 2; Length 450;
 Best Local Similarity 100.0%; Pred. No. 6.4e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 YLALDVLFCTSSIVHLCALISLDRYW 112
 |||||
 Db 109 YLALDVLFCTSSIVHLCALISLDRYW 133
 |||||

Search completed: February 6, 2004, 18:26:08
 Job time : 17.4448 secs

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OM protein - protein search, using sw model

Run on: February 6, 2004, 18:19:31 ; Search time 9.96656 Seconds
(without alignments)
2109.148 Million cell updates/sec

Title: US-09-692-077D-8

Perfect score: 447
Sequence: 1 MDHQDPYSVQATTAIAAAT.....QDFRRARFRLICRPTQTAW 447

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 20

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	306	68.5	450	1 A2AB_HUMAN	P18089 homo sapien
2	184	41.2	391	1 A2AB_ERIEU	O19012 erinaceus e
3	109	24.4	388	1 A2AB_ORYAE	O19032 oryctolopus
4	103	23.0	394	1 A2AB_RABIT	O77830 oryctolopus
5	100	22.4	384	1 A2AB_ELEMA	O19014 elephas max
6	96	21.5	389	1 A2AB_HORSE	O77721 equus cabal
7	81	18.1	390	1 A2AB_DUGOU	O77713 dugong dugo
8	75	16.8	448	1 A2AB_CAVPO	O60475 cavia porce
9	71	15.9	455	1 A2AB_MOUSE	P30545 mus musculu
10	63	14.1	382	1 A2AB_DIDMA	O77715 didelphis m
11	63	14.1	386	1 A2AB_AMBHO	O18935 amblysomus
12	63	14.1	387	1 A2AB_MACPR	O19025 microscelid
13	63	14.1	453	1 A2AB_RAT	P19328 rattus norv
14	62	13.9	389	1 A2AB_PROHA	O19054 procavia ca
15	62	13.9	392	1 A2AB_BOVIN	O77700 bos taurus
16	62	13.9	397	1 A2AB_TAIEU	O19091 talpa europ
17	38	8.5	384	1 A2AB_ECHTE	O77722 echinops te
18	26	5.8	455	1 A2AC_CAVPO	O60476 cavia porce
19	26	5.8	458	1 A2AC_MOUSE	O01337 mus musculu
20	26	5.8	458	1 A2AC_RAT	P22086 rattus norv
21	26	5.8	462	1 A2AC_HUMAN	P18825 homo sapien
22	26	5.8	469	1 A2AC_DIDMA	P35405 didelphis m
23	25	5.6	432	1 A2AR_LABOS	Q91081 labrus oasi
24	25	5.6	436	1 A2AR_CABAU	P32251 carassius a
25	25	5.6	450	1 A2AA_CAVPO	O60474 cavia porce
26	25	5.6	450	1 A2AA_HUMAN	P08913 homo sapien
27	25	5.6	450	1 A2AA_MOUSE	O01338 mus musculu
28	25	5.6	450	1 A2AA_PIG	P18871 sus scrofa
29	25	5.6	450	1 A2AA_RAT	P22909 rattus norv
30	25	5.6	452	1 A2AA_BOVIN	Q28838 bos taurus

ALIGNMENTS

RESULT 1
A2AB_HUMAN STANDARD; PRT; 450 AA.
AC P18089; Q9BZKO;
DT 01-NOV-1990 (Rel. 16, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Subtype C2).
GN ADRA2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90311349; PubMed=2164221;
RA Lomasney J.W., Lorenz W., Allen L.F., King K., Regan J.W.,
RA Yang-Feng T.L., Caron M.G., Lefkowitz R.J.;
RT "Expansion of the alpha 2-adrenergic receptor family: Cloning and
RT characterization of a human alpha 2-adrenergic receptor subtype, the
RT gene for which is located on chromosome 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5094-5098(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042469; PubMed=2172775;
RA Weinstein R.L., Zgonibick J.M., Macchi M., Adham N., Lichtblau H.,
RA Branchek T.A., Hartig P.R.;
RT "Cloning, expression, and pharmacological characterization of a human
RT alpha 2B-adrenergic receptor.";
RL Mol. Pharmacol. 38:681-688(1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Cayla C., Schack S., Bouloumie A., Dovedjian J.C., Paris H.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT 301-GLU-GLU-303.
RX MEDLINE=21265012; PubMed=11056163;
RA Small K.M., Brown K.M., Forbes S.L., Liggett S.B.;
RT "Polymorphic deletion of three intracellular acidic residues of the
RT alpha 2B-adrenergic receptor decreases G protein-coupled receptor
RT kinase-mediated phosphorylation and desensitization.";
RL J. Biol. Chem. 276:4917-4922(2001).
RN [5]
RP SEQUENCE OF 95-389 FROM N.A.
RX MEDLINE=91054503; PubMed=2173582;
RA Chang A.C., Ho T.F., Chang N.-C.A.;
RT "In vitro amplification by polymerase chain reaction of a partial
RT gene encoding the third subtype of alpha-2 adrenergic receptor in
RT humans.";
RL Biochem. Biophys. Res. Commun. 172:817-823(1990).
RN [6]
RP FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
IS CLONIDINE > NOREPINEPHRINE > EPINEPHRINE > OXYMETAZOLINE >
DOPAMINE > P-TYRAMINE > PHENYLEPHRINE > SEROTONIN > P-SYNEPHRINE /
P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >
CHLORPROPAMAZINE > PHENTOLAMINE > MANSERINE > SPIPERONE > PRAZOSIN
> ALPRENOLOL > PROPRANOLOL > PINDOLOL.
RN [7]
RP SUBCELLULAR LOCATION: Integral membrane protein.
RN [8]
RP SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
RN [9]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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or send an email to license@isb-sib.ch).
DR EMBL; M34041; AAA51666.1; -;
DR EMBL; M36742; AAA62823.1; -;

Query Match 41.2%; Score 184; DB 1; Length 391;
 Best Local Similarity 100.0%; Pred. No. 2.1e-144;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITPLIFFTFGNALVILAVLTSRSLRAPONFLVSLAAADILVATLIIIPSLANELLGW 78
 DB 6 ITPLIFFTFGNALVILAVLTSRSLRAPONFLVSLAAADILVATLIIIPSLANELLGW 65
 QY 79 YFRRTWCEVYIALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPTKICITLTVWL 138
 DB 66 YFRRTWCEVYIALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPTKICITLTVWL 125
 QY 139 IAAVISLPEPLIYKDGQPGPRGPOCKXNDQAWYILASSISGFPAPCLIMILVYRIYLI 198
 DB 126 IAAVISLPEPLIYKDGQPGPRGPOCKXNDQAWYILASSISGFPAPCLIMILVYRIYLI 185
 QY 199 AKRS 202
 DB 186 AKRS 189

RESULT 3
 A2AB ORYAP STANDARD; PRT; 388 AA.
 AC 019032;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADRA2B.
 OS Oryctolagus ather (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Tubulidentata; Orycteropodidae; Orycteropus.
 NC NCBI_TaxID=99818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97357151; PubMed=9214502;
 RA Springer M.S., Clevon G.C., Madsen O.J., de Jong W.W., Maddell V.G.,
 RA "Endemic African mammals shake the phylogenetic tree";
 RL Nature 368:61-64(1997).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: Y12523; CA73122.2; ALT SEQ.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 KM Phosphorylation; Lipoprotein; Palmitate.
 FT NON_TER 1
 FT TRANSMEM <1 25 1 (POTENTIAL).
 FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 37 62 2 (POTENTIAL).
 FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 73 95 3 (POTENTIAL).
 FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 118 140 4 (POTENTIAL).
 FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 157 180 5 (POTENTIAL).

FT DOMAIN 181 352 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 353 376 6 (POTENTIAL).
 FT DOMAIN 377 385 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 386 >388 7 (POTENTIAL).
 FT DISULFID 72 151 BY SIMILARITY.
 FT DOMAIN 280 291 ASP/GLU-RICH (ACIDIC).
 FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
 SIMILARITY).
 FT SITE 163 163 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT NON_TER 388 388
 SQ SEQUENCE 388 AA; 42429 MW; 1810DC767B38897 CRC64;

Query Match 24.4%; Score 109; DB 1; Length 388;
 Best Local Similarity 100.0%; Pred. No. 1.7e-82;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITPLIFFTFGNALVILAVLTSRSLRAPONFLVSLAAADILVATLIIIPSLANELLGW 78
 DB 6 ITPLIFFTFGNALVILAVLTSRSLRAPONFLVSLAAADILVATLIIIPSLANELLGW 65
 QY 79 YFRRTWCEVYIALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPT 127
 DB 66 YFRRTWCEVYIALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPT 114

RESULT 4
 A2AB RABIT STANDARD; PRT; 394 AA.
 AC 077830;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADRA2B.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stanhope M.J., Madsen O.J., Maddell V.G., Clevon G.C., de Jong W.W.,
 RA Springer M.S., Madsen O.O.M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: Y16189; CA76115.1; -
 DR EMBL: Y15946; CA75899.2; -
 DR HSBP; P29274; 1MMH.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT NON_TER 1
 FT TRANSMEM <1 25 1 (POTENTIAL).
 FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 37 62 2 (POTENTIAL).

FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 73 95 3 (POTENTIAL).
 FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 118 140 4 (POTENTIAL).
 FT TRANSMEM 141 156 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 157 180 5 (POTENTIAL).
 FT TRANSMEM 181 358 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 359 382 6 (POTENTIAL).
 FT TRANSMEM 383 391 7 (POTENTIAL).
 FT TRANSMEM 392 394 7 (POTENTIAL).
 FT DISULFID 72 151 BY SIMILARITY.
 FT DOMAIN 282 297 ASP/GLU-RICH (ACIDIC).
 FT NON TER 394 394
 SQ SEQUENCE 394 AA; 42906 MM; 5D520975AC6916A CRC64;

Query Match 23.0%; Score 103; DB 1; Length 394;
 Best Local Similarity 100.0%; Pred. No. 1.5e-77;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLIFFTFGNALVILAVLTGSRAPONTFLVSLAADILVATLIPSLANELLGYW 78
 DB 6 ITFLIFFTFGNALVILAVLTGSRAPONTFLVSLAADILVATLIPSLANELLGYW 65
 QY 79 YFRRTWCEVYIALDVLFCTSSIVHCAISLDRYNAVSRALEYN 121
 DB 66 YFRRTWCEVYIALDVLFCTSSIVHCAISLDRYNAVSRALEYN 108

RESULT 5

AZAB_ELEMA STANDARD; PRT; 384 AA.
 ID AZAB_ELEMA
 AC 019014;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADR2B.
 OS Elephas maximus (Indian elephant).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
 CX NCBI_TaxID=9783;
 [1]

SEQUENCE FROM N.A.
 RA Springer M.S.; Clevon G.C.; Madsen O.J.; de Jong W.W.; Maddell V.G.;
 RA "Endemic African mammals shake the phylogenetic tree."
 RT Nature 388:61-64(1997).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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EMBL; Y12525; CA73125.1;
 DR HSPB; P29274; 1MW.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PR00037; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECP FL 2; 1.
 KM G-protein coupled receptor; Transmembrane; Multigene family;
 FT Phosphorylation; Lipoprotein; Palmitate.
 FT NON TER 1 1
 FT TRANSMEM <1 25 1 (POTENTIAL).

FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 37 62 2 (POTENTIAL).
 FT TRANSMEM 63 72 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 73 95 3 (POTENTIAL).
 FT TRANSMEM 96 117 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 118 140 4 (POTENTIAL).
 FT TRANSMEM 141 156 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 157 180 5 (POTENTIAL).
 FT TRANSMEM 181 348 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 349 372 6 (POTENTIAL).
 FT TRANSMEM 373 381 7 (POTENTIAL).
 FT TRANSMEM 382 384 7 (POTENTIAL).
 FT DISULFID 72 151 BY SIMILARITY.
 FT DOMAIN 281 285 ASP/GLU-RICH (ACIDIC).
 FT SITE 163 163 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
 FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
 FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
 FT NON TER 384 384
 SQ SEQUENCE 384 AA; 41911 MM; CF41B56C35B94F CRC64;

Query Match 22.4%; Score 100; DB 1; Length 384;
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLIFFTFGNALVILAVLTGSRAPONTFLVSLAADILVATLIPSLANELLGYW 78
 DB 6 ITFLIFFTFGNALVILAVLTGSRAPONTFLVSLAADILVATLIPSLANELLGYW 65
 QY 79 YFRRTWCEVYIALDVLFCTSSIVHCAISLDRYNAVSRALEYN 118
 DB 66 YFRRTWCEVYIALDVLFCTSSIVHCAISLDRYNAVSRALEYN 105

RESULT 6

AZAB_HORSE STANDARD; PRT; 389 AA.
 ID AZAB_HORSE
 AC 077721;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADR2B.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CX NCBI_TaxID=9796;
 [1]

SEQUENCE FROM N.A.
 RA Springer M.S.; Madsen O.J.; Maddell V.G.; Clevon G.C.; de Jong W.W.;
 RA "Highly conserved molecular support for a diverse superordinal clade
 RT of endemic African mammals."
 RT Mol. Phylogenet. Evol. 9:501-508(1998).
 CC REVISIONS.
 CC Madsen O.J.;
 RA Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.

-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL; Y15945; CAA75898.2; -.
DR HSSP; P29274; IMM.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family.
FT NON_TER 1 1
FT TRANSSEM 1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 363 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 364 387 6 (POTENTIAL).
FT DOMAIN 388 >389 EXTRACELLULAR (POTENTIAL).
FT DISULFD 72 151 BY SIMILARITY.
FT DOMAIN 281 302 POLY-GLU.
FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 163 163 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT NON_TER 389 389
FT SEQUENCE 389 AA; 42257 MW; 99217943167980FD CRC64;
Query Match 21.5%; Score 96; DB 1; Length 389;
Best Local Similarity 100.0%; Pred. No. 8.9e-72;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 19 ITPIILFTFGNALVITAVLTSRSLRAPONFLVLSLAADILVATLIPFSLANELLGYW 78
Db 6 ITPIILFTFGNALVITAVLTSRSLRAPONFLVLSLAADILVATLIPFSLANELLGYW 65
Qy 79 YFRRTWCEVYALDVLFCTSSIVHCAISLDRYNAV 114
Db 66 YFRRTWCEVYALDVLFCTSSIVHCAISLDRYNAV 101
RESULT 7
A2AB_DUGDU STANDARD; PRT; 390 AA.
ID A2AB_DUGDU
AC 077713
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoreceptor) (Fragment).
GN ADRA2B.
OS Dugong dugon (Dugong).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Sirenia; Dugongidae; Dugong.
OX NCBI_TaxID=29137;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanhope M.J., Maden O.J., Madell V.G., Cleven G.C., de Jong W.W.,
RA Springer M.S., Maden O.O.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RT FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL; Y15947; CAA75900.2; -.
DR HSSP; P29274; IMM.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family.
FT NON_TER 1 1
FT TRANSSEM 1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 354 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 355 378 6 (POTENTIAL).
FT DOMAIN 379 >390 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 281 291 ASP/GLU-RICH (ACIDIC).
FT DISULFD 72 151 BY SIMILARITY.
FT NON_TER 390 390
FT SEQUENCE 390 AA; 42562 MW; 779F849267F9F314 CRC64;
Query Match 18.1%; Score 81; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.1e-59;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 61 VATIILFSLANELLGYWYFRTWCEVYALDVLFCTSSIVHCAISLDRYNAVSRLEY 120
Db 48 VATIILFSLANELLGYWYFRTWCEVYALDVLFCTSSIVHCAISLDRYNAVSRLEY 107
Qy 121 NSKRTPRRIKIILTWLIAA 141
Db 108 NSKRTPRRIKIILTWLIAA 128
RESULT 8
A2AB_CAVPO STANDARD; PRT; 448 AA.
ID A2AB_CAVPO
AC 060475;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoreceptor).
GN ADRA2B.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Hartley;
RC MEDLINE=66152573; PubMed=8573196;
RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.,
RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
RT and alpha 2C adrenoreceptor subtypes. Radioligand binding and
RT functional coupling to a CAMP-responsive reporter gene";
RL Biochem. Pharmacol. 51:291-300 (1996).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----

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CC
DR EMBL; U25723; AAA67075.1; -
DR HSSP; P29274; IMM.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS00263; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane;
KW Phosphorylation; Hydrophobic; Palmitoylation;
Multi-pass transmembrane protein; Multi-pass transmembrane protein family;

SEQUENCE	448 AA; 49597 NM; 8364F8157E404777	CRC64;
FT	DOMAIN	1
FT	DOMAIN	12
FT	DOMAIN	38
FT	DOMAIN	39
FT	TRANSMEM	50
FT	DOMAIN	76
FT	TRANSMEM	86
FT	DOMAIN	109
FT	TRANSMEM	131
FT	DOMAIN	153
FT	TRANSMEM	168
FT	DOMAIN	192
FT	TRANSMEM	193
FT	TRANSMEM	371
FT	DOMAIN	395
FT	TRANSMEM	403
FT	DOMAIN	427
FT	DOMAIN	428
FT	DISULFID	85
FT	LIPID	440
FT	DOMAIN	294
FT	SIZE	92
FT	SIZE	175
FT	SIZE	179
FT	SIZE	179

Query Match	16.8%;	Score 75;	DB 1;	Length 448;
Best Local Similarity	100.0%;	Pred. No. 2.1e-54;		
Matches 75;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	82	RTWCEVYIALDVLTCTSSIVHLCASIDRVAASRALEYNKSKTPPRICILITWLLA	141	
DB	62	RTWCEVYIALDVLTCTSSIVHLCASIDRVAASRALEYNKSKTPPRICILITWLLA	141	
QY	142	VISLPLEPIYKDGQP	156	
DB	142	VISLPLEPIYKDGQP	156	

RESULT 9		
A2AB_MOUSE		
ID	A2AB_MOUSE	STANDARD; PRT; 455 AA.
MAC	P30545;	
DT	01-APR-1993 (Rel. 25, Created)	
DT	01-APR-1993 (Rel. 25, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
NAME	ADRB2	
DESCRIPTION	adrenorenergic receptor (Alpha-2B adrenoceptor).	

CS
Mus musculus (Mouse) .
CC
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10099;

```

RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=DBA/2; TISSUE=Liver;
RX      MEDLINE=93129625; Pubmed=1336396;

```

RA Chen W.-M., Chang A.C., Shie B.J., Chang Y.-H., Chang N.-C.A.
RT "Molecular cloning and characterization of a mouse alpha 2C2
RT adrenoreceptor subtype gene." *J*
RN Biochim. Biophys. Acta 1171:219-223 (1992).
[2]
SEQUENCE FROM N.A.
RP

CC MEDLINE=92378586; Pubmed=3354956.
 RA Chruscielnski A. J., Link R.B., Daunt D.A., Barsh G.S., Koblikka B.K.;
 RT "Cloning and expression of the mouse homolog of the human alpha 2-C2
 RT adrenergic receptor.";
 RL Biochem. Biophys. Res. Commun. 186:1280-1287(1992).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE
 CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY RECORD

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C  -----
C  EMBL, M94563, AAA73895.1, "-"
C  EMBL, L00979, AAA37131.1, ALT_INIT.
C  PIR, S28221, S28221.
C  HSSP, P29274, IMMH.
C  MGDB, MGI:87935, Adm2b.
C  GO, GO:0004938, F:alphan2-adennergic receptor activity, IDA.
C  GO, GO:0001555, P:angiogenesis, IMP.
C  GO, GO:0000185, P:MAPKKK cascade, IMP.
C  InterPro, IPR000276, GPCR Rhodopsn.

```

PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.
PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
G-protein coupled receptor; Transmembrane
phosphorylation; Lipoprotein; Palmitate.
DOMAIN 1 17
EXTRACELLULAR (POTENTIAL).

1	TRANSMEM	18	42	1 (POTENTIAL).
2	DOMAIN	43	54	CYTOPLASMIC (POTENTIAL).
3	TRANSMEM	55	50	2 (POTENTIAL).
4	DOMAIN	81	90	EXTRACELLULAR (POTENTIAL).
5	TRANSMEM	91	113	3 (POTENTIAL).
6	DOMAIN	114	135	4 (POTENTIAL).
7	TRANSMEM	136	158	CYTOPLASMIC (POTENTIAL).
8	DOMAIN	159	174	EXTRACELLULAR (POTENTIAL).
9	TRANSMEM	175	198	5 (POTENTIAL).
10	DOMAIN	199	377	CYTOPLASMIC (POTENTIAL).
11	TRANSMEM	378	401	6 (POTENTIAL).
12	DOMAIN	402	430	EXTRACELLULAR (POTENTIAL).
13	TRANSMEM	411	414	7 (POTENTIAL).

T	DOPAMIN	435	455	/ POTENTIAL).
T	LIPID	90	169	CYTOPLASMIC (POTENTIAL).
T	DOPAMIN	447	447	BY SIMILARITY.
T	SITE	306	316	PALMITATE (POTENTIAL).
T	SITE	97	97	ASP/GLU-RICH (ACIDIC).
T	SITE	181	181	IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
T	SITE	185	185	IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
T	CONFLICT	229	202	IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
T	SEQUENCE	455 AA;	50615 MM;	V -> L (IN REF. 1).
T				MISSENGER (IN REF. 2).
T				A3954AD76B0E6263 C6C64:

Query Match	15.9%	Score 71;	DB 1;	Length 455;
Best Local Similarity	100.0%;	Pred. No. 4,3e-51;		
Matches 71;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0
84	MCEVYALDVLCSTSIYHLCAISLDIKMAVSRALAEYNSKRTPRRIKCIITLVMLIAAVI	143		

Db 89 WCEVTLADVLFCTSSIVHLCAISLDKRWAVSALEVNSKRTPRKICILTWMLIAVI 148
Qy 144 SLPLIYKGDQ 154
Db 149 SLPLIYKGDQ 159

RESULT 10
A2AB_DIDMA STANDARD: PRT; 382 AA.
ID A2AB_DIDMA
AC 077715;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
NCBI_TaxID=9267;
RX MEDLINE=9667998;
RA Stanhope M.J., Madsen O.J., Waddell V.G., de Jong W.W.,
RA Springer M.S.;
RT "Highly congruent molecular support for a diverse superordinal clade
of endemic African mammals.";
RL Mol. Phylogenet. Evol. 9:501-508(1998).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL: Y15943; CAA75896.1; -.
DR HSSP; P29274; IMM.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein.
FT NON_TER 1
FT TRANSSEM <1 25
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 346 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 347 370 6 (POTENTIAL).
FT DOMAIN 371 379 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 380 >382 7 (POTENTIAL).
FT DISULFID 72 151 BY SIMILARITY.
FT DOMAIN 271 283 ASP/GLU-RICH (ACIDIC).
FT NON_TER 382 382
SQ SEQUENCE 382 AA; 41870 MW; EAFPI2DDP44B2A19 CRC64;

Query Match 14.1%; Score 63; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ITFLIFLIFGNALVILAVLTSRLAPQNLFLVSLAADILVATLLIFPSLANELLGYW 78
Db 6 ITFLIFLIFGNALVILAVLTSRLAPQNLFLVSLAADILVATLLIFPSLANELLGYW 65

Qy 79 YFR 81
Db 66 YFR 68

RESULT 11
A2AB_AMEHO STANDARD: PRT; 386 AA.
ID A2AB_AMEHO
AC 018935;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Amblyomus hottentotus (Hottentot golden mole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Chrysochloridae; Amblyomus.
NCBI_TaxID=5391;
RX MEDLINE=9214502;
RA Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
RA Amrine H.W., Stanhope M.J.;
RT "Endemic African mammals shake the phylogenetic tree.";
RL Nature 388:61-64(1997).
RN [2]
RP REVISION TO 121.
RA Madsen O.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL: Y12526; CAA73126.2; -.
DR HSSP; P29274; IMM.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Multigene family;
Phosphorylation; Lipoprotein; Palmitate.
FT NON_TER 1
FT TRANSSEM <1 25
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 350 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 351 374 6 (POTENTIAL).
FT DOMAIN 375 383 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 384 >386 7 (POTENTIAL).
FT DOMAIN 280 289 ASP/GLU-RICH (ACIDIC).
FT DISULFID 72 151 BY SIMILARITY.

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FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
FT SITE 163 163 SIMILARITY)
FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 167 167 (BY SIMILARITY)
FT NON TER 386 386 IMPLICATED IN CATECHOL AGONIST BINDING
SQ SEQUENCE 386 AA; 42157 MM; ECE11E0B7192D95E CRC64;

Query Match 14.1%; Score 63; DB 1; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFTLFTIFGNALVILAVLTSRSIRAPONLFLVSLAADIIVATLIPPSLANELLGYW 78
DB 6 ITFTLFTIFGNALVILAVLTSRSIRAPONLFLVSLAADIIVATLIPPSLANELLGYW 65

QY 79 YFR 81
DB 66 YFR 68

RESULT 12
A2AB MACPR STANDARD; PRT; 387 AA.
AC 019025;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Macrosclerides proboscideus (Short-eared elephant shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Macroscelidea; Macroscelididae; Macroscelides.
NX NCBI_TaxID=29082;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97357151; PubMed=9214502;
RA Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
RT "Endemic African mammals shake the phylogenetic tree.";
RN Nature 388:61-64 (1997).
RN [2]
RP REVISIONS TO 148 AND 255
RA Springer M.S., Cleven G.C., Madsen O., de Jong W.W., Waddell V.G.,
RX Amrine H.W., Stanhope M.J.;
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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or send an email to license@1ab-sib.ch).
CC -----
CC EMBL: Y12524; CA73124.2; -.
CC DR HSRP; P29274; IMM.
CC DR InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR000237; GPCR_Rhodopsn.
CC PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
CC PROSITE: PS50262; G-PROTEIN RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.
FT NON TER 1 1
FT TRANSMEM <1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 37 62
FT DOMAIN 63 72 2 (POTENTIAL).
FT TRANSMEM 73 95 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 96 117 3 (POTENTIAL).
FT TRANSMEM 118 140 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 141 140 4 (POTENTIAL).
FT TRANSMEM 141 156 4 (POTENTIAL).
FT TRANSMEM 157 180 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 181 351 5 (POTENTIAL).
FT TRANSMEM 352 375 6 (POTENTIAL).
FT TRANSMEM 376 384 6 (POTENTIAL).
FT TRANSMEM 385 >387 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 280 288 7 (POTENTIAL).
FT DISULFD 72 151 ASP/GLU-RICH (ACIDIC).
FT SITE 79 79 BY SIMILARITY.
FT SITE 163 163 IMPLICATED IN LIGAND BINDING (BY
FT SITE 167 167 SIMILARITY).
FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
FT NON TER 387 387 (BY SIMILARITY).
SQ SEQUENCE 387 AA; 42587 MM; B74AD5F0E23BD5A CRC64;

Query Match 14.1%; Score 63; DB 1; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFTLFTIFGNALVILAVLTSRSIRAPONLFLVSLAADIIVATLIPPSLANELLGYW 78
DB 6 ITFTLFTIFGNALVILAVLTSRSIRAPONLFLVSLAADIIVATLIPPSLANELLGYW 65

QY 79 YFR 81
DB 66 YFR 68

RESULT 13
A2AB RAT STANDARD; PRT; 453 AA.
AC P19328; O63021;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
GN ADRA2B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RC MEDLINE=9022217; PubMed=2158103;
RA Zeng D., Harrison J.K., D'Angelo D.D., Barber C.M., Tucker A.L.,
RT "Molecular characterization of a rat alpha 2B-adrenergic receptor.";
RN Proc. Natl. Acad. Sci. U.S.A. 87:3102-3106 (1990).
RN [2]
RP SEQUENCE OF 6-453 FROM N.A.
RX STRAIN=Sabra; TISSUE=Kidney;
RC MEDLINE=95275492; PubMed=7755946;
RA le Joesec M., Cloix J.F., Pecquery R., Giudicelli Y., Dauvise J.P.;
RT "Different sodium regulation between salt-sensitive and salt-
resistant Sabra rats is not due to any mutation in the renal alpha
2B-adrenoceptor gene.";
RN Am. J. Hypertens. 8:177-182 (1995).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Search completed: February 6, 2004, 18:24:04
Job time : 9.96656 secs

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DE Alpha-2B adrenergic receptor (Alpha-2B adrenoreceptor) (Fragment).
GN ADRAB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98334573; PubMed=9667998;
RA Stanhope M.J., Madsen O.J., Maddell V.G., Cleven G.C., de Jong W.W.,
RA Springer M.S.;
RT "Highly congruent molecular support for a diverse superordinal clade
RT of endemic African mammals.";
RL Mol. Phylogenet. Evol. 9:501-508 (1998).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, Y15944; CAA75897.2; -.
DR HSP; P29274; IMM.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family.
FT NON_TER 1
FT TRANSMEM <1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 356 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 357 380 6 (POTENTIAL).
FT DOMAIN 381 >392 EXTRACELLULAR (POTENTIAL).
FT DISULFD 72 151 BY SIMILARITY.
FT DOMAIN 283 292 POLY-GLU.
FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
FT SIMILARITY).
FT SITE 163 163 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 167 167 (BY SIMILARITY).
FT IMPLICATED IN CATECHOL AGONIST BINDING
FT IMPLICATED IN CATECHOL AGONIST BINDING
SQ SEQUENCE 392 AA; 42839 MW; 471596A7446475E0 CRC64;
Query Match 13.9%; Score 62; DB 1; Length 392;
Best Local Similarity 100.0%; Pred. No. 1e-43;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 19 ITFLFTIFGNALVTLAVLRSRAPONFLVSLAADIIVATLIIIPSLANELIGYW 78
DB 6 ITFLFTIFGNALVTLAVLRSRAPONFLVSLAADIIVATLIIIPSLANELIGYW 65
OY 79 YF 80
DB 66 YF 67
```

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OM protein - protein search, using sw model

Run on: February 6, 2004, 18:20:16 ; Search time 32.8896 Seconds
(without alignments)
3507.169 Million cell updates/sec

Title: US-09-692-077D-8
Perfect score: 447
Sequence: 1 MDHQDEYSVQATAIAAAIT.....QDFRAFRRLICRPMGTAW 447

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 20

Total number of hits satisfying chosen parameters: 100

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_bacteria:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	43.0	389	6	Q9GKZ5
2	190	42.5	451	6	Q8HYX8
3	184	41.2	387	6	Q9GL17
4	184	41.2	389	6	Q8S095
5	184	41.2	391	6	Q8MIES
6	184	41.2	399	6	Q8MID0
7	171	38.3	388	6	Q9GL18
8	159	35.6	401	6	Q8MK45
9	145	32.4	392	11	Q8KIU3
10	145	32.4	392	11	Q8KAY3
11	142	31.8	391	11	Q8KJ37
12	140	31.3	383	6	Q9GL20
13	140	31.3	389	6	Q9GL07
14	140	31.3	389	11	Q8KIW8
15	140	31.3	389	11	Q8CG78
16	140	31.3	391	11	Q8KIR1

17	140	31.3	395	11	Q8KIU9	Q8kiu9 erehizon d
18	140	31.3	406	11	Q8KIN6	Q8kin6 thomomys ta
19	139	31.1	395	6	Q9SN91	Q9sn91 tonatus bid
20	139	31.1	395	11	Q8KIU7	Q8kiu7 myoxus glis
21	137	30.6	395	6	Q9GL12	Q9gl12 manis sp..a
22	136	30.4	399	6	Q8MK51	Q8mk51 lama guanac
23	135	30.2	383	6	Q8MK50	Q8mk50 roussetus a
24	130	29.1	383	6	Q9SN93	Q9sn93 pteropus ra
25	130	29.1	389	6	Q9SN94	Q9sn94 hispidodero
26	130	29.1	390	6	Q9SN95	Q9sn95 tapozosus s
27	130	29.1	392	6	Q9SN95	Q9sn95 megaderma l
28	130	29.1	393	11	Q8KIP2	Q8kip2 trichys fas
29	127	28.4	383	11	Q8KIW3	Q8kiw3 dipus sagit
30	127	28.4	397	11	Q8KIW6	Q8kiw6 castor cana
31	125	28.0	393	6	Q8MIR1	Q8mir1 lama guanac
32	122	27.3	365	6	Q8SQ08	Q8sq08 rhinopoma h
33	122	27.3	391	6	Q9GL06	Q9gl06 sus scrota
34	116	26.0	391	6	Q8SQ00	Q8sq00 emballonura
35	115	25.7	393	6	Q8MK55	Q8mk55 cyclopes di
36	113	25.3	389	6	Q8S089	Q8s089 rhinolophus
37	112	25.1	398	6	Q8MK49	Q8mk49 sorex ciner
38	110	24.6	401	11	Q8KIV7	Q8kiv7 dipodomys m
39	106	23.7	385	6	Q8HXU9	Q8hxu9 choicopus d
40	103	23.0	399	6	Q8MIE3	Q8mie3 lepus craws
41	103	23.0	403	6	Q8MHV6	Q8mhv6 ochotona pr
42	101	22.6	393	11	Q8KIV5	Q8kiv5 dryomys nit
43	99	22.1	398	6	Q8SQ02	Q8sq02 natalus str
44	85	19.0	393	6	Q9GL15	Q9gl15 macrotus ca
45	85	19.0	394	6	Q8SQ01	Q8sq01 desmodus ro

ALIGNMENTS

RESULT 1
ID Q9GKZ5 PRELIMINARY; PRT; 389 AA.
AC Q9GKZ5;
DT 01-MAR-2001 (TREMBLER1, 16, Created)
DT 01-MAR-2001 (TREMBLER1, 16, Last sequence update)
DT 01-OCT-2002 (TREMBLER1, 22, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Tupaiia tana (Large tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=70687;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082081; PubMed=11214318;
RA Maassen O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer M.,
RT "Parallel adaptive radiations in two major clades of placental
mammals".
RT Nature 409:610-614(2001).
RL -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC EMBL: AJ251187; CAC16698.1; -
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN RECEPTOR_F2_1; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 389
SQ SEQUENCE 389 AA; 42631 MW; A9DC6F864487A2B5 CRC64;
Query Match 43.0%; Score 192; DB 6; Length 389;
Best Local Similarity 100.0%; Pred. No. 3.7e-178;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19 ITPLIFLFTFGNALVILAVLTSRLAPQNLFLVSLAAADILVATLIPPSLNEELGYN 78

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Db 6 ITFLILFTFGNALVILAVLTSLRAPQNLFLVSLAADIIVATLIIIPSLANELLGW 65
Qy 79 YFRRTWCENVIALDVLFCTSSIVHLCALISLDRYAVASRALEYNSKRTPRRIKCIITLWVL 138
Db 66 YFRRTWCENVIALDVLFCTSSIVHLCALISLDRYAVASRALEYNSKRTPRRIKCIITLWVL 125
Qy 139 IAAVTSIPPLIYKDGQOPGRPOCKLNOEAWYILASSIGSFAPCLIMILVLRITLYI 198
Db 126 IAAVTSIPPLIYKDGQOPGRPOCKLNOEAWYILASSIGSFAPCLIMILVLRITLYI 185
Qy 199 AKRSNRGRPRAK 210
Db 186 AKRSNRGRPRAK 197

RESULT 2
Q8HY8 PRELIMINARY; PRT; 451 AA.
AC O8HY8;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Alpha-2B adrenoceptor.
OS Tupaiia belangeri (Northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
CX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RA Heilbronner U., Van Kampen M., Isovich E., Fluegge G.;
RT "Thalamic alpha-2B adrenoceptors under chronic stress: persistent
RT upregulation in the paraventricular nucleus.";
RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY150333; AAN7436.1; -
SQ SEQUENCE 451 AA; 50356 MW; 3172403011F3BC60 CRC64;

Query Match 42.5%; Score 190; DB 6; Length 451;
Best Local Similarity 100.0%; Pred. No. 3.8e-176;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ITFLILFTFGNALVILAVLTSLRAPQNLFLVSLAADIIVATLIIIPSLANELLGW 78
Db 19 ITFLILFTFGNALVILAVLTSLRAPQNLFLVSLAADIIVATLIIIPSLANELLGW 78
Qy 79 YFRRTWCENVIALDVLFCTSSIVHLCALISLDRYAVASRALEYNSKRTPRRIKCIITLWVL 138
Db 79 YFRRTWCENVIALDVLFCTSSIVHLCALISLDRYAVASRALEYNSKRTPRRIKCIITLWVL 138
Qy 139 IAAVTSIPPLIYKDGQOPGRPOCKLNOEAWYILASSIGSFAPCLIMILVLRITLYI 198
Db 139 IAAVTSIPPLIYKDGQOPGRPOCKLNOEAWYILASSIGSFAPCLIMILVLRITLYI 198
Qy 199 AKRSNRGRPR 208
Db 199 AKRSNRGRPR 208
Qy 199 AKRSNRGRPR 208
Db 199 AKRSNRGRPR 208

RESULT 3
Q9GL17 PRELIMINARY; PRT; 387 AA.
AC Q9GL17;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
CX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=21082081; PubMed=11214318;
RA Madsen O., Scally M., Douady C., Kao D., DeBry R., Adkins R.,
RA Armitage H., Stanhope M., de Jong W., Springer M.;
RT "Parallel adaptive radiations in two major clades of placental
RT mammals.";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ251174; CAC16689.1; -
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 387
SQ SEQUENCE 387 AA; 42546 MW; 2C1CD5D4B43F8D9B CRC64;

Query Match 41.2%; Score 184; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.3e-170;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ITFLILFTFGNALVILAVLTSLRAPQNLFLVSLAADIIVATLIIIPSLANELLGW 78
Db 6 ITFLILFTFGNALVILAVLTSLRAPQNLFLVSLAADIIVATLIIIPSLANELLGW 65
Qy 79 YFRRTWCENVIALDVLFCTSSIVHLCALISLDRYAVASRALEYNSKRTPRRIKCIITLWVL 138
Db 79 YFRRTWCENVIALDVLFCTSSIVHLCALISLDRYAVASRALEYNSKRTPRRIKCIITLWVL 125
Qy 139 IAAVTSIPPLIYKDGQOPGRPOCKLNOEAWYILASSIGSFAPCLIMILVLRITLYI 198
Db 126 IAAVTSIPPLIYKDGQOPGRPOCKLNOEAWYILASSIGSFAPCLIMILVLRITLYI 185
Qy 199 AKRS 202
Db 186 AKRS 189

RESULT 4
Q8SQ95 PRELIMINARY; PRT; 389 AA.
AC Q8SQ95;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN ADRA2B.
OS Nyctimene albigenter (common tube-nosed fruit bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
OC Pteropodidae; Nyctimene.
CX NCBI_TaxID=48988;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21819367; PubMed=11805285;
RX Teeling E.C., Madsen O., Van Den Bussche R.A., de Jong W.W.,
RA Stanhope M.J., Springer M.S.;
RT "Microbat paraphyly and the convergent evolution of a key innovation
RT in Old world rhinolophid microbats.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:1431-1436(2002).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ419805; CAD11972.1; -
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 389
SQ SEQUENCE 389 AA; 42907 MW; C203401584C560EE CRC64;
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Query Match 41.2%; Score 184; DB 6; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.3e-170;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFTLFTTGNALVLAVALTSRLAPQNFVLSLAADLVATLTIIPSLANELLGYW 78
DB 6 ITFTLFTTGNALVLAVALTSRLAPQNFVLSLAADLVATLTIIPSLANELLGYW 65
QY 79 YFRTWCEVYALADVLCFTSSIVHLCASIDRYAVSRALRYNSKRTPRRIKCIITVWL 138
DB 66 YFRTWCEVYALADVLCFTSSIVHLCASIDRYAVSRALRYNSKRTPRRIKCIITVWL 125
QY 139 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYILASSIGSFAPCLIMILVYLRITLYI 198
DB 126 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYILASSIGSFAPCLIMILVYLRITLYI 185
QY 199 AKRS 202
DB 186 AKRS 189

RESULT 5

Q8MTES ID Q8MTES PRELIMINARY; PRT; 391 AA.
AC Q8MTES;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
RT "Molecular evolution of the alpha 2B adrenergic receptor."
RL Submitted (AUG-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ505819; CAD4330.1; -
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 391 391
SQ SEQUENCE 391 AA; 43133 MW; EB55AAD36B8A9769 CRC64;

Query Match 41.2%; Score 184; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 2.3e-170;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFTLFTTGNALVLAVALTSRLAPQNFVLSLAADLVATLTIIPSLANELLGYW 78
DB 6 ITFTLFTTGNALVLAVALTSRLAPQNFVLSLAADLVATLTIIPSLANELLGYW 65
QY 79 YFRTWCEVYALADVLCFTSSIVHLCASIDRYAVSRALRYNSKRTPRRIKCIITVWL 138
DB 66 YFRTWCEVYALADVLCFTSSIVHLCASIDRYAVSRALRYNSKRTPRRIKCIITVWL 125
QY 139 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYILASSIGSFAPCLIMILVYLRITLYI 198
DB 126 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYILASSIGSFAPCLIMILVYLRITLYI 185
QY 199 AKRS 202
DB 186 AKRS 189

RESULT 6

Q8MID0 ID Q8MID0 PRELIMINARY; PRT; 399 AA.

AC Q8MID0;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
RT "Molecular evolution of the alpha 2B adrenergic receptor."
RL Submitted (AUG-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ505820; CAD4321.1; -
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 399 399
SQ SEQUENCE 399 AA; 43888 MW; 910ECAPB10659EDD CRC64;

Query Match 41.2%; Score 184; DB 6; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.4e-170;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFTLFTTGNALVLAVALTSRLAPQNFVLSLAADLVATLTIIPSLANELLGYW 78
DB 6 ITFTLFTTGNALVLAVALTSRLAPQNFVLSLAADLVATLTIIPSLANELLGYW 65
QY 79 YFRTWCEVYALADVLCFTSSIVHLCASIDRYAVSRALRYNSKRTPRRIKCIITVWL 138
DB 66 YFRTWCEVYALADVLCFTSSIVHLCASIDRYAVSRALRYNSKRTPRRIKCIITVWL 125
QY 139 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYILASSIGSFAPCLIMILVYLRITLYI 198
DB 126 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYILASSIGSFAPCLIMILVYLRITLYI 185
QY 199 AKRS 202
DB 186 AKRS 189

RESULT 7

Q9GL18 ID Q9GL18 PRELIMINARY; PRT; 388 AA.
AC Q9GL18;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
RT "Molecular evolution of the alpha 2B adrenergic receptor."
RL Submitted (AUG-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ505819; CAD4330.1; -
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 388 388
SQ SEQUENCE 388 AA; 43133 MW; EB55AAD36B8A9769 CRC64;

Query Match 41.2%; Score 184; DB 6; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.3e-170;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFTLFTTGNALVLAVALTSRLAPQNFVLSLAADLVATLTIIPSLANELLGYW 78
DB 6 ITFTLFTTGNALVLAVALTSRLAPQNFVLSLAADLVATLTIIPSLANELLGYW 65
QY 79 YFRTWCEVYALADVLCFTSSIVHLCASIDRYAVSRALRYNSKRTPRRIKCIITVWL 138
DB 66 YFRTWCEVYALADVLCFTSSIVHLCASIDRYAVSRALRYNSKRTPRRIKCIITVWL 125
QY 139 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYILASSIGSFAPCLIMILVYLRITLYI 198
DB 126 IAAVISLPLIYKDGQPGPRGPOCKLNOEAWYILASSIGSFAPCLIMILVYLRITLYI 185
QY 199 AKRS 202
DB 186 AKRS 189

DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR000237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1 1
FT NON_TER 388 388
SQ SEQUENCE 388 AA; 42546 MW; 14EB08C6FB4C371 CRC64;

Query Match 38.3%; Score 171; DB 6; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-157;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 LVTLAVLTSRSLRAPONLFLVSLAADIIVATLIIPESLANELLGYWFRRTWCVYIAL 91
DB 19 LVTLAVLTSRSLRAPONLFLVSLAADIIVATLIIPESLANELLGYWFRRTWCVYIAL 78
QY 92 DVLFTSSIVHLCAISLDRYMAVSRALEYNSKRTPRRIKCIITLFWMLAAVSLPPLIYK 151
DB 79 DVLFTSSIVHLCAISLDRYMAVSRALEYNSKRTPRRIKCIITLFWMLAAVSLPPLIYK 138
QY 152 GQGGQPRRPOCKLNOEAMYLASSISGFAPCLIMILVIRIYLAKS 202
DB 139 GQGGQPRRPOCKLNOEAMYLASSISGFAPCLIMILVIRIYLAKS 189

RESULT 8

QY 08MK45 PRELIMINARY; PRT; 401 AA.
AC 08MK45;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
RT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN ADRA2B.
OS Tapirus terrestris (lowland tapir) (Brazilian tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608557; PubMed=11743200;
RA Murphy W.J., Elzirik E., O'Brien S.J., Madsen O., Scally M.,
RA Donady C.J., Teeling E., Ryder O.A., Stanhope M.J., de Jong W.W.,
RA Springer M.S.;
RT "Resolution of the early placental mammal radiation using Bayesian
phylogenetics";
RL Science 294:2348-2351(2001).
DR EMBL; AJ315939; CAC87003.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 401 401
SQ SEQUENCE 401 AA; 43835 MW; 8D01F4C2548E9EB6 CRC64;

Query Match 35.6%; Score 159; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.3e-146;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLILFTFGNALVILAVLTSRSLRAPONLFLVSLAADIIVATLIIPESLANELLGYW 78
DB 6 ITFLILFTFGNALVILAVLTSRSLRAPONLFLVSLAADIIVATLIIPESLANELLGYW 65
QY 79 YFRRTWCVYIALDVLFTSSIVHLCAISLDRYMAVSRALEYNSKRTPRRIKCIITLWML 138
DB 66 YFRRTWCVYIALDVLFTSSIVHLCAISLDRYMAVSRALEYNSKRTPRRIKCIITLWML 125
QY 139 IAAVISLPLIYKDGQPRGRPOCKLNOEAMYLASSIS 177

DB 126 IAAVISLPLIYKDGQPRGRPOCKLNOEAMYLASSIS 164

RESULT 9

QY 08KIU3 PRELIMINARY; PRT; 392 AA.
AC 08KIU3;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
RT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN A2AB.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., Stanhope M.,
RA Catzeflis F., de Jong W.W., Douzery E.J.P.;
RT "Rodent phylogeny and a timescale for the evolution of Glires:
evidence from an extensive taxon sampling using three nuclear genes";
RL Mol. Biol. Evol. 0:0-(2002).
DR EMBL; AJ427255; CAD20293.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 392 392
SQ SEQUENCE 392 AA; 42811 MW; 3F75BC3DA390587 CRC64;

Query Match 32.4%; Score 145; DB 11; Length 392;
Best Local Similarity 100.0%; Pred. No. 2.2e-132;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AIAAIFLILFTFGNALVILAVLTSRSLRAPONLFLVSLAADIIVATLIIPESLANE 73
DB 1 AIAAIFLILFTFGNALVILAVLTSRSLRAPONLFLVSLAADIIVATLIIPESLANE 60
QY 74 LGGYWRRTWCVYIALDVLFTSSIVHLCAISLDRYMAVSRALEYNSKRTPRRIKCIIT 133
DB 61 LGGYWRRTWCVYIALDVLFTSSIVHLCAISLDRYMAVSRALEYNSKRTPRRIKCIIT 120
QY 134 LTVWMLAAVISLPLIYKDGQPRP 158
DB 121 LTVWMLAAVISLPLIYKDGQPRP 145

RESULT 10
QY 08K4Y3 PRELIMINARY; PRT; 392 AA.
AC 08K4Y3;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
RT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN ADRA2B.
OS Sciurus vulgaris (Red squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sciurus.
OX NCBI_TaxID=55149;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608557; PubMed=11743200;
RA Murphy W.J., Elzirik E., O'Brien S.J., Madsen O., Scally M.,
RA Donady C.J., Teeling E., Ryder O.A., Stanhope M.J., de Jong W.W.,
RA Springer M.S.;

RT "Resolution of the early placental mammal radiation using Bayesian
phylogenetics.";
RL Science 294:2348-2351(2001).
DR EMBL; AJ315942; CAC97006.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 392 392
SQ SEQUENCE 392 AA; 42773 MW; 24894FD9B2E84D6 CRC64;
Query Match 32.4%; Score 145; DB 11; Length 392;
Best Local Similarity 100.0%; Pred. No. 2.2e-132;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 AIAAATFTLFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANE 73
DB 1 AIAAATFTLFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANE 60
QY 74 LLGWYRRRTWCEVYALDVLTCTSSIVHCAISLDRYWAVSRALVNSKRTPRRIKCI 133
DB 61 LLGWYRRRTWCEVYALDVLTCTSSIVHCAISLDRYWAVSRALVNSKRTPRRIKCI 120
QY 134 LTWVLAIVISLPPIYKGDGQPOP 158
DB 121 LTWVLAIVISLPPIYKGDGQPOP 145
RESULT 11
Q8K3R7 PRELIMINARY; PRT; 391 AA.
AC Q8K3R7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN A2AB.
OS Apodonta rufa (Mountain beaver).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Apodontidae; Apodontia.
OX NCBI_TaxID=51342;
RN [1]
RP SEQUENCE FROM N.A.
RA Huchon D., Maden O., Sibald M.J.B., Ament K., Stanhope M.,
RA Catzeffis F., de Jong W.W., Douzery E.J.P.;
RT "Rodent phylogeny and a timescale for the evolution of Glires:
RT evidence from an extensive taxon sampling using three nuclear genes";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL; AJ427256; CAD20294.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 391 391
SQ SEQUENCE 391 AA; 42710 MW; B6244DDF3936D8B2 CRC64;
Query Match 31.8%; Score 142; DB 11; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.9e-129;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 AATFTLFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANE 76
DB 1 AATFTLFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANE 60
QY 77 YWYRRRTWCEVYALDVLTCTSSIVHCAISLDRYWAVSRALVNSKRTPRRIKCI 136
DB 61 YWYRRRTWCEVYALDVLTCTSSIVHCAISLDRYWAVSRALVNSKRTPRRIKCI 120

QY 137 WLIAVVISLPPIYKGDGQPOP 158
DB 121 WLIAVVISLPPIYKGDGQPOP 142
RESULT 12
Q9GL20 PRELIMINARY; PRT; 383 AA.
AC Q9GL20;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Cynopercus sphinx (Indian short-nosed fruit bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
OC Pteropodidae; Cynopterus.
OX NCBI_TaxID=9400;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21082081; PubMed=11214318;
RA Maden O., Scally M., Douady C., Kao D., DeBry R., Adkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer M.;
RT "Parallel adaptive radiations in two major clades of placental
RT mammals";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ251181; CAC16684.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KM G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1 1
FT NON_TER 383 383
SQ SEQUENCE 383 AA; 41945 MW; C135809087196294 CRC64;
Query Match 31.3%; Score 140; DB 6; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.6e-127;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 ITFTLFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANE 78
DB 6 ITFTLFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADIIVATLIIIPSLANE 65
QY 79 YPRRTWCEVYALDVLTCTSSIVHCAISLDRYWAVSRALVNSKRTPRRIKCI 138
DB 66 YPRRTWCEVYALDVLTCTSSIVHCAISLDRYWAVSRALVNSKRTPRRIKCI 125
QY 139 IAAVISLPPIYKGDGQPOP 158
DB 126 IAAVISLPPIYKGDGQPOP 145
RESULT 13
Q9GL07 PRELIMINARY; PRT; 389 AA.
AC Q9GL07;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21082081; PubMed=11214318;
RA Maden O., Scally M., Donady C., Kao D., DeBry R., Atkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer W.,
RT "Parallel adaptive radiations in two major clades of placental
RT mammals";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ251176; CAC16696.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS50262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1 1
FT NON_TER 389 389
SQ SEQUENCE 389 AA; 42278 MW; E42F177873FE47FF CRC64;

Query Match 31.3%; Score 140; DB 6; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.6e-127;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLILFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIIVATLIIPSLANELGYW 78
DB 6 ITFLILFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIIVATLIIPSLANELGYW 65
QY 79 YFRRTWCCEVYLAADVLCFTSSIVHLCAISIDRYWAVSRALFVNSKRTPRRIKCIITLTVWL 138
DB 66 YFRRTWCCEVYLAADVLCFTSSIVHLCAISIDRYWAVSRALFVNSKRTPRRIKCIITLTVWL 125
QY 139 IAAVISLPLIYKDGQGP 158
DB 126 IAAVISLPLIYKDGQGP 145

RESULT 14
O8KIW8 PRELIMINARY; PRT; 389 AA.
AC O8KIW8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN A2AB.
OS Batyergus nullus (Cape dune mole-rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Batyergidae;
OC Batyergus.
OX NCBI_TaxID=10172;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=#5234';
RA Huchon D., Maden O., Sibbald M.J.J.B., Ament K., Stanhope M.,
RA Catzeffis F., de Jong W.W., Douzery E.J.P.;
RT "Rodent phylogeny and a timescale for the evolution of Glires:
RT evidence from an extensive taxon sampling using three nuclear genes";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL; AJ427257; CAD20290.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS50262; G PROTEIN RECEPTOR FL 2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 389 389
SQ SEQUENCE 389 AA; 42278 MW; F731C298F5FD81BC CRC64;

Query Match 31.3%; Score 140; DB 11; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.6e-127;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLILFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIIVATLIIPSLANELGYW 78
DB 6 ITFLILFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIIVATLIIPSLANELGYW 65
QY 79 YFRRTWCCEVYLAADVLCFTSSIVHLCAISIDRYWAVSRALFVNSKRTPRRIKCIITLTVWL 138
DB 66 YFRRTWCCEVYLAADVLCFTSSIVHLCAISIDRYWAVSRALFVNSKRTPRRIKCIITLTVWL 125
QY 139 IAAVISLPLIYKDGQGP 158
DB 126 IAAVISLPLIYKDGQGP 145

RESULT 15
O8CG78 PRELIMINARY; PRT; 389 AA.
AC O8CG78;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha 2B adrenergic receptor (Fragment).
GN A2AB.
OS Chinchilla lanigera.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Chinchillidae;
OC Chinchilla.
OX NCBI_TaxID=34839;
RN (1)
RP SEQUENCE FROM N.A.
RA Huchon D., Maden O., Sibbald M.J.J.B., Ament K., Stanhope M.,
RA Catzeffis F., de Jong W.W., Douzery E.J.P.;
RT "Rodent phylogeny and a timescale for the evolution of Glires:
RT evidence from an extensive taxon sampling using three nuclear genes";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL; AJ427271; CAD20309.1; -;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 389 389
SQ SEQUENCE 389 AA; 42657 MW; 826BA4A7FAF7E901 CRC64;

Query Match 31.3%; Score 140; DB 11; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.6e-127;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ITFLILFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIIVATLIIPSLANELGYW 78
DB 6 ITFLILFTFGNALVTLAVTSRSLRAPQNLFLVSLAADIIVATLIIPSLANELGYW 65
QY 79 YFRRTWCCEVYLAADVLCFTSSIVHLCAISIDRYWAVSRALFVNSKRTPRRIKCIITLTVWL 138
DB 66 YFRRTWCCEVYLAADVLCFTSSIVHLCAISIDRYWAVSRALFVNSKRTPRRIKCIITLTVWL 125
QY 139 IAAVISLPLIYKDGQGP 158
DB 126 IAAVISLPLIYKDGQGP 145

Search completed: February 6, 2004, 18:25:23
Job time : 33.8896 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:50:45 ; Search time 37.8729 Seconds
(without alignments)
1873.391 Million cell updates/sec

Title: US-09-692-077d-8
Perfect score: 2363
Sequence: 1 MDHQDPYSVQATTAIAAAT.....QDFRAFRILCRPTQTAW 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_GeneSeq_19Jun03:*

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10:	/SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT:*
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12:	/SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:*
13:	/SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:*
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19:	/SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:*
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21:	/SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
22:	/SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
23:	/SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*
24:	/SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2363	100.0	447	22	AAW52118 Human alpha-2BAR t
2	2363	100.0	447	22	AAE00989 Human alpha-2B-adre
3	2363	100.0	447	23	AAE26633 Human alpha-2B-adr
4	2351.5	99.5	450	22	AAW52117 Human alpha-2BAR t
5	2351.5	99.5	450	22	AAE00990 Human alpha-2B-adre
6	2351.5	99.5	450	23	AAE26634 Human alpha-2B-adr
7	2343.5	99.2	450	24	ABP81780 Human alpha 2B-adr
8	2302.5	97.4	487	12	AAAR1419 Human alpha 2 beta
9	2302.5	97.4	487	18	AAW11804 Human alpha-2b adr

10	1626	68.8	330	15	AAAR48699 G-protein coupled
11	1626	68.8	330	17	AAW02671 G-protein coupled
12	1126	47.7	450	22	AAW52123 Human alpha-2BAR v
13	1124	47.6	450	22	AAW52122 Human alpha-2BAR p
14	1117	47.3	450	24	ABP81779 Human alpha 2a-adr
15	1082	45.8	457	22	AAW52126 Human alpha-2CAR v
16	1080	45.7	461	22	AAW52124 Human alpha-2CAR p
17	1080	45.7	461	24	ABP81781 Human alpha 2c-adr
18	1079.5	45.7	458	15	AAAR48674 Human derived adre
19	1029	43.5	334	15	AAAR48701 G-protein coupled
20	1029	43.5	334	17	AAW02673 G-protein coupled
21	1003	42.4	330	15	AAAR48700 G-protein coupled
22	1003	42.4	330	17	AAW02672 G-protein coupled
23	992	42.0	324	10	AAAP0552 Hamster beta-2 -ad
24	986.5	41.7	330	15	AAAR48698 G-protein coupled
25	986.5	41.7	330	17	AAW02670 G-protein coupled
26	957.5	40.5	307	24	ABG73558 Human alpha2-adren
27	955.5	40.4	307	22	AAU08334 Human alpha 2 adre
28	652.5	27.6	601	13	AAAR21931 D.melanogaster oct
29	652.5	27.6	601	22	ABP63318 D. melanogaster oc
30	652.5	27.6	601	23	AAAG0701 D. melanogaster oc
31	652.5	27.6	601	23	AAAR17036 Drosophila melanog
32	647	27.4	379	18	AAW33185 Corn barnacle G-pr
33	599.5	25.4	476	18	AAW24089 Balanus amphitrite
34	599	25.3	467	24	ABP81811 Human dopamine rec
35	593.5	25.1	415	24	ABG73546 Rat dopamine D2 re
36	593	25.1	467	15	AAAR48950 Sequence encoded b
37	593	25.1	467	17	AAAR96215 Recombinant human
38	590.5	25.0	415	11	AAAR05539 Rat D2 dopamine re
39	590.5	25.0	415	10	AAAV01598 Mouse dopamine D2
40	589.5	24.9	415	17	AAW09388 Human/rat alpha-1B
41	589	24.9	515	15	AAAR70995 Human/rat hybrid a
42	588	24.9	515	16	AAAR90041 Sequence encoded b
43	588	24.9	419	15	AAAR48949 Recombinant human
44	588	24.9	419	17	AAAR96214 Sequence of human
45	588	24.9	520	15	AAAR52831

ALIGNMENTS

RESULT 1	
ID	AAW52118 standard; Protein; 447 AA.
AC	AAW52118;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Human alpha-2BAR third intracellular loop variant.
XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2BAR.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Domain
FT	Region
FT	Domain
FT	Location/Qualifiers
FT	170..193
FT	/label= transmembrane_domain
FT	307..309
FT	/label= polymorphic_site
FT	370..393
FT	/label= transmembrane_domain
XX	
PN	W0200179561-A2.
XX	
PD	25-OCT-2001.
XX	
PF	17-APR-2001; 2001WO-US12575.
XX	
PR	17-APR-2000; 2000US-0551744.

Query Match	100.0%;	Score 2363;	DB 22;	Length 447;
Best Local Similarity	100.0%;	Pred. No. 7.3e-199;		
Matches 447;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 MDHDDPSVQNTAAIAAIIITLLIIFTTIGNALVILAVITSSSLRAPQNLFLVLSIAADITL	60		
DB	1 MDHDDPSVQNTAAIAAIIITLLIIFTTIGNALVILAVITSSSLRAPQNLFLVLSIAADITL	60		
QY	61 VATTIIPPSLNLNELGYVFPRTCEVYLAADVLCFTSSIVYHCAISIDRWANASRLLEY	120		
DB	61 VATTIIPPSLNLNELGYVFPRTCEVYLAADVLCFTSSIVYHCAISIDRWANASRLLEY	120		
QY	121 NSKSTPRRIKIIITLWILIAVISLPLIITYGDDGPQPRGRPOCKLQNEAWYIIASSIGS	180		
DB	121 NSKSTPRRIKIIITLWILIAVISLPLIITYGDDGPQPRGRPOCKLQNEAWYIIASSIGS	180		
QY	181 PFAACILMILVYLKTYLIIAKRSNRRGPAAKGGPOGSGSKOPRPHGALASAKIIPALASV	240		
DB	181 PFAACILMILVYLKTYLIIAKRSNRRGPAAKGGPOGSGSKOPRPHGALASAKIIPALASV	240		
QY	241 ASAEVNGHSGKSTGEKEGETPEDTGTTRALPPSWAALPNSGQGGKEGVCGASPEDAELEE	300		
DB	241 ASAEVNGHSGKSTGEKEGETPEDTGTTRALPPSWAALPNSGQGGKEGVCGASPEDAELEE	300		
QY	301 EEEBEECEPQAVVPSPASACSPILQOQGSRYVLTATAGVYLIRGVGVALIGQWRRRAQL	360		
DB	301 EEEBEECEPQAVVPSPASACSPILQOQGSRYVLTATAGVYLIRGVGVALIGQWRRRAQL	360		

QY	361	TRERPEVLAIVIGVTCMPPEPSSSLGICPKXKXPHGLFOFFPMIGYSSSLNP	420
Db	361	TRERPEVLAIVIGVTCMPPEPSSSLGICPKXKXPHGLFOFFPMIGYSSSLNP	420
QY	421	VIYTFNODFRFRFRIILCRPMTOTAW	447
Db	421	VIYTFNODFRFRFRIILCRPMTOTAW	447

RESULT 2
AAE00989
ID AAE00989 standard; Protein; 447 AA.

DT 04-JUL-2001 (first entry)

Human α 2B-adrenoceptor (α 2B-AR) variant protein.

KM Human, cardiac; gene therapy; alpha2-adrenoceptor; 2
KM glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KM norepinephrine; epinephrine; therapy; vascular contraction; variant;
KM coronary artery; coronary heart disease; CHD; chronic angina pectoris;
KM acute myocardial infarction; AMI; Pritinmetals variant.

OS Homo sapiens

Key	Location/Qualifiers
FH	298..306
FT	
FT	/note= "Glutamic acid repeat"

PN W0200129082-A1.

PD 26-APR-2001.

PF 20-OCT-2000; 2000WO-FI00913.

PR 22-OCT-1999; 99US-0422985.

PA (JUVA-) JUVANTIA PHARMA LTD OY.

PI Snapiir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;

PI Salonen R, Kauphanen J, Valkonen V;

DR WPI; 2001-300318/31.

2000

deletion of specific amino acids located in the third intracellular

PT arteries

PS Claim 8; Page 26-27; 37pp; English.
xx

The present sequence is human α 2B-adrenoceptor (α 2B-AR) variant protein. α 2B-AR has a glutamic acid repeat element (amino acids 288-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. The variant is obtained by deletion of three glutamates from the Glu repeat (amino acids 307-309). α 2B-AR gene is located on chromosome 2. α 2-AR mediates many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of α 2B-AR-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heart disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). α 2B-AR gene is used in gene therapy.

SQ Sequence 447 AA;

Query Match	Similarity	100.0%	Score 2363	DB 22	Length 447
Best Local	Similarity	100.0%	Pred. No. 7,3e-199		
Matches	447	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
Qy	1	MDHDPYSVOATPAIAAAITFLILFTIFGNALVITAVLTSRSILRAPQNLFLVSLAAADIL	60		
Db	1	MDHDPYSVOATPAIAAAITFLILFTIFGNALVITAVLTSRSILRAPQNLFLVSLAAADIL	60		
Qy	61	VATLIIPPSLANELLGYWFRFTWCEVYIALDLVLTSSIVHLCAISLDRYAAVSRLEY	120		
Db	61	VATLIIPPSLANELLGYWFRFTWCEVYIALDLVLTSSIVHLCAISLDRYAAVSRLEY	120		
Qy	121	NSKRPRIKICILVWVILAAVYISLPILYKGDQGPGRPOCKLNOEAWYTLASSTGS	180		
Db	121	NSKRPRIKICILVWVILAAVYISLPILYKGDQGPGRPOCKLNOEAWYTLASSTGS	180		
Qy	181	FPAPCLIMLVILYRIYLIAKRSNRGRPAKGGPGGSGSKQPPDPHGALASAKLPALASV	240		
Db	181	FPAPCLIMLVILYRIYLIAKRSNRGRPAKGGPGGSGSKQPPDPHGALASAKLPALASV	240		
Qy	241	ASAREVNHGSKSTGKEGETPEDTGTALPSPMAALPNSGQGQKEGVCGASPEDAESE	300		
Db	241	ASAREVNHGSKSTGKEGETPEDTGTALPSPMAALPNSGQGQKEGVCGASPEDAESE	300		
Qy	301	EEEEEECPQAVPVSPASACSPLOOPOGSRVATLIRGVILGRTGVALGQWRRRAQL	360		
Db	301	EEEEEECPQAVPVSPASACSPLOOPOGSRVATLIRGVILGRTGVALGQWRRRAQL	360		
Qy	361	TREKRFTEVLAVVIGVFLVCMPPFFFSYSIGAICPHKCVPHGLFOFFFMIGYCNSSILNP	420		
Db	361	TREKRFTEVLAVVIGVFLVCMPPFFFSYSIGAICPHKCVPHGLFOFFFMIGYCNSSILNP	420		
Qy	421	VYITIFNODFRRAFRRIICRPWTQTAW	447		
Db	421	VYITIFNODFRRAFRRIICRPWTQTAW	447		
RESULT 3					
AAE26633					
ID	AAE26633	standard; Protein; 447 AA.			
XX	AAE26633;				
AC	13-DEC-2002	(first entry)			
DT	13-DEC-2002				
XX	Human alpha-2B-adrenoceptor variant.				
DE	Human alpha-2B-adrenoceptor variant.				
XX	Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;				
KM	hypertension; hypotensive; variant.				
XX	Homo sapiens.				
OS	Synthetic.				
XX	WO200266617-A1.				
PN	29-AUG-2002.				
XX	13-FEB-2002; 2002WO-FI00113.				
XX	20-FEB-2001; 2001FI-0000323.				
PR	(JURI-)	JURILAB LTD OY.			
XX	Salonen J;				
XX	WPI; 2002-667063/71.				
DR	N-PSDB; AAD44388.				
XX	Detecting a risk of hypertension and targeting treatment in a subject				
PT	by determining the pattern of alleles encoding a variant				
PT	alpha-2-adrenoceptor				
XX	Disclosure; Page 26-27; 35pp; English.				

[illegible]

FT	Region	310..312	(AAM52118) "
FT		/label= Polymorphic_site	
FT	Domain	373..396	
FT		/label= transmembrane_domain	
PN	WO200179561-A2.		
XX			
XX	25-OCT-2001.		
PD			
PF	17-APR-2001; 2001WO-US12575.		
XX			
XX	17-APR-2000; 2000US-0551744.		
PR	10-AUG-2000; 2000US-0636259.		
PR	19-OCT-2000; 2000US-0692077.		
PA	(LIGG/) LIGGETT S B.		
PA	(SMAL/) SMALL K M.		
XX			
PI	Liggett SB, Small KM;		
DR	WPI, 2001-611728/70.		
DR	N-PSDB; AAI99905.		
XX			
PT	Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for		
PT	determining whether an individual is at increased risk of developing a		
PT	disease associated with the corresponding receptor comprises detecting		
PT	a polymorphic site -		
PS	Claim 20; Page 146-147; 163pp; English.		
XX			
CC	The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic		
CC	receptor gene (I)-(III) by detecting a polymorphic site, comprising;		
CC	(a) obtaining a sample having a polynucleotide encoding an alpha-2B,		
CC	alpha2A or alpha2C or fragment or complement of; and		
CC	(b) detecting a polymorphic site comprising nucleotide positions 901-909		
CC	of (I), a site comprising cytosine or guanine at position 753 of (III)		
CC	or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctga) at		
CC	positions 961-972 of (III). The method may be used for genotyping an		
CC	alpha2B, alpha2A or alpha2C receptor gene and further used to determine		
CC	whether an individual is at increased risk of developing a disease		
CC	associated with alpha2B, alpha2A or alpha2, comprising detecting a		
CC	polymorphic site which correlate to disease selected from cardiovascular		
CC	disease, central nervous system disease and combinations of these. In		
CC	addition, the technique may be used to predict an individual's response		
CC	to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,		
CC	norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and		
CC	combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,		
CC	rauwolscine, idaroxan, tolazoline, phenclolamine and combinations of		
CC	these) by detecting the polymorphic site and correlating the site to a		
CC	predetermined response (where the response is correlated to adenylyl		
CC	cyclase, MAP kinase activity, phosphorylation or inositol phosphate		
CC	levels). The present sequence is that of the third intracellular loop of		
CC	the human alpha-2BAR protein, the sequence includes 3 amino acid		
CC	polymorphic site at residues 301-303 (EEE), absent in the alpha-2BAR		
CC	variant protein (AAM52118).		
XX			
XX	Sequence 450 AA;		
Query Match	99.5%; Score 2351.5; DB 22; Length 450;		
Best Local Similarity	99.3%; Pred. No.7,6e-198;		
Matches 447; Conservative	0; Mismatches 0; Indels 3; Gaps 1;		
QY	1 MDHDPYVQVATAIAAAITFLITFTIGNALVIAVLTSSRLRPQNLFTVSLAAADIL 60		
DB	1 MDHDPYVQVATAIAAAITFLITFTIGNALVIAVLTSSRLRPQNLFTVSLAAADIL 60		
QY	61 VATLIIPSLNELIGWYFRRTWCVEYIALDVLFTCTSSIVHLCAISLDRYAVSRALEY 120		
DB	61 VATLIIPSLNELIGWYFRRTWCVEYIALDVLFTCTSSIVHLCAISLDRYAVSRALEY 120		
QY	121 NSKTPRRIKCIIILTWVILAAVISLPPLIYKGDQFQRRGRPOCKLNDQAWYIIASSIGS 180		

Db	121	NSKRTFRRIKCIITLVTWLIANAISLPLLYKGDOGQPCRGRRGCKLNQEMAYTIIASSIGS	160
Qy	181	FPAPCLIMLIVYIRIYLIAKSNRRGPPAKGGPGGSGSKQRPDPHGALASAKLPALASV	240
Db	181	FPAPCLIMLIVYIRIYLIAKSNRRGPPAKGGPGGSGSKQRPDPHGALASAKLPALASV	240
Qy	241	ASAREVNGSHKSTGKEKEGETPEDTGTALPPSWALLPNSGQGGKEGVCGASPEDEA---	297
Db	241	ASAREVNGSHKSTGKEKEGETPEDTGTALPPSWALLPNSGQGGKEGVCGASPEDEAEE	300
Qy	298	EEEEEEBCEBPAYVPVSPASCSPPLOOPGSRVLATLRQYLLIRGVGALIGQWRRR	357
Db	301	EEEEEEBCEBPAYVPVSPASCSPPLOOPGSRVLATLRQYLLIRGVGALIGQWRRR	360
Qy	358	AQLTREKRFYVLAVAVIGVFLCWFPPFFSYSLGACPKHCKVPHGLFOFFFWIGYCNSS	417
Db	361	AQLTREKRFYVLAVAVIGVFLCWFPPFFSYSLGACPKHCKVPHGLFOFFFWIGYCNSS	420
Qy	418	LNPIVYITINODPRRAFRRIICRPMYOTAW	447
Db	421	LNPIVYITINODPRRAFRRIICRPMYOTAW	450

ID	AAE00990	standard; Protein; 450 AA.
AC	AAE00990;	
DT	04-JUL-2001	(first entry)
DE	Human alpha2B-adrenoceptor (alpha2B-AR) protein.	
KW	Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;	
KW	glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;	
KW	norepinephrine; epinephrine; therapy; vascular contraction;	
KW	coronary artery; coronary heart disease; CHD; chronic angina pectoris;	
KW	acute myocardial infarction; AMI; Prinzmetal's variant.	
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
XX	FH Region	298..309
XX	FT	/note= "Glutamic acid repeat"
XX	FT	
XX	FN	WO200129082-A1.
XX		
XX	PD	26-APR-2001.
XX		
XX	PF	20-OCT-2000; 2000WO-FI00913.
XX		
XX	PR	22-OCT-1999; 99US-0422985.
XX		
XX	PA	(JUVV-) JUVANTIA PHARMA LTD OY.
PI	Snapir A, Heinonen P, Alhopuro P, Kärönen M, Koulu M, Pesonen U,	
PI	Scheinin R, Salonen JT, Tuomainen T, Lakka TA, Nyssönen K,	
PI	Salonen R, Kahanen J, Valkonen V;	
XX		
XX	WP1; 2001-300318/31.	
DR	N-PSDB; AAD04762.	
XX		
PT	New DNA molecule encoding variant specific adrenoceptor protein with	
PT	detection of specific amino acids located in the third intracellular	
PT	loop of the polypeptide, for treating vascular contraction of coronary	
PT	arteries -	
XX		
XX		
PS	Disclosure; Page 29-31; 37pp; English.	
CC		
CC	The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) protein	
CC	Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of	
CC	12 glutamates, in an acidic stretch of 18 amino acids (amino acids	
CC	294-311), located in the third intracellular loop of the receptor	

CC polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR
CC mediate many of the physiological effects of the catecholamines,
CC norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is
CC useful for treating a mammal suffering from vascular contraction of
CC coronary arteries and a disease involving vascular contraction of
CC coronary arteries which is clinically expressed as coronary heart disease
CC (CHD), unstable chronic angina pectoris which is clinically expressed as
CC Prinzmetal's variant form or acute myocardial infarction (AMI).
CC Alpha2B-AR gene is used in gene therapy.

XX
SQ Sequence 450 AA;

Query Match 99.5%; Score 2351.5; DB 22; Length 450;
Best Local Similarity 99.3%; Pred. No. 7.6e-198;

Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MDHODPVSQVATAIAAATFTLFTFGNALVTLAVTSRSLRAPONLFLVSLAADIL 60
DB 1 MDHODPVSQVATAIAAATFTLFTFGNALVTLAVTSRSLRAPONLFLVSLAADIL 60
QY 61 VATTIIFPSLANELLGTYWFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRLLEY 120
DB 61 VATTIIFPSLANELLGTYWFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRLLEY 120
QY 121 NSKRTPRRIKCIITLWVLIANAVISLPLIYKDGQPOPRGRPOCKLQNEAMYLASSIGS 180
DB 121 NSKRTPRRIKCIITLWVLIANAVISLPLIYKDGQPOPRGRPOCKLQNEAMYLASSIGS 180
QY 181 FPARCLIMILVYLRITYLIARSNRGRPRAGKGGQSGSKOPRPHGALASAKLPALASV 240
DB 181 FPARCLIMILVYLRITYLIARSNRGRPRAGKGGQSGSKOPRPHGALASAKLPALASV 240
QY 241 ASAREVNGSHKSTGEKEGETPEDTGTALPSPWALPNSGQGGKEVCGASPEDAE--- 297
DB 241 ASAREVNGSHKSTGEKEGETPEDTGTALPSPWALPNSGQGGKEVCGASPEDAE--- 297
QY 298 EEEEEECEPEQAVPVSPASACSPPLQOPQSGRVLTATLGRGVATIGQWRRR 357
DB 298 EEEEEECEPEQAVPVSPASACSPPLQOPQSGRVLTATLGRGVATIGQWRRR 357
QY 301 EEEEEECEPEQAVPVSPASACSPPLQOPQSGRVLTATLGRGVATIGQWRRR 360
DB 301 EEEEEECEPEQAVPVSPASACSPPLQOPQSGRVLTATLGRGVATIGQWRRR 360
QY 358 AQLTREKRTFTVLAIVGVFLCMPPFFSYSLGATCPKCKVPHGLFQFFPMWIGYCNSS 417
DB 358 AQLTREKRTFTVLAIVGVFLCMPPFFSYSLGATCPKCKVPHGLFQFFPMWIGYCNSS 417
QY 361 AQLTREKRTFTVLAIVGVFLCMPPFFSYSLGATCPKCKVPHGLFQFFPMWIGYCNSS 420
DB 361 AQLTREKRTFTVLAIVGVFLCMPPFFSYSLGATCPKCKVPHGLFQFFPMWIGYCNSS 420
QY 418 LNPVIYTIENODFRARFRILCRPWOTAW 447
DB 418 LNPVIYTIENODFRARFRILCRPWOTAW 447
QY 421 LNPVIYTIENODFRARFRILCRPWOTAW 450
DB 421 LNPVIYTIENODFRARFRILCRPWOTAW 450

RESULT 6

AAE26634
ID AAE26634 standard; Protein; 450 AA.

XX
AC AAE26634;

XX
DT 13-DEC-2002 (first entry)

XX
DE Human alpha-2B-adrenoceptor protein.

XX
KM Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
XX hypertension; hypotensive.

XX
OS Homo sapiens.

XX
PN WO200266617-A1.

XX
PD 29-AUG-2002.

XX
PF 13-FEB-2002; 2002WO-FI00113.

XX
PR 20-FEB-2001; 2001FI-0000323.

XX
PA (JURI-) JURILAB LTD OY.

XX
PI Salonen J;

XX
DR WPI: 2002-667063/71.

XX
DR N-PSDB; AAE26634.

XX
PT Detecting a risk of hypertension and targeting treatment in a subject
XX by determining the pattern of alleles encoding a variant
XX alpha-2B-adrenoceptor

XX
PS Disclosure; Page 30-31; 35pp; English.

XX
CC The invention relates to a method for detecting a risk of hypertension
XX by determining the pattern of alleles encoding a variant alpha-2B-
XX adrenoceptor (AR) protein. The methods and compositions of the invention
XX are useful for detecting risks and targeting treatment for hypertension.
XX The kit is also useful for selecting for clinical drug trials testing
XX the antihypertensive effect of compounds. The present sequence is human
XX alpha-2B-adrenoceptor protein.

XX
SQ Sequence 450 AA;

Query Match 99.5%; Score 2351.5; DB 23; Length 450;
Best Local Similarity 99.3%; Pred. No. 7.6e-198;

Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MDHODPVSQVATAIAAATFTLFTFGNALVTLAVTSRSLRAPONLFLVSLAADIL 60
DB 1 MDHODPVSQVATAIAAATFTLFTFGNALVTLAVTSRSLRAPONLFLVSLAADIL 60
QY 61 VATTIIFPSLANELLGTYWFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRLLEY 120
DB 61 VATTIIFPSLANELLGTYWFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRLLEY 120
QY 121 NSKRTPRRIKCIITLWVLIANAVISLPLIYKDGQPOPRGRPOCKLQNEAMYLASSIGS 180
DB 121 NSKRTPRRIKCIITLWVLIANAVISLPLIYKDGQPOPRGRPOCKLQNEAMYLASSIGS 180
QY 181 FPARCLIMILVYLRITYLIARSNRGRPRAGKGGQSGSKOPRPHGALASAKLPALASV 240
DB 181 FPARCLIMILVYLRITYLIARSNRGRPRAGKGGQSGSKOPRPHGALASAKLPALASV 240
QY 241 ASAREVNGSHKSTGEKEGETPEDTGTALPSPWALPNSGQGGKEVCGASPEDAE--- 297
DB 241 ASAREVNGSHKSTGEKEGETPEDTGTALPSPWALPNSGQGGKEVCGASPEDAE--- 297
QY 298 EEEEEECEPEQAVPVSPASACSPPLQOPQSGRVLTATLGRGVATIGQWRRR 357
DB 298 EEEEEECEPEQAVPVSPASACSPPLQOPQSGRVLTATLGRGVATIGQWRRR 357
QY 301 EEEEEECEPEQAVPVSPASACSPPLQOPQSGRVLTATLGRGVATIGQWRRR 360
DB 301 EEEEEECEPEQAVPVSPASACSPPLQOPQSGRVLTATLGRGVATIGQWRRR 360
QY 358 AQLTREKRTFTVLAIVGVFLCMPPFFSYSLGATCPKCKVPHGLFQFFPMWIGYCNSS 417
DB 358 AQLTREKRTFTVLAIVGVFLCMPPFFSYSLGATCPKCKVPHGLFQFFPMWIGYCNSS 417
QY 361 AQLTREKRTFTVLAIVGVFLCMPPFFSYSLGATCPKCKVPHGLFQFFPMWIGYCNSS 420
DB 361 AQLTREKRTFTVLAIVGVFLCMPPFFSYSLGATCPKCKVPHGLFQFFPMWIGYCNSS 420
QY 418 LNPVIYTIENODFRARFRILCRPWOTAW 447
DB 418 LNPVIYTIENODFRARFRILCRPWOTAW 447
QY 421 LNPVIYTIENODFRARFRILCRPWOTAW 450
DB 421 LNPVIYTIENODFRARFRILCRPWOTAW 450

RESULT 7

ABP81780
ID ABP81780 standard; Protein; 450 AA.

XX
AC ABP81780;

XX
DT 04-MAR-2003 (first entry)

XX
DE Human alpha 2b-adrenoceptor protein SEQ ID NO:42.

XX
KM G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 ulcer.
 KW Homo sapiens.
 XX WO200261087-A2.
 XX 08-AUG-2002.
 XX 19-DEC-2001; 2001WO-US50107.
 XX 19-DEC-2000; 2000US-257144P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX Burner GC, Roush CL, Brown JP;
 XX WPI: 2003-046718/04.
 XX N-PSDB; ABZ42624.
 DR New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases
 PT
 PS Disclosure; Fig 1; 523pp; English.
 XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.
 CC
 XX Sequence 450 AA:
 SO Query Match 99.2%; Score 2343.5; DB 24; Length 450;
 Best Local Similarity 98.9%; Pred. No. 3.8e-197;
 Matches 445; Conservative 1; Mismatches 1; Indels 3; Gaps 1;
 QY 1 MDHDDPSVQATATAAATFTLFTFGNALVILAVITRSRLRAPQNLFLVSLAADIL 60
 DB 1 MDHDDPSVQATATAAATFTLFTFGNALVILAVITRSRLRAPQNLFLVSLAADIL 60
 QY 61 VATLIPSLANELLGYWFRRTQCEVIALDVLTCTSSIVHLCAISIDRYVAASRALEY 120
 DB 61 VATLIPSLANELLGYWFRRTQCEVIALDVLTCTSSIVHLCAISIDRYVAASRALEY 120
 QY 121 NSKTRPRRIKCIITLWMLIAVILSLPILYKGDGPQGRPOCKLNOEAWYIIASSIGS 180

DB 121 NSKTRPRRIKCIITLWMLIAVILSLPILYKGDGPQGRPOCKLNOEAWYIIASSIGS 180
 QY 161 PPAPCLMILVLYRLYLAKXSNRGRPAKGGPGGSEKOPRPHGALASAKLPALASV 240
 DB 161 PPAPCLMILVLYRLYLAKXSNRGRPAKGGPGGSEKOPRPHGALASAKLPALASV 240
 QY 241 ASAREVNGSHKSTGKEGETPEDTGTALPPSWALPNSGGQKEGVCGASPEDEA--- 297
 DB 241 ASAREVNGSHKSTGKEGETPEDTGTALPPSWALPNSGGQKEGVCGASPEDEAEE 300
 QY 298 EEEEEEEBCEPOAVPVSPASACSPPLQOPQGSRLATLRQVLLRGVGAIGQMMWRR 357
 DB 301 EEEEEEEBCEPOAVPVSPASACSPPLQOPQGSRLATLRQVLLRGVGAIGQMMWRR 360
 QY 358 AQLTREKRTFLVAVIGVFLCWFPPFSSYLGAICPHKCVPHGLPQFFFIWIGYCNSS 417
 DB 361 AHVTEKRTFLVAVIGVFLCWFPPFSSYLGAICPHKCVPHGLPQFFFIWIGYCNSS 420
 QY 418 LNPVITYTIFNODFRRAFRRLICRPWTQTAW 447
 DB 421 LNPVITYTIFNODFRRAFRRLICRPWTQTAW 450
 RESULT 8
 AAR14149
 ID AAR14149 standard; Protein; 487 AA.
 XX AAR14149;
 AC 06-JAN-1992 (first entry)
 DT Human alpha 2 beta adrenergic receptor.
 XX Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta.
 KW Homo sapiens.
 OS US053337-A.
 XX 01-OCT-1991.
 PD 30-OCT-1989; 89US-0428856.
 PF 30-OCT-1989; 89US-0428856.
 XX 30-OCT-1989; 89US-0428856.
 XX (NEUR-) NEUROGENETIC CORP.
 PA Weinshank RJ, Hartig PR;
 XX WPI: 1991-310087/42.
 DR N-PSDB; AAQ14151.
 XX Isolated DNA encoding human adrenergic receptor - for detecting
 PT nucleic acids encoding alpha, 2-beta adrenergic receptor, for
 PT screening drugs.
 PT
 XX Disclosure; Fig 2; 15pp; English.
 PS Clone NGC-alpha2beta was isolated from a human spleen genomic
 CC library by screening with a fragment of the human 5-HT1A receptor
 CC gene. The gene was used to express recombinant receptor protein
 CC which can be used to produce antibodies for inhibition of receptor
 CC function.
 CC
 XX Sequence 487 AA:
 SO Query Match 97.4%; Score 2302.5; DB 12; Length 487;
 Best Local Similarity 97.6%; Pred. No. 1.7e-193;
 Matches 439; Conservative 2; Mismatches 6; Indels 3; Gaps 1;
 QY 1 MDHDDPSVQATATAAATFTLFTFGNALVILAVITRSRLRAPQNLFLVSLAADIL 60

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Db      38 MDHODPYSVQATAIAAAITFLIFTFGNALVILAVLTSRSMRAPQNLFLVSLAAADIL 97
Qy      61 VATTIIPFSLANELLGWYFRRTWCEVYALADVIFCTSSIVHLCAISLDRYMAVSRALEY 120
Db      98 VATTIIPFSLANELLGWYFRRTWCEVYALADVIFCTSSIVHLCAISLDRYMAVSRALEY 157
Qy      121 NSKTRPRRIKCIITLWVLAIAVISLPLIYKDGQPPGRGRPOCKLNOEAWYIIASSIGS 180
Db      158 NSKTRPRRIKCIITLWVLAIAVISLPLIYKDGQPPGRGRPOCKLNOEAWYIIASSIGS 217
Qy      181 FPAFLIMILVYLAIVYLAIAKSNRGRPRAGKGPQGESKOPRPHGALASAKLPALASV 240
Db      218 FPAFLIMILVYLAIVYLAIAKSNRGRPRAGKGPQGESKOPRPHGALASAKLPALASV 277
Qy      241 ASAREVNGHSKSTKEGGETPEDTGTALPPSWAALPNSGQGGQKEGVCGASPEDA--- 297
Db      278 ASAREVNGHSKSTKEGGETPEDTGTALPPSWAALPNSGQGGQKEGVCGASPEDAEE 337
Qy      298 EEEEEECEPQAVPVSPASACSPPLQOPGSRVLAIRGQVLLGRGVGAIIGQWRRR 357
Db      338 EEEEEECEPQAVPVSPASACSPPLQOPGSRVLAIRGQVLLGRGVGAIIGQWRRR 397
Qy      358 AQLTRERKFTFVLAVVIGVFLCMFPFFSYSLGAIKPKCKVPHGLFOFFFWIYCNS 417
Db      398 AHTREKRFTEVLAVVIGVFLCMFPFFSYSLGAIKPKCKVPHGLFOFFFWIYCNS 457
Qy      418 LNPVIYITIFNDPFRARFRILCRPWTOTAW 447
Db      458 LNPVIYITIFNDPFRARFRILCRPWTOTAW 487

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RESULT 9

AAW11804
ID AAW11804 standard; Protein: 487 AA.

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XX AC AAW11804;
XX DT 25-MAR-2003 (updated)
XX DT 06-MAY-1997 (first entry)
XX DE Human alpha-2b adrenergic receptor.
XX KM Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
XX KM epinephrine; signal transduction; neurotransmitter; ligand.
XX OS Homo sapiens.
XX PN US5595880-A.
XX PD 21-JAN-1997.
XX PF 22-OCT-1992; 92US-0965040.
XX PR 30-OCT-1989; 89US-0428856.
XX PR 30-MAY-1991; 91US-0707604.
XX PR 22-OCT-1992; 92US-0965040.
XX PA (SYNA-) SYNAPTIC PHARM CORP.
XX PI Hartig PR, Weisshank RL;
XX PI WPI: 1997-107576/10.
XX DR N-PSDB; AAT59499.
XX PT Assay for alpha-2b adrenergic receptor ligands - using membranes of
XX PT cells expressing recombinant receptor
XX PS Disclousure; Fig 2A-E; 16pp; English.
XX CC Human alpha-2b adrenergic receptor (AAW11804) is a member of the
XX CC rhodopsin-like signal transducer family. Its amino acid sequence
XX CC was deduced from a genomic DNA clone (AAT59499) obcd. from a human
XX CC spleen DNA library. Vectors have been adapted to allow prodn. of

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CC alpha-2b adrenoceptor in bacterial, yeast or mammalian cells;
CC transfected Ltk- cells, designated L-NGC-alpha-2b, are deposited as
CC ATCC CRL 10275. Membranes of transfected mammalian cells can used
CC in novel methods to identify drugs which specifically interact
CC with, and bind to, the alpha-2b adrenergic receptor.
CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 487 AA;

Query Match 97.4%; Score 2302.5; DB 18; Length 487;

Best Local Similarity 97.6%; Pred. No. 1.7e-193; Indels 3; Gaps 1;

Matches 439; Conservative 2; Mismatches 6;

```

Qy      1 MDHODPYSVQATAIAAAITFLIFTFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL 60
Db      38 MDHODPYSVQATAIAAAITFLIFTFGNALVILAVLTSRSMRAPQNLFLVSLAAADIL 97
Qy      61 VATTIIPFSLANELLGWYFRRTWCEVYALADVIFCTSSIVHLCAISLDRYMAVSRALEY 120
Db      98 VATTIIPFSLANELLGWYFRRTWCEVYALADVIFCTSSIVHLCAISLDRYMAVSRALEY 157
Qy      121 NSKTRPRRIKCIITLWVLAIAVISLPLIYKDGQPPGRGRPOCKLNOEAWYIIASSIGS 180
Db      158 NSKTRPRRIKCIITLWVLAIAVISLPLIYKDGQPPGRGRPOCKLNOEAWYIIASSIGS 217
Qy      181 FPAFLIMILVYLAIVYLAIAKSNRGRPRAGKGPQGESKOPRPHGALASAKLPALASV 240
Db      218 FPAFLIMILVYLAIVYLAIAKSNRGRPRAGKGPQGESKOPRPHGALASAKLPALASV 277
Qy      241 ASAREVNGHSKSTKEGGETPEDTGTALPPSWAALPNSGQGGQKEGVCGASPEDA--- 297
Db      278 ASAREVNGHSKSTKEGGETPEDTGTALPPSWAALPNSGQGGQKEGVCGASPEDAEE 337
Qy      298 EEEEEECEPQAVPVSPASACSPPLQOPGSRVLAIRGQVLLGRGVGAIIGQWRRR 357
Db      338 EEEEEECEPQAVPVSPASACSPPLQOPGSRVLAIRGQVLLGRGVGAIIGQWRRR 397
Qy      358 AQLTRERKFTFVLAVVIGVFLCMFPFFSYSLGAIKPKCKVPHGLFOFFFWIYCNS 417
Db      398 AHTREKRFTEVLAVVIGVFLCMFPFFSYSLGAIKPKCKVPHGLFOFFFWIYCNS 457
Qy      418 LNPVIYITIFNDPFRARFRILCRPWTOTAW 447
Db      458 LNPVIYITIFNDPFRARFRILCRPWTOTAW 487

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RESULT 10

AAAR48699
ID AAR48699 standard; Protein: 330 AA.

```

XX AC AAR48699;
XX DT 05-JUN-1996 (first entry)
XX DE G-protein coupled human alpha-2 C2 adrenergic receptor protein.
XX KM G-protein coupled receptor; ligand binding assay; transmembrane domain;
XX KM psychotic disorder; schizophrenia; dopamine; AMP; adenosine; thrombin;
XX KM muscarinic acetylcholine; adrenergic; endocannabin; bombesin; endocrine;
XX KM rhodopsin; opsin; odorant; cytomagalovirus.
XX OS Homo sapiens.
XX PN WO9405695-A1.
XX PD 17-MAR-1994.
XX PF 09-SEP-1993; 93WO-US08528.
XX PR 10-SEP-1992; 92US-0943236.
XX PR (UNYV ) UNIV NEW YORK STATE.
XX PA

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PI Murphy RB, Schuster DI;
 XX WPI; 1994-101120/12.
 XX
 PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 PT binding GPR ligands or modulating GPR binding
 XX
 PS Disclosure; Page 72-73; 160pp; English.
 XX
 CC Proteins AAR4865-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
 CC of polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 XX
 SQ Sequence 330 AA;
 Query Match 68.8%; Score 1626; DB 15; Length 330;
 Best Local Similarity 73.6%; Pred. No. 2.4e-134;
 Matches 321; Conservative 6; Mismatches 3; Indels 106; Gaps 4;
 QY 12 TAAIAAATFLIFITFGNALVILAVLTSRSLAPQNLFLVSLAAADILVATLIPSLA 71
 DB 1 TAAIAAATFLIFITFGNALVILAVLTSRSLAPQNLFLVSLAAADILVATLIPSLA 60
 QY 72 NELGWTFRRTWCCEVYALADVLFCSTSIYHLCASIDRYWAVSRALFVNSKRTPRRIKC 131
 DB 61 NELGWTFRRTWCCEVYALADVLFCSTSIYHLCASIDRYWAVSRALFVNSKRTPRRIKC 120
 QY 132 ILLTWLAAVLSLPLIYKDGQGPGRPOCKNOEAWYLLASISGFAPCLIMILV 191
 DB 121 ILLTWLAAVLSLPLIYKDGQGPGRPOCKNOEAWYLLASISGFAPCLIMILV 178
 QY 192 YLRITVLIARSNRGRPRAGKGPQGESKOPRPHGALASAKLPALASVASAREVNGHSK 251
 DB 179 YLRITVLIARSNRGRPRAGKGPQGESKOPRPHGALASAKLPALASVASAREVNGHSK 251
 QY 252 STGEKEGETPEDTGTALPESWALPNSGQKQKGVCSAPDEABEEBEEBCECPQA 311
 DB 227 -----
 QY 312 VVSPASACSPPLQOPQGSRLVATLRGVLLGRGVGAIIGQWRRRAQLTREKRTFTVLA 371
 DB 227 -----GRGVGAIIGQWRRRAQLTREKRTFTVLA 255
 QY 372 VVIGVFVLCMPFFFSYSLGAIICPKKCKVPHGLFOFFFWIGYCNSSLNPVITYITFNODR 431
 DB 256 VVIGVFVLCMPFFFSYSLGAIICPKKCKVPHGLFOFFFWIGYCNSSLNPVITYITFNODR 314
 QY 432 RAFRRIICRPWTQTAM 447
 DB 315 RMFRRIICRPWTQTAM 330
 RESULT 11
 ID AAM02671 standard; peptide; 330 AA.
 XX AAM02671;
 XX
 XX 25-MAR-2003 (updated)
 DT 12-NOV-1996 (first entry)
 XX
 DE G-protein coupled human alpha-2 C2 adrenergic receptor.
 XX
 KM G-protein coupled receptor; ligand binding assay; transmembrane domain.

KM schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KM muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KM odorant; cytomagalovirus; serotonergic.
 OS Homo sapiens.
 XX
 XX US5508384-A.
 XX
 XX 16-APR-1996.
 XX
 XX 09-SEP-1993; 93US-0118270.
 XX
 XX 09-SEP-1993; 93US-0118270.
 XX
 XX 10-SEP-1992; 92US-0943236.
 XX
 XX (UNYV) UNIV NEW YORK STATE.
 PA
 XX
 XX Murphy RB, Schuster DI;
 PI WPI; 1996-208785/21.
 DR
 XX
 PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrenia
 XX
 PS Disclosure; Column 69-72; 184pp; English.
 XX
 CC Proteins AAM02657-W02720 represent a range of G-protein coupled receptor
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other GPR proteins. The receptor proteins
 CC were used to design polypeptides, pref. based on the transmembrane
 CC domains, for use in G-protein coupled receptor ligand binding assays.
 CC The polypeptide fragments retain biological activity such as binding a
 CC GPR ligand or modulating GPR ligand binding to a GPR (see
 CC AAM02747-W02999 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 330 AA;
 Query Match 68.8%; Score 1626; DB 17; Length 330;
 Best Local Similarity 73.6%; Pred. No. 2.4e-134;
 Matches 321; Conservative 6; Mismatches 3; Indels 106; Gaps 4;
 QY 12 TAAIAAATFLIFITFGNALVILAVLTSRSLAPQNLFLVSLAAADILVATLIPSLA 71
 DB 1 TAAIAAATFLIFITFGNALVILAVLTSRSLAPQNLFLVSLAAADILVATLIPSLA 60
 QY 72 NELGWTFRRTWCCEVYALADVLFCSTSIYHLCASIDRYWAVSRALFVNSKRTPRRIKC 131
 DB 61 NELGWTFRRTWCCEVYALADVLFCSTSIYHLCASIDRYWAVSRALFVNSKRTPRRIKC 120
 QY 132 ILLTWLAAVLSLPLIYKDGQGPGRPOCKNOEAWYLLASISGFAPCLIMILV 191
 DB 121 ILLTWLAAVLSLPLIYKDGQGPGRPOCKNOEAWYLLASISGFAPCLIMILV 178
 QY 192 YLRITVLIARSNRGRPRAGKGPQGESKOPRPHGALASAKLPALASVASAREVNGHSK 251
 DB 179 YLRITVLIARSNRGRPRAGKGPQGESKOPRPHGALASAKLPALASVASAREVNGHSK 251
 QY 252 STGEKEGETPEDTGTALPESWALPNSGQKQKGVCSAPDEABEEBEEBCECPQA 311
 DB 227 -----
 QY 312 VVSPASACSPPLQOPQGSRLVATLRGVLLGRGVGAIIGQWRRRAQLTREKRTFTVLA 371
 DB 227 -----GRGVGAIIGQWRRRAQLTREKRTFTVLA 255
 QY 372 VVIGVFVLCMPFFFSYSLGAIICPKKCKVPHGLFOFFFWIGYCNSSLNPVITYITFNODR 431
 DB 256 VVIGVFVLCMPFFFSYSLGAIICPKKCKVPHGLFOFFFWIGYCNSSLNPVITYITFNODR 314

XX WPI: 2001-611728/70.
 DR N-PSDB; AAI99917.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 PS
 XX Claim 48; Page 152-154; 163pp; English.

XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (ggggcggggccg) or (B) (ggggcgctcag) at
 CC positions 961-972 of (IIIV). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK4304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2AAR protein.

XX Sequence 450 AA;

Query Match 47.6%; Score 1124; DB 22; Length 450;
 Best Local Similarity 53.2%; Pred. No. 4.1e-90;
 Matches 243; Conservative 49; Mismatches 103; Indels 62; Gaps 14;

QY 6 PYSQATATAAATFLITFTFGNALVTLAVTSRSRAQONFLVSLAADIVATLI 65
 DB 27 PYSQAVTLTLCAGLMLTIVFGNVLITAVFTSRALKAPQNFVSLAADIVATLV 86
 QY 66 I PFSLANELGAWVRRTWCCEVYLAIDLFCSTSVHCAISLDRYVMSALFENSKRT 125
 DB 87 I PFSLANEVMGWTFGKAWCEIYLAIDLFCSTSVHCAISLDRYMSITDAIEYNLKT 146
 QY 126 PRRIKCIITLWTLAAVLSLPLI----YKGDQGPQPRGRPOCKLNDRAWYTLASIGSF 181
 DB 147 PRRIKAIITLWVAVISFPLISIEKKGGGCGQP--AEPRCEINDQKMWISSICISF 205
 QY 182 PAPCIIMLVLYRLYLAKR-----SNRRGPRAKGGPGQSGSKQPR--PHGGAASAK 233
 DB 206 PAPCIIMLVLYRLYLAKR-----SNRRGPRAKGGPGQSGSKQPR--PHGGAASAK 265
 QY 234 LPALASVASAEVNHSGSTGEKEGEPEDTGTALPPSMALPNSGQKXGVCASGP 293
 DB 266 AEPLPT-----QLAN--APGEPAAP--GPRDIALDLSES-----SS 298
 QY 294 EDEAE-----EEEBEECEPQAVPVSAPASCPLOQPOGSRVLTALRGVLLGRG- 345
 DB 299 SDHARPPGP RPGRKGRKARASQYKGP--SLPRRGG-----ATGIGTAPAGPGE 351
 QY 346 --VGAIGQMMRRRAQLTRKRFVTVAIVIGFVLCMPFPFSSYSLGATCPKCKVPHG 403
 DB 352 ERVGAAKASRRRGQ--NREKRFVTLAVVIGFVVCWFPEFTYTLAV--GCSYVRT 406
 QY 404 LFOFFWTCGNSNINPIYITTFNDPRARPRICR 440
 DB 407 LKFFFWGTCGNSNINPIYITTFNDPRARPRICR 443

RESULT 14
 ABP81779
 ID ABP81779 standard; Protein; 450 AA.
 XX
 AC ABP81779;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human alpha 2a-adrenoceptor protein SEQ ID NO:40.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW growth-related receptor; modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiovascular; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW proriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 ulcer.

OS Homo sapiens.
 XX
 PN W0200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US50107.
 XX
 PF 19-DEC-2000; 2000US-257144P.
 XX
 PR 19-DEC-2000; 2000US-257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burner GC, Roush CL, Brown JP;
 XX
 DR WPI: 2003-046718/04.
 XX
 DR N-PSDB; ABZ42623.

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating diseases
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX
 PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

Sequence 450 AA;

Query Match 47.3%; Score 1117; DB 24; Length 450;
Best Local Similarity 52.7%; Pred. No. 1.7e-89;
Matches 241; Conservative 52; Mismatches 102; Indels 62; Gaps 13;

QY 6 PYSQATTAATAATFLFTFTFGNALVYLAATSRSLRAPONLFLVSLAADIIVATLI 65
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 27 PYSQATTAATAATFLFTFTFGNALVYLAATSRSLRAPONLFLVSLAADIIVATLI 86
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 66 IPFSLANELLGYWYFRTWCEVYALDVLFTCTSSIVHCAISLDRYVAASALEYNSKRT 125
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 87 IPFSLANELLGYWYFRTWCEVYALDVLFTCTSSIVHCAISLDRYVAASALEYNSKRT 146
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 126 PRRKCIITLFWLIAAVISLPLI---YKDGQPOPRGRPOCKLANDEAWYILASISGSF 181
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 147 PRRKCIITLFWLIAAVISLPLI---YKDGQPOPRGRPOCKLANDEAWYILASISGSF 205
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 182 PAPCLIMILYLRILYIAKR---SNRGRPRAGGEGGSGKOPR---PDHGALASAK 233
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 206 PAPCLIMILYLRILYIAKR---SNRGRPRAGGEGGSGKOPR---PDHGALASAK 265
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 234 LPLASVASAREVNGHKSSTGEKEGETPDTGTALPSPMAALPNSGGQKEGVCAASP 293
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 266 AEPPLT---QLNG---APEEPAPA-GPRDTDALDEES-----SS 298
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 294 EDEAE-----EEEEECEPOAVPVSPASACSPLOQPOGSRVLAATLRGQVLA 346
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 299 SDHAERPPGRPRPRGRPKCKAKASQVKPDDSLRGAGRGKRS-----GRLOQRGR 351
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 347 GAIGQGMRRRAOL---TREKRTFLVAVIGVFLCMFPFESYSIGATCPKCKVPHG 403
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 352 SASGLP---RRRAGAGGONLEKRFTEFLAVVIGVFLCMFPFESYSIGATCPKCKVPHG 406
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 404 LFOFFWIGYCNSSLNPIVYITIFNODPRRARLTLR 440
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 407 LKFFWFGYCNSSLNPIVYITIFNODPRRARLTLR 443
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
RESULT 15
AAMS2126
ID AAMS2126 standard; Protein; 457 AA.
AC AAMS2126;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2CAR variant protein.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2CAR.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 208..231
FT Domain /label=transmembrane_domain
FT Domain 379..402
FT Domain /label=transmembrane_domain
PN MO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001MO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.

XX
PI Liggett SB, Small KM;
XX
DR WPI: 2001-611728/70.
DR N-PSDB; AA199933.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS
XX
PS Claim 78; Page 160-162; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C, or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (GGGCGGCGGCG) or (B) (GGGCGGCGGCG) at
CC position 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2CAR variant
CC protein, deleted for a 4 amino acid polymorphic site at residues 321-324
CC of the wildtype protein (AAMS2124).
XX
SQ Sequence 457 AA;
XX
Query Match 45.8%; Score 1082; DB 22; Length 457;
Best Local Similarity 51.5%; Pred. No. 2e-86;
Matches 235; Conservative 43; Mismatches 104; Indels 74; Gaps 9;

QY 7 YSVQATTAATAATFLFTFTFGNALVYLAATSRSLRAPONLFLVSLAADIIVATLI 66
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 46 YSAGAVAGLAAVGFLVFTVGVAVVIAVLSRALRAPONLFLVSLAADIIVATLI 105
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 67 PFSIANELLGYWYFRTWCEVYALDVLFTCTSSIVHCAISLDRYVAASALEYNSKRT 126
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 106 PFSIANELLGYWYFRTWCEVYALDVLFTCTSSIVHCAISLDRYVAASALEYNSKRT 165
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 127 RRIKCIITLFWLIAAVISLPLI---YKDGQPOPRGR---POCKLANDEAWYILASISGSF 182
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 166 RRVKATIVAVMLISAVISPPVLSVR-----QPDAGAYPQCGINDEBTWYILSSGISGF 220
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 183 APCIMILYLRILYIAKR---SNRGRPRAGGEGGSGKOPR---PDHGALASAKLPAASVAS 242
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 221 APCIMILYLRILYIAKR---SNRGRPRAGGEGGSGKOPR---PDHGALASAKLPAASVAS 257
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 243 AREVNGHKSSTGEKEGETPDTGT-RALPSW---PALPNSG-----QGG 284
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 258 PTTENGGAAGAAR-----TGTAPRPPTTSRTTRAORPRGAGAPLRRGRRRAGA 310
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 285 KEGVGASPEDEAESEEESECEPOAVPVSPASACSPLOQPOGSRVLAATLRGQVLA 344
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 311 EGGAGGADGGAAESGALTSRSRPGGRSLRASSSVFELRRARRASSV----- 362
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 345 GVAIGQGMRRRAOLTREKRTFLVAVIGVFLCMFPFESYSIGATCPKCKVPHGL 404
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 363 -----CRRKVAQAREKRFTEFLAVVIGVFLCMFPFESYSIGATCPKCKVPHGL 413
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 405 FQFFWIGYCNSSLNPIVYITIFNODPRRARLTLR 440
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Mon Feb 9 08:28:47 2004

us-09-692-077d-8.rag

Page 12

Db 414 KFFFWIGYCNSSLNPIVITVENODFRPSPKHLIFR 449

Search completed: February 6, 2004, 18:17:33
Job time : 39.8729 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 18:16:11 ; Search time 14.9498 Seconds
(Without alignments)
1265.095 Million cell updates/sec

Title: US-09-692-077D-8

Perfect score: 2363
Sequence: 1 MDHQDPYSVQATAIAAIR.....QDFRFRRLICRPWTGTAW 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfill1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1626	68.8	330	1 US-08-118-270-20	Sequence 20, Appl
2	1626	68.8	330	5 PCT-US93-08528-20	Sequence 20, Appl
3	1130	47.8	450	1 US-08-194-338-5	Sequence 5, Appl
4	1122	47.5	450	1 US-08-444-734A-8	Sequence 8, Appl
5	1065	45.1	461	1 US-08-194-338-4	Sequence 4, Appl
6	1029	43.5	334	1 US-08-118-270-22	Sequence 22, Appl
7	1029	43.5	334	5 PCT-US93-08528-22	Sequence 22, Appl
8	1027	43.5	358	2 US-08-465-971B-4	Sequence 4, Appl
9	1003	42.4	330	1 US-08-118-270-21	Sequence 21, Appl
10	1003	42.4	330	5 PCT-US93-08528-21	Sequence 21, Appl
11	986.5	41.7	330	1 US-08-118-270-19	Sequence 19, Appl
12	986.5	41.7	330	5 PCT-US93-08528-19	Sequence 19, Appl
13	954	40.4	450	1 US-08-196-989B-11	Sequence 11, Appl
14	954	40.4	450	2 US-08-760-931A-11	Sequence 11, Appl
15	954	40.4	450	2 US-09-225-024-11	Sequence 11, Appl
16	652.5	27.6	601	1 US-07-676-174A-2	Sequence 2, Appl
17	595.5	25.2	415	1 US-08-194-338-10	Sequence 10, Appl
18	593	25.1	467	1 US-08-056-051-6	Sequence 6, Appl
19	593	25.1	467	2 US-07-928-611-22	Sequence 22, Appl
20	593	25.1	467	1 US-08-487-811A-22	Sequence 22, Appl
21	593	25.1	467	3 US-09-060-694-22	Sequence 22, Appl
22	593	25.1	467	4 US-09-378-074-22	Sequence 22, Appl
23	593	25.1	467	5 PCT-US93-07370-22	Sequence 22, Appl
24	589	24.9	515	1 US-08-722-001-25	Sequence 25, Appl
25	588	24.9	419	1 US-08-056-051-4	Sequence 4, Appl
26	588	24.9	419	1 US-07-928-611-20	Sequence 20, Appl
27	588	24.9	419	2 US-08-487-811A-20	Sequence 20, Appl

28	588	24.9	419	3 US-09-060-694-20	Sequence 20, Appl
29	588	24.9	419	5 PCT-US93-07370-20	Sequence 20, Appl
30	588	24.9	419	4 US-09-378-074-20	Sequence 20, Appl
31	587	24.8	517	2 US-08-467-568-10	Sequence 10, Appl
32	587	24.8	517	2 US-09-030-582-10	Sequence 10, Appl
33	586	24.8	515	1 US-08-444-734A-7	Sequence 7, Appl
34	586	24.8	515	2 US-08-406-855A-22	Sequence 22, Appl
35	586	24.8	515	3 US-09-206-899-22	Sequence 22, Appl
36	586	24.8	520	1 US-08-334-698-4	Sequence 4, Appl
37	586	24.8	520	1 US-08-228-932-4	Sequence 4, Appl
38	586	24.8	520	1 US-08-468-939-4	Sequence 4, Appl
39	586	24.8	520	2 US-08-406-855A-4	Sequence 4, Appl
40	586	24.8	520	2 US-08-722-190-4	Sequence 4, Appl
41	586	24.8	520	3 US-08-244-354-4	Sequence 4, Appl
42	586	24.8	520	3 US-09-206-899-4	Sequence 4, Appl
43	586	24.8	520	4 US-09-444-783-4	Sequence 4, Appl
44	586	24.8	520	4 US-09-688-415-4	Sequence 4, Appl
45	586	24.8	520	5 PCT-US95-04203-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-118-270-20
Sequence 20, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-20
Query Match 68.8%; Score 1626; DB 1; Length 330;
Best Local Similarity 73.6%; Pred. No. 1.5e-107;
Matches 321; Conservative 6; Mismatches 3; Indels 106; Gaps 4;
CY 12 TAAIAATFLILFTIRGNLVILAVLTSSLRAPQVLFVSLAADIIVATIIIPSLA 71

Db 1 TAAIAAATFLILFTTIGNALVIAVLTSSRLAPQNLFLVSIADILVATLIIIPSLA 60
Qy 72 NELLGWYFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRALEVNSKRTPRKIC 131
Db 61 NELLGWYFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRALEVNSKRTPRKIC 120
Qy 132 ILLTWLIAAVISLPLIYKGDQGPGRPOCKLNOEAMVYIIASSIGSFAPCLIMTLV 191
Db 121 ILLTWLIAAVISLPLIYKGDQGPGRPOCKLNOEAMVYII-SSIGSFAPCLIMTLV 178
Qy 192 YLRITVLIARSNRGRPAKCGPGQGESKOPRPHGALASAKLPALASVASAEVNGHSK 251
Db 179 YLRITVLIARSNRGRPAKCGPGQGESKOPRPHGALASAKLPALAS- 226
Qy 252 STGEKEGETPEDTGTIRALPPSWALPNSGQCKEGVCASPEDAEEBEEBECEPQA 311
Db 227 - 226
Qy 312 VPVSPASACSPPLQOPQGSRLVLTALRGVILGRGVALIGGQWRRRAQLTREKRTFVLA 371
Db 227 -GRGVGALIGGQWRRRAHVTREKRTFVLA 255
Qy 372 VVIGVFLCWFPPFFSYSGAICPKHCKVPHGLFOFFFMWIGYCNSSLNPVITYTFNODR 431
Db 256 VVIGVFLCWFPPFFSYSGAICPKHCKVPHGLFOFFFMWIGYCNSSLNPVITYTFNODR- 314
Qy 432 RAEFRILCRPWTOTAM 447
Db 315 RAEFRILCRPWTOTAM 330

RESULT 2

PCT-US93-08528-20
Sequence 20, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

PCT-US93-08528-20

Query Match 68.8%; Score 1626; DB 5; Length 330;
Best Local Similarity 73.6%; Pred. No. 1.5e-107;
Matches 321; Conservative 6; Mismatches 3; Indels 106; Gaps 4;

Qy 12 TAAIAAATFLILFTTIGNALVIAVLTSSRLAPQNLFLVSIADILVATLIIIPSLA 71
Db 1 TAAIAAATFLILFTTIGNALVIAVLTSSRLAPQNLFLVSIADILVATLIIIPSLA 60
Qy 72 NELLGWYFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRALEVNSKRTPRKIC 131
Db 61 NELLGWYFRRTWCEVYALADVLFCTSSIVHLCAISLDRYMAVSRALEVNSKRTPRKIC 120
Qy 132 ILLTWLIAAVISLPLIYKGDQGPGRPOCKLNOEAMVYIIASSIGSFAPCLIMTLV 191
Db 121 ILLTWLIAAVISLPLIYKGDQGPGRPOCKLNOEAMVYII-SSIGSFAPCLIMTLV 178
Qy 192 YLRITVLIARSNRGRPAKCGPGQGESKOPRPHGALASAKLPALASVASAEVNGHSK 251
Db 179 YLRITVLIARSNRGRPAKCGPGQGESKOPRPHGALASAKLPALAS- 226
Qy 252 STGEKEGETPEDTGTIRALPPSWALPNSGQCKEGVCASPEDAEEBEEBECEPQA 311
Db 227 - 226
Qy 312 VPVSPASACSPPLQOPQGSRLVLTALRGVILGRGVALIGGQWRRRAQLTREKRTFVLA 371
Db 227 -GRGVGALIGGQWRRRAHVTREKRTFVLA 255
Qy 372 VVIGVFLCWFPPFFSYSGAICPKHCKVPHGLFOFFFMWIGYCNSSLNPVITYTFNODR 431
Db 256 VVIGVFLCWFPPFFSYSGAICPKHCKVPHGLFOFFFMWIGYCNSSLNPVITYTFNODR- 314
Qy 432 RAEFRILCRPWTOTAM 447
Db 315 RAEFRILCRPWTOTAM 330

RESULT 3

US-08-194-338-5
Sequence 5, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH01.001DV1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-194-338-5

Query Match 47.8%; Score 1130; DB 1; Length 450;
Best Local Similarity 53.2%; Pred. No. 2e-72;
Matches 243; Conservative 52; Mismatches 100; Indels 62; Gaps 13;

QY 6 PYSVQATPAIAAATLFTLFTFGNALVITAVTSRSIRAPQNTFLVSLAADIIVATLI 65
DB 27 PYSIQVTLTVCLAGLMLTLVFGNVLYITAVTSRALKAPQNTFLVSLAADIIVATLV 86
QY 66 IPFSLANELGYWFRRTWCSEVYALDVLCTSSIVHCAISDRYVAVSRALEYNSKRT 125
DB 87 IPFSLANENVGWYFGKTWCSEIYALDVLCTSSIVHCAISDRYWSITQAIETYNLKT 146
QY 126 PRRIKIIITVWLIAAVISLPLI---YKDGQPGPRGRPOCKLNOEAWYILASISGSF 181
DB 147 PRRIKALITVWVISAVISFPLISIEKGGGGGPGP-AEPRCEINDOKWYVLSCTIGSF 205
QY 182 PAPCLIMILVYLRITLYIAKR-----SNRGRPRAGGPGQGESKQPR---PDHGALASAK 233
DB 206 PAPCLIMILVYLRITLYIAKRTRVPSRRGPDVAAPGCTERRPGLGERSAGPGGAE 265
QY 234 LPALASVASAREVNGHSGKSTGEKEGETPEDTGTALPSPWALPNSGQGEVCGASP 293
DB 266 AEPLPT-----QING--APGEPPA-GRDITDALDEES-----SS 298
QY 294 EDEAE-----EEEBEECEPOAVPSPASCPPLQOPGSRVATLARGVLTGRGV 346
DB 299 SDHAERPPGRRPRGRGKAPASQVKGDSLRGARGRRS-----GRLLQGRGR 351
QY 347 GATGGQWRRRAQL---TREKRTFVLAVYIGVFLCMFPFFSYSIGALCPKHKCYPHG 403
DB 352 SASGLP--RRRAGAGGQGNREKRTFVLAVYIGVFLCMFPFFSYSITLTAV---GCSVPR 406
QY 404 LPOFFEWIGYCNSSLNPVITYITFNQDPRAPRILCR 440
DB 407 LKFFFWFGYCNSSLNPVITYITFNHDFRRAFKILCR 443

RESULT 4
US-08-444-734A-8
Sequence 8, Application US/08444734A
Patent No. 5610282
GENERAL INFORMATION:
APPLICANT: Sibley, David R.
APPLICANT: Monema, Frederick J.
APPLICANT: Mahan, Lawrence C.
APPLICANT: McVittie, Loris D.
TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and
TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobe, Marcens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,734A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,917
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/548,714
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH065.001FWL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-444-734A-8

Query Match 47.5%; Score 1122; DB 1; Length 450;
Best Local Similarity 52.7%; Pred. No. 7.5e-72;
Matches 241; Conservative 53; Mismatches 101; Indels 62; Gaps 13;

QY 6 PYSVQATPAIAAATLFTLFTFGNALVITAVTSRSIRAPQNTFLVSLAADIIVATLI 65
DB 27 PYSIQVTLTVCLAGLMLTLVFGNVLYITAVTSRALKAPQNTFLVSLAADIIVATLV 86
QY 66 IPFSLANELGYWFRRTWCSEVYALDVLCTSSIVHCAISDRYVAVSRALEYNSKRT 125
DB 87 IPFSLANENVGWYFGKTWCSEIYALDVLCTSSIVHCAISDRYWSITQAIETYNLKT 146
QY 126 PRRIKIIITVWLIAAVISLPLI---YKDGQPGPRGRPOCKLNOEAWYILASISGSF 181
DB 147 PRRIKALITVWVISAVISFPLISIEKGGGGGPGP-AEPRCEINDOKWYVLSCTIGSF 205
QY 182 PAPCLIMILVYLRITLYIAKR-----SNRGRPRAGGPGQGESKQPR---PDHGALASAK 233
DB 206 PAPCLIMILVYLRITLYIAKRTRVPSRRGPDVAAPGCTERRPGLGERSAGPGGAE 265
QY 234 LPALASVASAREVNGHSGKSTGEKEGETPEDTGTALPSPWALPNSGQGEVCGASP 293
DB 266 AEPLPT-----QING--APGEPPA-GRDITDALDEES-----SS 298
QY 294 EDEAE-----EEEBEECEPOAVPSPASCPPLQOPGSRVATLARGVLTGRGV 346
DB 299 SDHAERPPGRRPRGRGKAPASQVKGDSLRGARGRRS-----GRLLQGRGR 351
QY 347 GATGGQWRRRAQL---TREKRTFVLAVYIGVFLCMFPFFSYSIGALCPKHKCYPHG 403
DB 352 SASGLP--RRRAGAGGQGNREKRTFVLAVYIGVFLCMFPFFSYSITLTAV---GCSVPR 406
QY 404 LPOFFEWIGYCNSSLNPVITYITFNQDPRAPRILCR 440
DB 407 LKFFFWFGYCNSSLNPVITYITFNHDFRRAFKILCR 443

RESULT 5
US-08-194-338-4
Sequence 4, Application US/08194338

Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-194-338-4

Query Match 45.1%; Score 1065; DB 1; Length 461;
Best Local Similarity 51.6%; Pred. No. 8.1e-68;
Matches 236; Conservative 43; Mismatches 106; Indels 72; Gaps 12;

QY 7 YSVQATAAIAAIFLLIFITFGNALVLAIVTSRSLAPONLFLVSLAADIIVATLII 66
DB 46 YSAGVAGIAAVGLIVFTVGNLVIAVITSRALAPONLFLVSLAADIIVATLII 105
QY 67 PPSLANELIGWYFRTWCEVLAIDLVECTSSIVHLCAISIDRWAVSRALVNSKRT 126
DB 106 PPSLANELMAWYFRTWCEVLAIDLVECTSSIVHLCAISIDRWAVSRALVNSKRT 165
QY 127 RRIKCIITVWLIAVLSLPLI--YKGDQGPORGR--POCKLQEAAYIIASISGSPF 182
DB 166 RRVKATIAVWVLSAVISPPVLSLX--QPDGAAYVQCGLNDEFTWIISSCIQSF 220
QY 183 APCIMILIVLRIYLAIAKSNRGRPRAGKGGPQGGESKQPRPHGALASAKLPALASV 242
DB 221 APCIMILIVLRIYLAIAKSNRGRPRAGKGGPQGGESKQPRPHGALASAKLPALASV 257
QY 243 AREVNGHSKSTGEKEGETPEDTGT-RALPESMAL-----PNSG-----OGQ 284
DB 258 PTTENGIGLAAAGEAR-----TGARPRPTWATRAAQRGAPRLRGRRRGA 310
QY 285 KEGVAGSPEDAE 343
DB 311 EGGAGAG-----DGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357

QY 344 RGVGALGGQWRRRAQITREKFTVLAIVGVFLCWPEFFFSYSIGALCPKRCVPHG 403
DB 358 RRRRASSVCRRAVQ-AEKRTFTVLAIVGVFLCWPEFFFTYSIGICRACQVGP 416
QY 404 LPOFFWIGYCNSSINPVYITINQDPRRAFRIILCR 440
DB 417 LKFFFWIGYCNSSINPVYITINQDPRRAFRIILCR 453

RESULT 6
US-08-118-270-22
Sequence 22, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-22

Query Match 43.5%; Score 1029; DB 1; Length 334;
Best Local Similarity 47.6%; Pred. No. 2e-65;
Matches 210; Conservative 46; Mismatches 59; Indels 126; Gaps 8;

QY 12 TAAIAAIFLLIFITFGNALVLAIVTSRSLAPONLFLVSLAADIIVATLII 71
DB 1 TLTVICIAGLIMLFTVGNLVIAVITSRALAPONLFLVSLAADIIVATLII 60
QY 72 NELLGMYFRTWCEVLAIDLVECTSSIVHLCAISIDRWAVSRALVNSKRTPRIK 131
DB 61 NEVM-YWFGKWEIEVLAIDLVECTSSIVHLCAISIDRWAVSRALVNSKRTPRIK 119
QY 132 IITVWLIAVLSLPLIY-----KGDQGPORGRPOCKLQEAAYIIASISGSPFAPCLI 187
DB 120 IITVWVIAVLSAVISPPILISIEKKAGAGGQAPAPSCKINDQKYYVSSISGSPFAPCLI 179
QY 188 MILVYLRILYIAK-----SNRGRPRAGKGGPQGGESKQPR--PDHGALASAKLPALAS 239
DB 180 NMLVYVRIYQIAKRTVVPERRGPDACAPGADRRPNAVGBRGAGTA----- 230

QY	240	VASAEVNGHSGXSTGEKEGEPTPTGTRALPPSWALLPNSQOGKEGVGASPEDEAE	299
Db	231	-----GGGEE-----	236
QY	300	EEEEEECEPOAVPVSPASACSPPLQOPQSGHVLTATLRQVILGRGVGAIGQMMRRRAQ	359
Db	237	-----PAGGAKASRM---RGR	249
QY	360	LTRERKFEVLAVVIGVFLVLCWPEPFPSYSLGACPKHGVPHGLFQPFWMIGYCNSSIN	419
Db	250	ONREKRFFVLAIVGVFVVCWCFPPFFTYTLIAV--GCPVEYOLNFNPFPMFGYCNSSIN	306
QY	420	PVIYTIENQDFRRARFRIICR 440	
Db	307	PVIYTIENHDFRRARFKILCR 327	
RESULT 7			
PCT-US93-08528-22			
Sequence 22, Application PC/TUS9308528			
GENERAL INFORMATION:			
APPLICANT: New York University			
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN			
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF			
NUMBER OF SEQUENCES: 348			
CORRESPONDENCE ADDRESS:			
ADDRESS: BROWDY AND NEIMARK			
STREET: 419 Seventh Street, N.W., Suite 300			
CITY: Washington			
STATE: D.C.			
COUNTRY: USA			
ZIP: 20004			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: PCT/US93/08528			
FILING DATE: 09-SEP-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/943,236			
FILING DATE: 10-SEP-1992			
ATTORNEY/AGENT INFORMATION:			
NAME: Townsend, Kevin G.			
REGISTRATION NUMBER: 34,033			
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 202-628-5197			
TELEFAX: 202-737-3528			
TELEX: 248633			
INFORMATION FOR SEQ ID NO: 22:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 334 amino acids			
TYPE: amino acid			
STRADEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: peptide			
PCT-US93-08528-22			
Query Match			
Best Local Similarity 43.5%, Score 1029, DB 5, Length 334,			
Best Local Similarity 47.6%, Pred. No. 26-65,			
Matches 210, Conservative 46, Mismatches 59, Indels 126, Gaps			
QY	12	TAAIAAATPILFTFGNALVITLTSRSIRAFONFLVSLAADIIVATILIPFSLA	71
Db	1	TLTLVCIAGLIMLTFVFGNVLYITAVFTRALKAPQNFVLSIASADIVATVIVPFSLA	60
QY	72	NELGIVYFRRTWCVCVIALDVLFTCTSSIVHCAISLDRYAVASRLERNSKTRPRRIIC	131
Db	61	NEVW-YWFGKWCISYLAIDVLFTCTSSIVHCAISLDRYWSITQAIENNLKTRPRRIA	119

QY	132	ILITWMLAAVSLPLEPLY----	KDDQGPQPRGRPOCKNOEWMYLIASSISGFAPCL	187		
Db	120	ILITWMLAAVSLPLEPLISIKKAGGGQQAEBECKINDOKMYI	ISSISGFAPCL	179		
QY	188	MILVYLRIYLIAR-----	SNRGRPAKGPQGESKOPR-----	PDHGALASAKLPALAS	239	
Db	180	NHLVYVRIYQLAKRTRVPSPSRPGDACA	PGAGDRRNAVGPBKAGTA-----		230	
QY	240	VASAEVNGHSHKSTGEKEGETPEBDTGTRAL	PPSMALPNSGGQKGEVCGASPEDEAE		239	
Db	231	-----	GGQGE-----		236	
QY	300	EEEEEECEPQAVPVPSPASACSP	LQPGGSRLATLRQVLLRGVGAIGQWMRRRAQ		355	
Db	237	-----	-----	RAGAKASRW-----	RGR	249
QY	360	LTRERKFTVLAVVIGVFLCMFPFSSYL	GLCPKHCKVPHGLQFPFWIGYCNSSLN		419	
Db	260	QNRERKFTVLAVVIGVFLCMFPF	FTYTLAV--	GCVPYQLNFFPFGYCNSSLN		306
QY	420	PVIYTIENODFERARFRILICR				440
Db	307	PVIYTIENHDDRRAFKILICR				327

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01 RESULT 8
02 US-08-465-971B-4
03 ; Sequence 4, Application US/08465971B
04 ; Patent No. 5942414
05 ; GENERAL INFORMATION:
06 ; APPLICANT: Yi Li and Mark D. Adams
07 ; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
08 ; NUMBER OF SEQUENCES: 10
09 ; CORRESPONDENCE ADDRESSES:
10 ; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
11 ; ADDRESSEE: Cecchi, Stewart & Olstein
12 ; STREET: 6 Becker Farm Road
13 ; CITY: Roseland
14 ; STATE: NJ
15 ; COUNTRY: US
16 ; ZIP: 07068-1739
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Floppy disk
19 ; COMPUTER: IBM PC compatible
20 ; OPERATING SYSTEM: PC-DOS/MS-DOS
21 ; SOFTWARE: Wordperfect 5.1
22 ; CURRENT APPLICATION DATA:
23 ; APPLICATION NUMBER: US/08/465,971B
24 ; FILING DATE: 06-JUN-1995
25 ; CLASSIFICATION: 536
26 ; ATTORNEY/AGENT INFORMATION:
27 ; NAME: MULLINS, J.G.
28 ; REGISTRATION NUMBER: 33073
29 ; REFERENCE/DOCKET NUMBER: 325800-453 (PFI87)
30 ; TELECOMMUNICATION INFORMATION:
31 ; TELEPHONE: 201-994-1700
32 ; TELEFAX: 201-994-1744
33 ; INFORMATION FOR SEQ ID NO: 4:
34 ; SEQUENCE CHARACTERISTICS:
35 ; LENGTH: 358 amino acids
36 ; TYPE: amino acid
37 ; STRANDEDNESS: not relevant
38 ; TOPOLOGY: not relevant
39 ; MOLECULE TYPE: protein
40 ; US-08-465-971B-4
41
42 Query Match 43.5%; Score 1027; DB 2; Length 358;
43 Best Local Similarity 48.8%; Pred. No. 3e-65;
44 Matches 218; Conservative 39; Mismatches 56; Indels 134; Gaps 10;
45
46 6 PYSVQATPAIAAATFLILFTIFGNAIYLAVLTSSRSIRAQONFLV-SLAADIIV-- 62
47 PYSIQVTLITCLAGLMLTLTVFGNVAVITAVFTSRALKAQONFLVXYSASDILVXXX 86

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QY 63 TLIIPESLANELLGYWFRRTWCCEVYLADVLCTSTIVHCAISLDRYMAVSRALEYN 122
 DB 87 TLIVFISLANEWMGMYFGKAMCEIYLADVLCTSTIVHCAISLDRYMAVSRALEYN 146
 QY 123 KTRPRRIKIIITWLVIAVSLPPLI-----YKDGOPGPRGRPOCKLNQZAMYLIIAS 176
 DB 147 KTRPRRIKIIITWLVIAVSLPPLI-----YKDGOPGPRGRPOCKLNQZAMYLIIAS 205
 QY 177 SIGSFAPCLIMILVYRIYQIAKRRIVPPSRG-----PDAVAPPGGLQGRGASG 240
 DB 206 CIGSFAPCLIMILVYRIYQIAKRRIVPPSRG-----PDAVAPPGGLQGRGASG 260
 QY 237 LASVASAREVNGHSGKSTGEKEGETPBDTGTRALPPSWALPNSGQKEGVCGASPEDE 296
 DB 241 -----PDAVAPPGGLQGRGASG----- 260
 QY 297 ABEEREEBCEBPQAVPVSPASACSPILQOPGSRVLTATLGRGVALIGGQWRR 356
 DB 261 -----LPRRAGA-GGQ----- 271
 QY 357 RAQLTRERKFTVLAIVGVFLCWPFFESYSLGATCPKCKVPHGLFOFFFTIGYCN 416
 DB 272 -----NREKFTVLAIVGVFLCWPFFFTYTLAV---GCVPRTLKFFFWGYCNS 324
 QY 417 SLNPVITYTFNODFRRAFRRI---LCR 440
 DB 325 SLNPVITYTFNODFRRAFRRI---LCR 351

RESULT 9

US-08-118-270-21
 ; Sequence 21, Application US/08118270
 ; Patent No. 5508384
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Randall B.
 ; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 ; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 ; NUMBER OF SEQUENCES: 348
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/118,270
 ; FILING DATE: 09-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/943,236
 ; FILING DATE: 10-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Townsend, Kevin G.
 ; REGISTRATION NUMBER: 34,033
 ; REFERENCE/DOCKET NUMBER: MURPHY=2A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 330 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-118-270-21

Query Match 42.4%; Score 1003; DB 1; Length 330;
 Best Local Similarity 50.5%; Pred. No. 1,4e-63;
 Matches 214; Conservative 40; Mismatches 48; Indels 122; Gaps 12;

QY 26 TIRGNLVIAVLTNSLRAPQNLFLVLAADIIIVATLIIPESLANELLGYWFRRTWC 85
 DB 13 TIRGNLVIAVLTNSLRAPQNLFLVLAADIIIVATLIIPESLANELLGYWFRRTWC 71
 QY 86 EYIALDVLCTSTIVHCAISLDRYMAVSRALEYNKTRPRRIKIIITWLVIAVSL 145
 DB 72 EYIALDVLCTSTIVHCAISLDRYMAVSRALEYNKTRPRRIKIIITWLVIAVSL 131
 QY 146 PPLI-----YKDGOPGPRGRPOCKLNQZAMYLIIASIGSFAPCLIMILVYRIYIAK 201
 DB 132 PPLISIEKKGGGGGPPQ-APRCEINDQWYVYSSCIGSFAPCLIM-LVYVRIYIYIAK 189
 QY 202 -----SNRGPRAKGGPGGSGSKPRPDHGALASAKLPALASVASAREVNGHSGKSTGEK 256
 DB 190 RTVPPSRDPPDAVAPPGTERP-----NG----- 216
 QY 257 EREGTEPDTGTRALPPSWALPNSGQKEGVCGASPEDEABEEREEBCEBPQAVPSP 316
 DB 217 -----LGPERSAGPGGGR----- 231
 QY 317 ASACSPILQOPGSRVLTATLGRGVALIGGQWRRRAQLTRERKFTVLAIVGV 376
 DB 232 -SASGLP-----RRRAGA-GGQ-----NREKFTVIAVIGV 262
 QY 377 FVLCWPFPPFFSYSLGATCPKCKVPHGLFOFFFWGYCNSLNVPVITYTFNODFRAPR 436
 DB 263 FVLCWPFPPFFFTYTLAVL---GCVPRTLKFFFWGYCNSLNVPVITYTFNODFRAPR 319

RESULT 10

PCT-US93-08528-21
 ; Sequence 21, Application PC/TUS9308528
 ; GENERAL INFORMATION:
 ; APPLICANT: New York University
 ; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 ; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 ; NUMBER OF SEQUENCES: 348
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/08528
 ; FILING DATE: 09-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/943,236
 ; FILING DATE: 10-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Townsend, Kevin G.
 ; REGISTRATION NUMBER: 34,033
 ; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633

```

: INFORMATION FOR SEQ ID NO: 21:
:
: SEQUENCE CHARACTERISTICS:
:
:   LENGTH: 330 amino acids
:
:   TYPE: amino acid
:
:   STRANDEDNESS: single
:
:   TOPOLOGY: linear
:
:   MOLECULE TYPE: peptide
:
: PCT-US93-08528-21

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Query Match	42.4%	Score 1003	DB 5	Length 330
Best Local Similarity	50.5%	Pred No. 1.4e-63		
Matches 214	Conservative 40	Mismatches 48	Indels 122	Gaps 12

Qy	26	TIFGAAVYIATLVATRSRAPONLPLVLSAADIVATLIIFFSLANELIGWYFRRTWC	85
Db	13	TVFGVAVYIIAVTFSRALKAPONLPLVLSAADIVATLVIFPFSLANEVNGYTFGK-WC	71
Qy	86	EVYIALDVLFTCTSIYHLCAISLDERYMAVSRLAEYNSKRTPRRIKIIITWLIAAVISL	145
Db	72	EIYIALDVLFTCTSIYHLCAISLDERYMAVSITQAIENLAKTTPRIKAIITTVWIAVISF	131
Qy	146	PLII-----YKDGQGPGRGPOCKTNGEAWMYLASSISGFAPCLIMLVYRIYLIAR	201
Db	132	PLLIISIEKKGGGGGQOP-AEPRCEIENDQKMYVTSISGTSFFAPCLIM-LVYVRIYQIAR	189
Qy	202	-----SNRGPRAKGPGCGESKQRPDPHGALASAKLPALASVASAREVNGSHKSTGEK	256
Db	190	RTRVPSRRDDPAVAAPPGCTERR-----NG-----	216
Qy	257	EEGTEPBDTGTRALPPSWAALPLNSGOGQKEGVCGASPEDEAESEEEBEECEPOAVPSP	316
Db	217	-----LQPERASAGPGGGRG-----	231
Qy	317	ASACSPPIQOPQGSRVLATLNGQVLLGRGVGAIGGQWMMRRAQLTREKKEFTVLAVLIGV	376
Db	232	-SASGLP-----RRRAAG-GGQ-----NREKKEFTVIAVIGV	262
Qy	377	FVLCMFPPEFFSYSLGAIQPKHCKVPHGLFOPEFFWIGYCNSSLNPIYITIENODFRAAFER	436
Db	263	FVVCWFPPEFFTYTLTAVAL---CSVDRLEFKPEFFMGYCNSSLNPIYITIFNHDFFRAAFK	319
Qy	437	ILCR 440	
Db	320	ILCR 323	

RESULT 11
 US-08-118--270-19
 Sequence 19, Application US/08118270
 Patent No. 5508384
 GENERAL INFORMATION:
 APPLICANT: Murphy, Randall B.
 APPLICANT: Schuster, David I.
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 City: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/118,270
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236

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: FILING DATE: 10-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Townsend, Kevin G.
: REGISTRATION NUMBER: 34,033
: REFERENCE/DOCKET NUMBER: MURPHY=2A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 330 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-118-270-19

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Query Match	41.7%;	Score 986.5;	DB 1;	Length 330;
Best Local Similarity	48.6%;	Pred. No. 2e-62;		
Matches 210; Conservative	41;	Mismatches	66;	Gaps 9;

[illegible]

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RESULT 12
PCT-US93-08528-19
: Sequence 19, Application PC/TUS9308528
: GENERAL INFORMATION:
: APPLICANT: New York University
: TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
: TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
: NUMBER OF SEQUENCES: 348
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
:

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-19

Query Match 41.7%; Score 986.5; DB 5; Length 330;
Best Local Similarity 48.6%; Pred. No. 28-62;
Matches 210; Conservative 41; Mismatches 66; Indels 115; Gaps 9;

QY 13 AIAIAITFLITFTFGNALVILAVLTSRLAPONTPLVLSAADIIVATLIPESIAN 72
DB 2 AIAIAITFLITFTFGNALVILAVLTSRLAPONTPLVLSAADIIVATLIPESIAN 61
QY 73 ELGLGYWYFRTWCEYVLAIDVLFCTSSIVHLCALISLDRYMAVSRALEYSKRTPRIKCI 132
DB 62 EIM-TWYEGQWCGYVLAIDVLFCTSSIVHLCALISLDRYMAVSRALEYSKRTPRIKAT 120
QY 133 ILTWLILAVISLPLI--YKGDQGPQPRGR--POCKINOEWYILASSIGSPAPCLIM 188
DB 121 IVAWVLISAVISFPLVLSLYR-----OPDGAAPQCGINDETWYILASSIGSPAPCLIT 175
QY 189 ILVYRIYILAKSRGRPRAKGPGQGSKOPRPHDGGALASAKLPALASVAREVNG 248
DB 176 LLVYRIYIRVAKRR-----TISEKRAVPGPDGASPTTENG 212
QY 249 HSKSTGEKEGFTPDGTTRALPESWALPNSGQOGKGVGASPEDAESEEESECE 308
DB 213 LGAAAGEAR-----TGT-----ARFLRRRRARRSSVC----- 239
QY 309 PQAVVSPASACSPPLQOPQGSRLVATLRGOVLGRGVGALIGQWRRRAOLTEKRTFP 368
DB 240 -----RRKVAQAAREKRTFP 253
QY 369 VLAIVIGVFLCWPFFPSYSIGALCPGHCKVPHGLFOFFPMIGYCNSSINPVYITFNO 428
DB 254 VLAIVIGVFLCWPFFPSYSIGALCPGHCKVPHGLFOFFPMIGYCNSSINPVYITFNO 428
QY 429 DEPRARFRIILR 440
DB 311 DFRSFKHILFR 322

RESULT 13
US-08-196-989B-11
Sequence 11, Application US/08196989B
Patent No. 5583476
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-196-989B-11

Query Match 40.4%; Score 954; DB 1; Length 450;
Best Local Similarity 46.1%; Pred. No. 5,48-60;
Matches 202; Conservative 37; Mismatches 173; Indels 26; Gaps 4;

QY 6 PYVQATAAIAITFLITFTFGNALVILAVLTSRLAPONTPLVLSAADIIVATLIPESIAN 65
DB 27 PYVQATAAIAITFLITFTFGNALVILAVLTSRLAPONTPLVLSAADIIVATLIPESIAN 86
QY 66 IPFSLANELLGWYFRTWCEYVLAIDVLFCTSSIVHLCALISLDRYMAVSRALEYSKRT 125
DB 87 IPFSLANELLGWYFRTWCEYVLAIDVLFCTSSIVHLCALISLDRYMAVSRALEYSKRT 146
QY 126 PRIRKCIILTWLILAVISLPLI--YKGDQGPQPRGR--POCKINOEWYILASSIGSP 181
DB 147 PRIRKCIILTWLILAVISLPLI--YKGDQGPQPRGR--POCKINOEWYILASSIGSP 205
QY 182 FAPCLIMILVYRIYILAKSRGRPRAKGPGQGSKOPRPHDGGALASAKLPALASVA 241
DB 206 FAPCLIMILVYRIYILAKSRGRPRAKGPGQGSKOPRPHDGGALASAKLPALASVA 247
QY 242 SAREVNGHSGTGEKEGFTPDGTTRALPESWALPNSGQOGKGVGASPEDAESEEE 301
DB 248 XXX 307
QY 302 EEEBEEBPAVSPASACSPPLQOPQGSRLVATLRGOVLGRGVGALIGQWRRRAOLTE 361
DB 308 XXX 367
QY 362 REKRTFVLAIVIGVFLCWPFFPSYSIGALCPGHCKVPHGLFOFFPMIGYCNSSINPV 421
DB 368 REKRTFVLAIVIGVFLCWPFFPSYSIGALCPGHCKVPHGLFOFFPMIGYCNSSINPV 424
QY 422 IYTFNODPRARFRIILC 439
DB 425 IYTFNODPRARFRIILC 442

RESULT 14
US-08-760-936-11
Sequence 11, Application US/08760936
Patent No. 5856443
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John

Qy	362	REKRFTVLA	VIGVFLCWFPPFPSSY	SGAICPHCKVPHGLFQFPFWIGY	CNSLNPV	421
Db	368	REKRFTVLA	VIGVFLCWFPPFPSSY	SGAICPHCKVPHGLFQFPFWIGY	CNSLNPV	424
Qy	422	IVTIFNOD	FRRAFKKILC			439
Db	425	IVTIFNOD	FRRAFKKILC			442

Search completed: February 6, 2004, 18:20:53
Job time : 16.9498 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 6, 2004, 18:17:36 ; Search time 29.8997 Seconds
(without alignments)
3130.265 Million cell updates/sec

Title: US-09-692-077d-8
Perfect score: 2363
Sequence: 1 MDHQDPYSVQATRAIAAIR.....QDFRAFRRLCRPTQTAW 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2363	100.0	447	9	US-09-825-923-2
2	2363	100.0	447	15	US-10-077-870-2
3	2363	100.0	447	15	US-10-001-073-8
4	2351.5	99.5	450	9	US-09-825-923-4
5	2351.5	99.5	450	15	US-10-077-870-4
6	2351.5	99.5	450	15	US-10-001-073-7
7	2343.5	99.2	450	15	US-10-825-567A-42
8	1126	47.7	450	15	US-10-001-073-27
9	1124	47.6	450	15	US-10-001-073-26
10	1117	47.3	450	15	US-10-825-567A-40
11	1080	45.7	461	15	US-10-225-567A-44
12	1073.5	45.4	458	15	US-10-001-073-46
13	1071.5	45.3	462	15	US-10-001-073-44
14	960.5	40.6	307	15	US-10-060-795B-4
15	652.5	27.6	601	9	US-09-782-980-84

16	652.5	27.6	601	10	US-09-884-430-8	Sequence 8, Appl1
17	652.5	27.6	601	15	US-10-336-489-8	Sequence 8, Appl1
18	599	25.3	467	15	US-10-225-567A-106	Sequence 106, App
19	593	25.1	419	12	US-10-292-798-460	Sequence 460, App
20	593	25.1	467	15	US-10-224-260-22	Sequence 22, Appl1
21	590.5	25.0	415	15	US-10-060-795B-2	Sequence 2, Appl1
22	588	24.9	419	15	US-10-224-260-20	Sequence 20, Appl1
23	587	24.8	462	12	US-10-017-161-754	Sequence 754, App
24	587	24.8	517	10	US-09-951-622-10	Sequence 10, Appl1
25	587	24.8	517	15	US-10-325-930-10	Sequence 10, Appl1
26	586	24.8	497	14	US-10-052-589-2	Sequence 2, Appl1
27	586	24.8	520	15	US-10-185-991-4	Sequence 4, Appl1
28	586	24.8	520	15	US-10-338-129-4	Sequence 4, Appl1
29	586	24.8	520	15	US-10-238-667-4	Sequence 4, Appl1
30	586	24.8	520	15	US-10-225-567A-36	Sequence 36, Appl1
31	585	24.8	515	15	US-10-338-129-10	Sequence 10, Appl1
32	585	24.8	515	15	US-10-338-667-10	Sequence 10, Appl1
33	584	24.7	421	11	US-09-992-238-10	Sequence 10, Appl1
34	582.5	24.7	443	12	US-10-352-684A-2	Sequence 2, Appl1
35	582.5	24.7	443	15	US-10-060-795B-11	Sequence 11, Appl1
36	582.5	24.7	443	15	US-10-157-031-78	Sequence 78, Appl1
37	582.5	24.7	443	15	US-10-225-567A-102	Sequence 102, App
38	582.5	24.7	443	12	US-10-292-798-658	Sequence 658, App
39	581	24.6	515	15	US-10-054-616A-2	Sequence 2, Appl1
40	581	24.6	515	15	US-10-054-616A-4	Sequence 4, Appl1
41	581	24.6	515	15	US-10-054-616A-5	Sequence 5, Appl1
42	580	24.5	387	15	US-10-241-313-4	Sequence 4, Appl1
43	580	24.5	515	15	US-10-054-616A-3	Sequence 3, Appl1
44	579	24.5	560	15	US-10-238-129-8	Sequence 8, Appl1
45	579	24.5	560	15	US-10-238-667-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-09-825-923-2
Sequence 2, Application US/09825923
Patent No. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Kartonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuomala, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Nyyss'nen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Kaahonen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 447
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-923-2
Query Match 100.0%; Score 2363; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 2, 7e-166;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDHDPYSVQATATAAATAATFLLFTIFGNALVITLRSRLRAPQNLFLVSLAAADIL 60
DB 1 MDHDPYSVQATATAAATAATFLLFTIFGNALVITLRSRLRAPQNLFLVSLAAADIL 60
QY 61 VATLIIIPSLANELLGYWYFRRTWCEVYALDVLFCTSSIVHLCALSLDRYAVASRALEY 120
DB 61 VATLIIIPSLANELLGYWYFRRTWCEVYALDVLFCTSSIVHLCALSLDRYAVASRALEY 120
QY 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
DB 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
QY 181 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
DB 181 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
QY 241 ASAREVNGHSGKSTGKEGETPEDTGTALPPSMALPNSGGQKGVCGASPEDAEER 300
DB 241 ASAREVNGHSGKSTGKEGETPEDTGTALPPSMALPNSGGQKGVCGASPEDAEER 300
QY 301 EEEBEECEPOAVPVPASACSPPLQOPQGSRLATLRGQVLLGRGVGAIIGQWRRRAQL 360
DB 301 EEEBEECEPOAVPVPASACSPPLQOPQGSRLATLRGQVLLGRGVGAIIGQWRRRAQL 360
QY 361 TREKRTFTVLAVVIGVFLCWPFPPFSYSLGALCPKCKVPHGLQFPFFWIGYCNSSLNP 420
DB 361 TREKRTFTVLAVVIGVFLCWPFPPFSYSLGALCPKCKVPHGLQFPFFWIGYCNSSLNP 420
QY 421 VIYTFINQDFRRAFRRIICRPMTOTAM 447
DB 421 VIYTFINQDFRRAFRRIICRPMTOTAM 447

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RESULT 2

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US-10-077-870-2
; Sequence 2, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salomon, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 3.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo. sapiens
US-10-077-870-2

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Query Match 100.0%; Score 2363; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 2,7e-166;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDHDPYSVQATATAAATAATFLLFTIFGNALVITLRSRLRAPQNLFLVSLAAADIL 60
DB 1 MDHDPYSVQATATAAATAATFLLFTIFGNALVITLRSRLRAPQNLFLVSLAAADIL 60
QY 61 VATLIIIPSLANELLGYWYFRRTWCEVYALDVLFCTSSIVHLCALSLDRYAVASRALEY 120
DB 61 VATLIIIPSLANELLGYWYFRRTWCEVYALDVLFCTSSIVHLCALSLDRYAVASRALEY 120
QY 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
DB 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
QY 181 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
DB 181 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
QY 241 ASAREVNGHSGKSTGKEGETPEDTGTALPPSMALPNSGGQKGVCGASPEDAEER 300
DB 241 ASAREVNGHSGKSTGKEGETPEDTGTALPPSMALPNSGGQKGVCGASPEDAEER 300
QY 301 EEEBEECEPOAVPVPASACSPPLQOPQGSRLATLRGQVLLGRGVGAIIGQWRRRAQL 360
DB 301 EEEBEECEPOAVPVPASACSPPLQOPQGSRLATLRGQVLLGRGVGAIIGQWRRRAQL 360
QY 361 TREKRTFTVLAVVIGVFLCWPFPPFSYSLGALCPKCKVPHGLQFPFFWIGYCNSSLNP 420
DB 361 TREKRTFTVLAVVIGVFLCWPFPPFSYSLGALCPKCKVPHGLQFPFFWIGYCNSSLNP 420
QY 421 VIYTFINQDFRRAFRRIICRPMTOTAM 447
DB 421 VIYTFINQDFRRAFRRIICRPMTOTAM 447

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QY 241 ASAREVNGHSGKSTGKEGETPEDTGTALPPSMALPNSGGQKGVCGASPEDAEER 300
DB 241 ASAREVNGHSGKSTGKEGETPEDTGTALPPSMALPNSGGQKGVCGASPEDAEER 300
QY 301 EEEBEECEPOAVPVPASACSPPLQOPQGSRLATLRGQVLLGRGVGAIIGQWRRRAQL 360
DB 301 EEEBEECEPOAVPVPASACSPPLQOPQGSRLATLRGQVLLGRGVGAIIGQWRRRAQL 360
QY 361 TREKRTFTVLAVVIGVFLCWPFPPFSYSLGALCPKCKVPHGLQFPFFWIGYCNSSLNP 420
DB 361 TREKRTFTVLAVVIGVFLCWPFPPFSYSLGALCPKCKVPHGLQFPFFWIGYCNSSLNP 420
QY 421 VIYTFINQDFRRAFRRIICRPMTOTAM 447
DB 421 VIYTFINQDFRRAFRRIICRPMTOTAM 447

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RESULT 3

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US-10-001-073-8
; Sequence 8, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-073-8

```

```

Query Match 100.0%; Score 2363; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 2,7e-166;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDHDPYSVQATATAAATAATFLLFTIFGNALVITLRSRLRAPQNLFLVSLAAADIL 60
DB 1 MDHDPYSVQATATAAATAATFLLFTIFGNALVITLRSRLRAPQNLFLVSLAAADIL 60
QY 61 VATLIIIPSLANELLGYWYFRRTWCEVYALDVLFCTSSIVHLCALSLDRYAVASRALEY 120
DB 61 VATLIIIPSLANELLGYWYFRRTWCEVYALDVLFCTSSIVHLCALSLDRYAVASRALEY 120
QY 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
DB 121 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
QY 181 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
DB 181 NSKRTPRRIKCIITLTVMLIAAVISLPLIYKGDQGPQGRPOCKLNOEAWYTLASSIGS 180
QY 241 ASAREVNGHSGKSTGKEGETPEDTGTALPPSMALPNSGGQKGVCGASPEDAEER 300
DB 241 ASAREVNGHSGKSTGKEGETPEDTGTALPPSMALPNSGGQKGVCGASPEDAEER 300
QY 301 EEEBEECEPOAVPVPASACSPPLQOPQGSRLATLRGQVLLGRGVGAIIGQWRRRAQL 360
DB 301 EEEBEECEPOAVPVPASACSPPLQOPQGSRLATLRGQVLLGRGVGAIIGQWRRRAQL 360
QY 361 TREKRTFTVLAVVIGVFLCWPFPPFSYSLGALCPKCKVPHGLQFPFFWIGYCNSSLNP 420
DB 361 TREKRTFTVLAVVIGVFLCWPFPPFSYSLGALCPKCKVPHGLQFPFFWIGYCNSSLNP 420
QY 421 VIYTFINQDFRRAFRRIICRPMTOTAM 447
DB 421 VIYTFINQDFRRAFRRIICRPMTOTAM 447

```

RESULT 4
US-09-825-923-4
; Sequence 4, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Myrnes, Kjetil
; APPLICANT: Salonen, Ritta
; APPLICANT: Kaunonen, Jussi
; APPLICANT: Valtonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2b-adrenoceptor
; FILE REFERENCE: Alpha-2b-AR variant
; CURRENT APPLICATION NUMBER: US/09/825, 923
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422, 985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-4

Query Match 99.5%; Score 2351.5; DB 9; Length 450;
Best Local Similarity 99.3%; Pred. No. 1.9e-165;
Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 MDHODPYSVQATAIAAATFTLITFTFGNALVTLAVLTSTRSLRAPQNLFLVSLAADI 60
DB 1 MDHODPYSVQATAIAAATFTLITFTFGNALVTLAVLTSTRSLRAPQNLFLVSLAADI 60
QY 61 VATLIIPFSLANELGTYWYFRRTWCEVYALDVLCSTSYVHLCAISLDRYMAVSRALEY 120
DB 61 VATLIIPFSLANELGTYWYFRRTWCEVYALDVLCSTSYVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIILTWLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMVILASSIGS 180
DB 121 NSKRTPRRIKCIILTWLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMVILASSIGS 180
QY 121 NSKRTPRRIKCIILTWLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMVILASSIGS 180
DB 121 NSKRTPRRIKCIILTWLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMVILASSIGS 180
QY 181 PFAPCLIMILVYLRIRYLIARSNRRGPACGPGCGESKOPRPHGALASAKLPALASV 240
DB 181 PFAPCLIMILVYLRIRYLIARSNRRGPACGPGCGESKOPRPHGALASAKLPALASV 240
QY 181 PFAPCLIMILVYLRIRYLIARSNRRGPACGPGCGESKOPRPHGALASAKLPALASV 240
DB 181 PFAPCLIMILVYLRIRYLIARSNRRGPACGPGCGESKOPRPHGALASAKLPALASV 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWAALPNSGQGKEGVCGASPEDEA--- 297
DB 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWAALPNSGQGKEGVCGASPEDEA--- 297
QY 298 EEEEEECEPQAVPVSPASACSPLOQPOGSRVLTALRGQVILGRGVAIGQWMRRR 357
DB 298 EEEEEECEPQAVPVSPASACSPLOQPOGSRVLTALRGQVILGRGVAIGQWMRRR 357
QY 301 EEEEEECEPQAVPVSPASACSPLOQPOGSRVLTALRGQVILGRGVAIGQWMRRR 360
DB 301 EEEEEECEPQAVPVSPASACSPLOQPOGSRVLTALRGQVILGRGVAIGQWMRRR 360
QY 358 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGACPKCKVPHGLFOFFFWIGYCNS 417
DB 358 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGACPKCKVPHGLFOFFFWIGYCNS 417
QY 361 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGACPKCKVPHGLFOFFFWIGYCNS 420
DB 361 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGACPKCKVPHGLFOFFFWIGYCNS 420
QY 418 LNPVIYITIFNODFRARFRRIICRPWTOTAW 447
DB 418 LNPVIYITIFNODFRARFRRIICRPWTOTAW 447
QY 421 LNPVIYITIFNODFRARFRRIICRPWTOTAW 450
DB 421 LNPVIYITIFNODFRARFRRIICRPWTOTAW 450

; Sequence 4, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077, 870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 4
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-4

Query Match 99.5%; Score 2351.5; DB 15; Length 450;
Best Local Similarity 99.3%; Pred. No. 1.9e-165;
Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 MDHODPYSVQATAIAAATFTLITFTFGNALVTLAVLTSTRSLRAPQNLFLVSLAADI 60
DB 1 MDHODPYSVQATAIAAATFTLITFTFGNALVTLAVLTSTRSLRAPQNLFLVSLAADI 60
QY 61 VATLIIPFSLANELGTYWYFRRTWCEVYALDVLCSTSYVHLCAISLDRYMAVSRALEY 120
DB 61 VATLIIPFSLANELGTYWYFRRTWCEVYALDVLCSTSYVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIILTWLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMVILASSIGS 180
DB 121 NSKRTPRRIKCIILTWLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMVILASSIGS 180
QY 121 NSKRTPRRIKCIILTWLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMVILASSIGS 180
DB 121 NSKRTPRRIKCIILTWLIAAVISLPLIYKDGQPOPRGRPOCKLNOEAMVILASSIGS 180
QY 181 PFAPCLIMILVYLRIRYLIARSNRRGPACGPGCGESKOPRPHGALASAKLPALASV 240
DB 181 PFAPCLIMILVYLRIRYLIARSNRRGPACGPGCGESKOPRPHGALASAKLPALASV 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWAALPNSGQGKEGVCGASPEDEA--- 297
DB 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSWAALPNSGQGKEGVCGASPEDEA--- 297
QY 298 EEEEEECEPQAVPVSPASACSPLOQPOGSRVLTALRGQVILGRGVAIGQWMRRR 357
DB 298 EEEEEECEPQAVPVSPASACSPLOQPOGSRVLTALRGQVILGRGVAIGQWMRRR 357
QY 301 EEEEEECEPQAVPVSPASACSPLOQPOGSRVLTALRGQVILGRGVAIGQWMRRR 360
DB 301 EEEEEECEPQAVPVSPASACSPLOQPOGSRVLTALRGQVILGRGVAIGQWMRRR 360
QY 358 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGACPKCKVPHGLFOFFFWIGYCNS 417
DB 358 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGACPKCKVPHGLFOFFFWIGYCNS 417
QY 361 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGACPKCKVPHGLFOFFFWIGYCNS 420
DB 361 AQLTRERKFTFVLAIVGVFLCWFPPFFSYSLGACPKCKVPHGLFOFFFWIGYCNS 420
QY 418 LNPVIYITIFNODFRARFRRIICRPWTOTAW 447
DB 418 LNPVIYITIFNODFRARFRRIICRPWTOTAW 447
QY 421 LNPVIYITIFNODFRARFRRIICRPWTOTAW 450
DB 421 LNPVIYITIFNODFRARFRRIICRPWTOTAW 450

RESULT 6
US-10-001-073-7
; Sequence 7, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001, 073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-073-7

Query Match 99.5%; Score 2351.5; DB 15; Length 450;
Best Local Similarity 99.3%; Pred. No. 1.9e-165;
Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MDHODPYSVOATAAATAITFLFTIFGNALVLAVALTSRSLAPQNLPLVSLAADIL 60
DB 1 MDHODPYSVOATAAATAITFLFTIFGNALVLAVALTSRSLAPQNLPLVSLAADIL 60
QY 61 VATLIIPSLANELLGYWYFRRTWCEVYALDVLCFTSSIVHLCAISLDRYMAVSRALEY 120
DB 61 VATLIIPSLANELLGYWYFRRTWCEVYALDVLCFTSSIVHLCAISLDRYMAVSRALEY 120
QY 121 NSKTRPRRIKICILITWMLIAAVISLPLIYKGDGQPPRRPOCKLNOEMWYLLASISGS 180
DB 121 NSKTRPRRIKICILITWMLIAAVISLPLIYKGDGQPPRRPOCKLNOEMWYLLASISGS 180
QY 121 NSKTRPRRIKICILITWMLIAAVISLPLIYKGDGQPPRRPOCKLNOEMWYLLASISGS 180
DB 121 NSKTRPRRIKICILITWMLIAAVISLPLIYKGDGQPPRRPOCKLNOEMWYLLASISGS 180
QY 181 FFAPLIMILVYLIRIYLIARNSNRGRPRAGKPGQGSKOPRDPHGALASAKLPALASY 240
DB 181 FFAPLIMILVYLIRIYLIARNSNRGRPRAGKPGQGSKOPRDPHGALASAKLPALASY 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSMALPNSGQKQKGVCGASPEDAEER 297
DB 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSMALPNSGQKQKGVCGASPEDAEER 297
QY 298 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRLVATLRGQVLRGVGALIGQWRRR 357
DB 298 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRLVATLRGQVLRGVGALIGQWRRR 357
QY 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRLVATLRGQVLRGVGALIGQWRRR 360
DB 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRLVATLRGQVLRGVGALIGQWRRR 360
QY 358 AQLTRERKFTFVLAIVGVFLCMPPFPFSYSGALCPKHCVPKGLPQFFWIGYCNSS 417
DB 358 AQLTRERKFTFVLAIVGVFLCMPPFPFSYSGALCPKHCVPKGLPQFFWIGYCNSS 417
QY 418 LNPVIYITFNQDRRAFRRLICRPMWTQAM 447
DB 421 LNPVIYITFNQDRRAFRRLICRPMWTQAM 450

RESULT 7
US-10-225-567A-42
Sequence 42; Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-42

Query Match 99.2%; Score 2343.5; DB 15; Length 450;
Best Local Similarity 98.9%; Pred. No. 7.6e-165;
Matches 445; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 MDHODPYSVOATAAATAITFLFTIFGNALVLAVALTSRSLAPQNLPLVSLAADIL 60
DB 1 MDHODPYSVOATAAATAITFLFTIFGNALVLAVALTSRSLAPQNLPLVSLAADIL 60
QY 61 VATLIIPSLANELLGYWYFRRTWCEVYALDVLCFTSSIVHLCAISLDRYMAVSRALEY 120
DB 61 VATLIIPSLANELLGYWYFRRTWCEVYALDVLCFTSSIVHLCAISLDRYMAVSRALEY 120

QY 121 NSKTRPRRIKICILITWMLIAAVISLPLIYKGDGQPPRRPOCKLNOEMWYLLASISGS 180
DB 121 NSKTRPRRIKICILITWMLIAAVISLPLIYKGDGQPPRRPOCKLNOEMWYLLASISGS 180
QY 181 FFAPLIMILVYLIRIYLIARNSNRGRPRAGKPGQGSKOPRDPHGALASAKLPALASY 240
DB 181 FFAPLIMILVYLIRIYLIARNSNRGRPRAGKPGQGSKOPRDPHGALASAKLPALASY 240
QY 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSMALPNSGQKQKGVCGASPEDAEER 297
DB 241 ASAREVNGHSKSTGEKEGETPEDTGTALPPSMALPNSGQKQKGVCGASPEDAEER 297
QY 298 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRLVATLRGQVLRGVGALIGQWRRR 357
DB 298 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRLVATLRGQVLRGVGALIGQWRRR 357
QY 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRLVATLRGQVLRGVGALIGQWRRR 360
DB 301 EEEEEEECEPQAVPVSPASACSPPLQOPQGSRLVATLRGQVLRGVGALIGQWRRR 360
QY 358 AQLTRERKFTFVLAIVGVFLCMPPFPFSYSGALCPKHCVPKGLPQFFWIGYCNSS 417
DB 361 AQLTRERKFTFVLAIVGVFLCMPPFPFSYSGALCPKHCVPKGLPQFFWIGYCNSS 420
QY 418 LNPVIYITFNQDRRAFRRLICRPMWTQAM 447
DB 421 LNPVIYITFNQDRRAFRRLICRPMWTQAM 450

RESULT 8
US-10-001-073-27
Sequence 27; Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-073-27

Query Match 47.7%; Score 1126; DB 15; Length 450;
Best Local Similarity 53.2%; Pred. No. 4.9e-75;
Matches 243; Conservative 50; Mismatches 102; Indels 62; Gaps 14;

QY 6 PYSVOATAAATAITFLFTIFGNALVLAVALTSRSLAPQNLPLVSLAADILVATLI 65
DB 27 PYSVOATAAATAITFLFTIFGNALVLAVALTSRSLAPQNLPLVSLAADILVATLI 65
QY 66 IPFSLANELLGYWYFRRTWCEVYALDVLCFTSSIVHLCAISLDRYMAVSRALEYNSKRT 125
DB 87 IPFSLANELLGYWYFRRTWCEVYALDVLCFTSSIVHLCAISLDRYMAVSRALEYNSKRT 125
QY 126 PPRKICILITWMLIAAVISLPLI-----YKGDGQPPRRPOCKLNOEMWYLLASISGS 181
DB 147 PPRKICILITWMLIAAVISLPLI-----YKGDGQPPRRPOCKLNOEMWYLLASISGS 181
QY 182 FFAPLIMILVYLIRIYLIARNSNRGRPRAGKPGQGSKOPRDPHGALASAKLPALASY 240
DB 206 FFAPLIMILVYLIRIYLIARNSNRGRPRAGKPGQGSKOPRDPHGALASAKLPALASY 240
QY 234 LPALASASAREVNGHSKSTGEKEGETPEDTGTALPPSMALPNSGQKQKGVCGASPEDAEER 293
DB 266 AEPFLP-----QNG-----APGEPAPA-GRDLDALDEES-----SS 298
QY 294 EDAAE-----EEEEEECEPQAVPVSPASACSPPLQOPQGSRLVATLRGQVLRGVGALIGQWRRR 357
DB 299 SDAAEPPGPRRRPRGPRGKGRASQVPGD--SLPRRPG-----ATGIGTAPAGGE 351
QY 346 --VGAIGQWRRRRAQLTRERKFTFVLAIVGVFLCMPPFPFSYSGALCPKHCVPKGL 403

Db 352 ERVGAAKASRRGQ--NREKRFVLAIVGVVCMFPFFFTYTLAV---GCSVPT 406
Qy 404 LPOFFWIGYCNLSLNPVITYITFNQDPRRAFRILCR 440
Db 407 LFKFFWFGYCNLSLNPVITYITFNHDFRRAFKILCR 443

RESULT 9

US-10-001-073-26
; Sequence 26, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCR
; CURRENT APPLICATION NUMBER: US/10/001.073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-073-26

Query Match 47.6%; Score 1124; DB 15; Length 450;
Best Local Similarity 53.2%; Pred. No. 6.9e-75;
Matches 243; Conservative 49; Mismatches 103; Indels 62; Gaps 14;

Qy 6 PYSVQATAAIAAATPFLFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLI 65
Db 27 PYSLOVTLTVCLAGLMLTVFQNVVITAVFTSRALKAPQNLFLVSLASADILVATLV 86
Qy 66 IPFSLANELLGWYFRRTWCEVYIALDVLFTCTSSIVHLCAISLDRYAVASRALFYNSKRT 125
Db 87 IPFSLANENVGWYFGKAWCEIYIALDVLFTCTSSIVHLCAISLDRYAVSITQAIENYLNKRT 146
Qy 126 PRRIKCIILTWLILAAVLSLPLI---YKGDQPGRRGPOCKLQDQSGRLVATLRGVLGRG 181
Db 147 PRRIKCIITCWVLSAVISPEPLISIKKGGGGPQP-AEPRCINDQKMWISSCIGSF 205
Qy 182 FAPCLIMILVYRIYLIYAKR-----SNRGRPRAGCGQGESKOPR---PDHGALASAK 233
Db 206 FAPCLIMILVYRIYLIYAKRTRVPSRRGPDVAAPPGTERPNGLGPERASGPGAE 265
Qy 234 LPALASVASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQKQEGVCGASP 293
Db 266 AEPLPT-----QNG--APGEPAPA-GPRDTDALDLEES-----SS 298
Qy 294 EDEAE-----ESEECEPOAVPVSPASACSPLOQDQSGRLVATLRGVLGRG- 345
Db 299 SDHAERPPGRRPRGRGKAKASQVKPGD--SLPRRGPG-----ATGTFPAAPGGE 351
Qy 346 --VGATGGQWRRRAQL--TREKRFVLAIVGVVLCMPPEFFSYSGAICPKKCKYPHG 403
Db 352 ERVGAAKASRRGQ--NREKRFVLAIVGVVCMFPFFFTYTLAV---GCSVPT 406
Qy 404 LPOFFWIGYCNLSLNPVITYITFNQDPRRAFRILCR 440
Db 407 LFKFFWFGYCNLSLNPVITYITFNHDFRRAFKILCR 443

RESULT 10
US-10-225-567A-40
; Sequence 40, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-40

Query Match 47.3%; Score 1117; DB 15; Length 450;
Best Local Similarity 52.7%; Pred. No. 2.3e-74;
Matches 241; Conservative 52; Mismatches 102; Indels 62; Gaps 13;

Qy 6 PYSVQATAAIAAATPFLFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLI 65
Db 27 PYSLOVTLTVCLAGLMLTVFQNVVITAVFTSRALKAPQNLFLVSLASADILVATLV 86
Qy 66 IPFSLANELLGWYFRRTWCEVYIALDVLFTCTSSIVHLCAISLDRYAVASRALFYNSKRT 125
Db 87 IPFSLANENVGWYFGKAWCEIYIALDVLFTCTSSIVHLCAISLDRYAVSITQAIENYLNKRT 146
Qy 126 PRRIKCIILTWLILAAVLSLPLI---YKGDQPGRRGPOCKLQDQSGRLVATLRGVLGRG 181
Db 147 PRRIKCIITCWVLSAVISPEPLISIKKGGGGPQP-AEPRCINDQKMWISSCIGSF 205
Qy 182 FAPCLIMILVYRIYLIYAKR-----SNRGRPRAGCGQGESKOPR---PDHGALASAK 233
Db 206 FAPCLIMILVYRIYLIYAKRTRVPSRRGPDVAAPPGTERPNGLGPERASGPGAE 265
Qy 234 LPALASVASAREVNGSHKSTGEKEGETPEDTGTALPPSWAALPNSGQKQEGVCGASP 293
Db 266 AEPLPT-----QNG--APGEPAPA-GPRDTDALDLEES-----SS 298
Qy 294 EDEAE-----ESEECEPOAVPVSPASACSPLOQDQSGRLVATLRGVLGRG 346
Db 299 SDHAERPPGRRPRGRGKAKASQVKPGD--SLPRRGPG-----GRLQGRGR 351
Qy 347 GAIGGQWRRRAQL--TREKRFVLAIVGVVLCMPPEFFSYSGAICPKKCKYPHG 403
Db 352 SASGLP--RRRAGGQNLKRTFTVLAIVGVVCMFPFFFTYTLAV---GCSVPT 406
Qy 404 LPOFFWIGYCNLSLNPVITYITFNQDPRRAFRILCR 440
Db 407 LFKFFWFGYCNLSLNPVITYITFNHDFRRAFKILCR 443

RESULT 11
US-10-225-567A-44
; Sequence 44, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-44

Query Match 45.7%; Score 1080; DB 15; Length 461;
 Best Local Similarity 52.5%; Pred. No. 1.3e-71;
 Matches 240; Conservative 41; Mismatches 104; Indels 72; Gaps 12;

7 YSVQATAAIAAATFTLFTFGNALVLAIVTSRLAPQNLFLVSLAADIIVATLII 66
 46 YSAGAVAGLAAVGFLIVFTVGNVLAIVLTSRLAPQNLFLVSLAADIIVATLII 105
 67 PPSLANELGYWYRRRTWCEVYALDVLCFCTSSIVHLCAISLDRYWASRLAEVNSKRT 126
 106 PPSLANELMAWYFGQWCGVYALDVLCFCTSSIVHLCAISLDRYWASVQAVEINLKRT 165
 127 RRIKCIITLWMLIAVISLPELI--YKGDQGPQPRGR--POCKINOAWYILASSIGSF 182
 166 RRVKATIVAVMLISAVISFPPLVSLYR--QPDGAAYPQCGLNDEWTYILSSCIGSFF 220
 183 APCLIMILVYLRIRYIAKSNRGRPRAGKPGQGESKOPRPHGALASAKLPALASVAS 242
 221 APCLIMGLVYARIYRAKRTTR-----TISEKRAVPYDQAS 257
 243 AREVNGHSGTGEKEGETPEDTGT-RALPSM-----ALPNSG-----QCG 284
 258 PTTENGGAAGBAR-----GTARPPPTWMSKTRAAQRRGAPGLRRGRRRAGA 310
 285 KEVCYCASPEDAEHEEEEECEPOAVPVSPASCSPLLOQPOGSRVLAITLRC-QVILG 343
 311 EGGAGCA-----DQAGAPGAAGSALTASRSP--GPGRLSRASRSVFEPLS 357
 344 RGVGAIIGQWWRRAQOLTRERFTFLAVVIGFVLCWPFPPFSYSLGICPKHCKVPHG 403
 358 RRRRARSSVCRKVAQ--AREKRTFVLAVMGCVFLCMWPFPIYSLVIGICREAOVGP 416
 404 LPOFFWIGYCNSSLNPVITYITFNODFRARFRILCR 440
 417 LKFFPFIQYCNSSLNPVITYITFNODFRPSEKHLFR 453

RESULT 12
 US-10-001-073-46
 ; Sequence 46, Application US/10001073
 ; Publication No. US20030113725A1
 ; GENERAL INFORMATION: Stephen
 ; APPLICANT: Liggett, Stephen
 ; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
 ; FILE REFERENCE: 13073-PCT
 ; CURRENT APPLICATION NUMBER: US/10/001,073
 ; CURRENT FILING DATE: 2001-11-01
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 46
 ; LENGTH: 458
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-001-073-46

Query Match 45.4%; Score 1073.5; DB 15; Length 458;
 Best Local Similarity 52.9%; Pred. No. 3.8e-71;
 Matches 236; Conservative 47; Mismatches 110; Indels 53; Gaps 11;

7 YSVQATAAIAAATFTLFTFGNALVLAIVTSRLAPQNLFLVSLAADIIVATLII 66
 46 YSAGAVAGLAAVGFLIVFTVGNVLAIVLTSRLAPQNLFLVSLAADIIVATLII 105
 67 PPSLANELGYWYRRRTWCEVYALDVLCFCTSSIVHLCAISLDRYWASRLAEVNSKRT 126
 106 PPSLANELMAWYFGQWCGVYALDVLCFCTSSIVHLCAISLDRYWASVQAVEINLKRT 165
 127 RRIKCIITLWMLIAVISLPELI--YKGDQGPQPRGR--POCKINOAWYILASSIGSF 182
 166 RRVKATIVAVMLISAVISFPPLVSLYR--QPDGAAYPQCGLNDEWTYILSSCIGSFF 220

183 APCLIMILVYLRIRYIAKSNR--RGRPRAGKPGQGESKOPRPHGALASAKLPALASV 240
 221 APCLIMGLVYARIYRAKRTTRTISEKRAVPYD-----DQASPTTENG-----LGA 267
 241 ASAREVNGH---SKSTGEKEGETPEDTGTALPESMALPNSGQ---GQKEVCGASPE 294
 268 AGAGE-NHGCAPPADVEPDESSAAERRRR---GALRRGRRRAGAEAGAGAGQ 321
 295 DEAEHEEECEPOAVPVSPASCSPLLOQPOGSRVLAITLRCQVILGRVGAIGQW 354
 322 GAESGALTASRSPQGGRLSRASRSVFEPLRRRRASV-----C 364
 355 RRAQOLTRERFTFLAVVIGFVLCWPFPPFSYSLGICPKHCKVPHGLPQFFWIGIC 414
 365 RRVKARERKRTFLAVVIGFVLCWPFPIYSLVIGICREAOVGPFLKFFFWIGY 424
 415 NSSLNPVITYITFNODFRARFRILCR 440
 425 NSSLNPVITYITFNODFRPSEKHLFR 450

RESULT 13
 US-10-001-073-44
 ; Sequence 44, Application US/10001073
 ; Publication No. US20030113725A1
 ; GENERAL INFORMATION: Stephen
 ; APPLICANT: Liggett, Stephen
 ; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
 ; FILE REFERENCE: 13073-PCT
 ; CURRENT APPLICATION NUMBER: US/10/001,073
 ; CURRENT FILING DATE: 2001-11-01
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 44
 ; LENGTH: 462
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-001-073-44

Query Match 45.3%; Score 1071.5; DB 15; Length 462;
 Best Local Similarity 53.9%; Pred. No. 5.3e-71;
 Matches 241; Conservative 45; Mismatches 110; Indels 51; Gaps 14;

7 YSVQATAAIAAATFTLFTFGNALVLAIVTSRLAPQNLFLVSLAADIIVATLII 66
 46 YSAGAVAGLAAVGFLIVFTVGNVLAIVLTSRLAPQNLFLVSLAADIIVATLII 105
 67 PPSLANELGYWYRRRTWCEVYALDVLCFCTSSIVHLCAISLDRYWASRLAEVNSKRT 126
 106 PPSLANELMAWYFGQWCGVYALDVLCFCTSSIVHLCAISLDRYWASVQAVEINLKRT 165
 127 RRIKCIITLWMLIAVISLPELI--YKGDQGPQPRGR--POCKINOAWYILASSIGSF 182
 166 RRVKATIVAVMLISAVISFPPLVSLYR--QPDGAAYPQCGLNDEWTYILSSCIGSFF 220
 183 APCLIMILVYLRIRYIAKSNR--RGRPRAGKPGQGESKOPRPHGALASAKLPALASV 240
 221 APCLIMGLVYARIYRAKRTTRTISEKRAVPYD-----DQASPTTENG-----LGA 267
 241 ASAREVNGH---SKSTGEKEGETPEDTGTALPESMALPNSGQ---GQKEVCGASPE 294
 268 AGAGE-NHGCAPPADVEPDESSAAERRRR---GALRRGRRRAGAEAGAGAGQ 318
 295 DEAEHEEECEPOAVPVSPASCSPLLOQPOGSRVLAITLRC-QVILGRVGAIGQW 353
 319 -----DQAGAPGAAGSALTASRSP--GPGRLSRASRSVFEPLRRRRASV 368
 354 WRRRAQOLTRERFTFLAVVIGFVLCWPFPPFSYSLGICPKHCKVPHGLPQFFWIGY 413
 369 RRVKARERKRTFLAVVIGFVLCWPFPIYSLVIGICREAOVGPFLKFFFWIGY 427
 414 CNSSLNPVITYITFNODFRARFRILCR 440

Db 428 CNSSLNPFVITVFNODRPSFKILFR 454

RESULT 14
US-10-060-795B-4

/ Sequence 4, Application US/10060795B
/ Publication No. US20030040022A1
/ GENERAL INFORMATION:
/ APPLICANT: Cliveall Olivier
/ APPLICANT: Bunzow, James R.
/ APPLICANT: Grandy, David K.
/ APPLICANT: Machida, Curtis A.
/ TITLE OF INVENTION: Dopamine Receptors and Genes
/ FILE REFERENCE: 90-1092-CCC
/ CURRENT APPLICATION NUMBER: US/10/060, 795B
/ CURRENT FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: 09/238977
/ PRIOR FILING DATE: 1999-01-27
/ PRIOR APPLICATION NUMBER: 08/474892
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: 07/973588
/ PRIOR FILING DATE: 1992-11-09
/ PRIOR APPLICATION NUMBER: 07/438544
/ PRIOR FILING DATE: 1989-11-20
/ PRIOR APPLICATION NUMBER: 07/273373
/ PRIOR FILING DATE: 1988-11-18
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 307
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-060-795B-4

Query Match 40.6%; Score 960.5; DB 15; Length 307;
Best Local Similarity 44.2%; Pred. No. 5.1e-63;
Matches 194; Conservative 42; Mismatches 40; Indels 163; Gaps 4;

QY 6 PYSVQATMAIAAATITLFTTIGNALVILAVLTSRLAPQVLFVSLAAADILVATLI 65
DB 27 PYSVQATLTLVCLAGLMLTTFVGMVLIIVFTSRALKAPQVLFVSLAAADILVATLI 86
QY 66 IPESLANELLGYXPRRTWCEVYALDVLCFTSSIVHLCAISIDRYAVSRALEVNSKRT 125
DB 87 LPESLANEWMQVYFCKTWCEIYALDVLCFTSSIVHLCAISIDRYAVSRALEVNSKRT 146
QY 126 PARIKCIITLWVLAIVISLPLI---YKDGQPGQPRGRPOCKLQDEAWYIIASSIGSF 181
DB 147 PRRIKAIITVWVLAIVISFPLISIEKKGGGGPQP-APRCEINDQKMYVSSCIGSF 205
QY 182 FAPCLIMILVYLAIVYLIYIAKSNRRGPRAKGPGQGESKOPRPHGALASAKLPALASVA 241
DB 206 FAPLLIMILVYVRIYIOLAK----- 224
QY 242 SAREVNGHSKSTKEKEGETPEDTGTALRPPSWAALPNSGQKQEGVCGASPEDAESEE 301
DB 225 ----- 224
QY 302 EEEBCEPQAVPVSPASACSPPLQPGQSHVLAITLNGVLLGRGVAGIGQWRRRAQLT 361
DB 225 -----RRTTRVP 230
QY 362 REKRFFVLAIVIGVNLCPFFPFYSYSGAICPKKCKVPHGLPQFFPMWIGYCNSSLNPF 421
DB 231 REKRFFVLAIVIGVNLCPFFPFYSYSGAICPKKCKVPHGLPQFFPMWIGYCNSSLNPF 287
QY 422 IYTFINODPRRARPRITCR 440
DB 288 IYTFINODPRRARPRITCR 306

RESULT 15

US-09-782-980-84
/ Sequence 84, Application US/09782980
/ Patent No. US20020072089A1
/ GENERAL INFORMATION:
/ APPLICANT: Khodadouc, Mehran M.
/ APPLICANT: Macbeth, Kyle J.
/ APPLICANT: Busfield, Samantha J.
/ APPLICANT: McCarthy, Sean A.
/ APPLICANT: Holzman, Douglas A.
/ APPLICANT: Gu, Wei
/ APPLICANT: White, David
/ APPLICANT: Pan, Yang
/ TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDF, LRSG, AND
/ TITLE OF INVENTION: STMT PROTEIN AND NUCLEIC ACID MOLECULES AND USES
/ FILE REFERENCE: MNI-121CP
/ CURRENT APPLICATION NUMBER: US/09/782, 980
/ CURRENT FILING DATE: 2001-02-13
/ PRIOR APPLICATION NUMBER: PCT/US00/02125
/ PRIOR FILING DATE: 2000-01-27
/ PRIOR APPLICATION NUMBER: 09/448, 076
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: 09/276, 400
/ PRIOR FILING DATE: 1999-03-25
/ PRIOR APPLICATION NUMBER: 60/117, 580
/ PRIOR FILING DATE: 1999-01-27
/ PRIOR APPLICATION NUMBER: 09/014, 195
/ PRIOR FILING DATE: 1998-01-27
/ PRIOR APPLICATION NUMBER: 09/014, 348
/ PRIOR FILING DATE: 1998-01-27
/ PRIOR APPLICATION NUMBER: 09/086, 892
/ PRIOR FILING DATE: 1998-05-29
/ PRIOR APPLICATION NUMBER: 09/296, 208
/ PRIOR FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: 09/063, 950
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 09/561, 381
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: 09/561, 810
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: 09/087, 121
/ PRIOR FILING DATE: 1998-05-29
/ PRIOR APPLICATION NUMBER: 09/672, 721
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 09/049, 799
/ PRIOR FILING DATE: 1998-03-27
/ NUMBER OF SEQ ID NOS: 176
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 84
/ LENGTH: 601
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-09-782-980-84

Query Match 27.6%; Score 652.5; DB 9; Length 601;
Best Local Similarity 33.6%; Pred. No. 5.8e-40;
Matches 167; Conservative 74; Mismatches 171; Indels 85; Gaps 12;

QY 16 AAATITLFTTIGNALVILAVLTSRLAPQVLFVSLAAADILVATLIIPESLANELL 75
DB 113 ALVLSIVITLITIGNLVILSVFTYKPLRIYQNFIVSLAVDLTVALLVLPNVAYSIL 172
QY 76 GYVFPRTWCEVYALDVLCFTSSIVHLCAISIDRYAVSRALEVNSKRTPRRIKCIILT 135
DB 173 GRWEPFHLCKMLTCDVLCCTSSIIINLCAIALDRYMAITDPINVAOKRTVGHVLLISG 232
QY 136 VWLIAVLSLPLIYGDGQPGQPRGRPOCKLQDEAWYIIASSIGSFAPCLIMILVYLR 195
DB 233 VWLISLISLPLIYGDGQPGQPRGRPOCKLQDEAWYIIASSIGSFAPCLIMILVYLR 292
QY 196 YL-----IAKSNRRGPRAKGPG----- 214
DB 293 FVATRRRLRERANKLNTIALKSTLEPMAVNSPVAANSNGSKSRLLASWLCGRDRAQ 352

us-09-692-077d-8.rapb

Mon Feb 9 08:28:47 2004

```

OY 215 -----OGESKQPRPD-----HCGALASAK-----LPALASVASAREVNGHSKS 252
Db 353 FATPMIQNQESISSETHQPODSSKQGFHNSDPQOQHVVVLVKSRRAKTOSTKHGT 412
OY 253 TG--EKEEGETPRDUTGRALPPSMALPNSGQOKEGVC-----GASPEDAEIEEIEEIEE 306
Db 413 RGRKSSQSSSTCEPHGEQOL-----LPAGDPG--GSCOPGGHSGGCKSDAISTESG 463
OY 307 CEPQA---VPVSPA-SACSPPLQOPGSGRYLATLRQVLLGRGVGALGGOMRRRAQLTR 362
Db 464 SDPKGCIQVCTQADEQTSKLTIPQOSTGVAASVTPLQKXISGWNQFIEEKXISLSK 523
OY 363 EKRFTEVLAVVIGVFLCWFPPFPSPYSLGALCDKCKVPHGLFO-FFWIGICNSLNPV 421
Db 524 ERRAARTLGIINGVFVICMLPFLMVVILPFCOTCC-PTNKKNFITWIGYNSGLNPV 581
OY 422 IYTIENQDFRRAFRIL 438
Db 582 IYTIENLDYRRAPKRL 598

```

Search completed: February 6, 2004, 18:22:05
 Job time : 30.8997 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 6, 2004, 18:13:11 ; Search time 16.4448 Seconds
(without alignments)
2614.040 Million cell updates/sec

Title: US-09-692-077D-8

Perfect score: 2363

Sequence: 1 MDHQDPYSVQATAAIAAAT.....QDFRAFRRLICRPMQTAW 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being predicted,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2343.5	99.2	450	2 A37223	alpha-2B-adrenergic
2	1993.5	84.4	448	2 I51863	alpha-2B-adrenergic
3	1985.5	84.0	453	2 A35642	alpha-2B-adrenergic
4	1951.5	82.6	455	2 S28221	alpha-2-C2 adrenergic
5	1437	60.8	276	2 I53161	alpha-2-adrenergic
6	1143	48.4	450	2 B40392	alpha-2-adrenergic
7	1135	48.0	450	2 I49481	alpha-2-adrenergic
8	1124	47.6	450	2 A34169	alpha-2A-adrenergic
9	1114	47.1	450	2 A38316	alpha-2-adrenergic
10	1101	46.6	432	2 I50829	alpha-2-adrenergic
11	1091	46.2	450	2 JH0190	alpha-2-adrenergic
12	1084.5	45.9	458	2 A40392	alpha-2-adrenergic
13	1083.5	45.9	458	2 I49480	alpha-2-adrenergic
14	1080.5	45.7	458	2 A48392	alpha-2C4 adrenoce
15	1080	45.7	461	2 A41327	alpha-2C-adrenergic
16	1075.5	45.5	458	2 A37869	alpha-2B-adrenergic
17	685.5	29.0	484	2 S5868	G protein-coupled
18	652.5	27.6	601	2 JH1004	tyramine receptor
19	652.5	27.6	601	2 JH0170	octopamine receptor
20	647	27.4	379	2 JH0178	serotonin receptor
21	599.5	25.4	476	2 JH0142	G protein-coupled
22	587	24.8	517	2 A45121	alpha-1B adrenoce
23	586.5	24.8	422	2 JH0315	serotonin receptor
24	586.5	24.8	444	1 DYB02	dopamine receptor
25	586	24.8	515	2 A40491	alpha-1-adrenergic
26	584	24.7	421	2 I49375	serotonin receptor
27	584	24.7	564	2 A38271	serotonin receptor
28	582.5	24.7	443	1 DYH02	dopamine receptor
29	582	24.6	511	2 C56849	dopamine receptor

30	581	24.6	442	1 DYXLD2	dopamine receptor
31	580	24.5	387	1 DYH02	dopamine receptor
32	580	24.5	444	1 DYMSD2	dopamine receptor
33	580	24.5	444	1 S08146	dopamine receptor
34	579	24.5	560	2 A38731	alpha-1A adrenoce
35	578	24.5	422	2 I38209	serotonin receptor
36	578	24.5	514	2 D56849	dopamine receptor
37	576	24.4	515	2 JH1525	alpha-1B-adrenergic
38	575	24.3	377	2 B30341	G protein-coupled
39	574.5	24.3	509	2 A47174	serotonin receptor
40	573	24.2	377	2 S68423	serotonin receptor
41	570	24.1	572	2 I39369	alpha-1A-adrenergic
42	567	24.0	430	2 T16079	hypothetical prote
43	567	24.0	501	2 JH0447	alpha-1A-adrenergic
44	564	23.9	501	2 T18663	hypothetical prote
45	557	23.6	377	2 A53279	serotonin receptor

ALIGNMENTS

RESULT 1
A37223
alpha-2B-adrenergic receptor - human
N/Alternate names: alpha-2C2-adrenergic receptor
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 29-Oct-1999
C/Accession: A37223, I39407, S14308, A36158
R/Weinmann, R.L.; Zgombick, J.W.; Macchi, M.; Adham, N.; Lichtblau, H.; Branchek, T.A.; Mol. Pharmacol. 38, 681-688, 1990
A/Title: Cloning, expression, and pharmacological characterization of a human alpha-2B-adrenergic receptor
A/Reference number: A37223; MUID:91042469; PMID:2172775
A/Accession: A37223
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-450 <MB1>
R/Lomasney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, T.L.; Caron MG. J. Biol. Chem. 265, 1241-1244, 1990
A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic receptor family: cloning and characterization
A/Reference number: I39407; MUID:90311345; PMID:2164221
A/Accession: I39407
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-450 <LCM>
A/Cross-references: GB:M34041; NID:9178197; PIDN:AAA51666.1; PID:9178198
R/Chen, J.; Kang, N.; Uhl, S.; Wikberg, J.E.S. FEBS Lett. 280, 241-244, 1991
A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic receptor family: cloning and characterization
A/Reference number: S14308; MUID:91192139; PMID:1849485
A/Accession: S14308
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 56-185 <CH>
A/Cross-references: GB:X59684; NID:928635
A/Note: This translation is not annotated in GenBank entry H5ALPH218, release 111.0
R/Chang, A.C.; Ho, T.F.; Chang, N.C. Biochem. Biophys. Res. Commun. 172, 817-823, 1990
A/Title: In vitro amplification by polymerase chain reaction of a partial gene encoding the alpha-2B-adrenergic receptor
A/Reference number: A36158; MUID:91054503; PMID:2173582
A/Accession: A36158
A/Molecule type: DNA
A/Residues: 95-361, 'OL', 364-389 <CHA>
A/Cross-references: GB:M38742; NID:9177867; PIDN:AAA62823.1; PID:9177868
C/Genetics:
A/Genes: GDB:ADRA2B; ADRA2L1; ADRA2R1
A/Cross-references: GDB:120539; OMIM:104260
A/Map position: 2p13-2p13
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
Query Match 99.2%; Score 2343.5; DB 2; Length 450;
Best Local Similarity 98.9%; Pred. No. 1.1e-154;
Matches 445; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 MDHODPVSQVQATTAIAAATFTLFTTIGNALVTIAVLTSSRLAPQNLFLVSLAAADIL 60
DB 1 MDHODPVSQVQATTAIAAATFTLFTTIGNALVTIAVLTSSRLAPQNLFLVSLAAADIL 60
QY 61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
DB 61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 180
DB 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 180
QY 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 180
DB 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 180
QY 181 FFAPCLIMILVYLRIYLAIRKSNRRGPRAKGGPGQSGSKQPRPHGALASAKLPALASV 240
DB 181 FFAPCLIMILVYLRIYLAIRKSNRRGPRAKGGPGQSGSKQPRPHGALASAKLPALASV 240
QY 241 ASAREVNGHSKSTGEKGETPEDTGTALPPSWAALPNSGQKQKGVCGASPEDAE-- 297
DB 241 ASAREVNGHSKSTGEKGETPEDTGTALPPSWAALPNSGQKQKGVCGASPEDAE-- 297
QY 241 ASAREVNGHSKSTGEKGETPEDTGTALPPSWAALPNSGQKQKGVCGASPEDAE-- 297
DB 241 ASAREVNGHSKSTGEKGETPEDTGTALPPSWAALPNSGQKQKGVCGASPEDAE-- 297
QY 298 EEEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRQVTLGRGVGAIIGQWRRR 357
DB 298 EEEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRQVTLGRGVGAIIGQWRRR 357
QY 301 EEEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRQVTLGRGVGAIIGQWRRR 360
DB 301 EEEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRQVTLGRGVGAIIGQWRRR 360
QY 358 AQLRREKFTFVLAVVIGVFLCWPFPFSSYSLGICPKHCKVPHGLFQFPFMIYGCNS 417
DB 358 AQLRREKFTFVLAVVIGVFLCWPFPFSSYSLGICPKHCKVPHGLFQFPFMIYGCNS 417
QY 418 LNPVIYITFNODFRRAFRRIICRPMTQTAM 447
DB 421 LNPVIYITFNODFRRAFRRIICRPMTQTAM 450

RESULT 2

151883
alpha-2b-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C:Accession: J51883
R:Le Joesec, M.; Cloit, J.F.; Pecquery, R.; Giudicelli, Y.; Dausse, J.P.
Am. J. Hypertens. 8, 177-182, 1995
A:Title: Differential sodium regulation between salt-sensitive and salt-resistant Sabra
A:Reference number: 151883; PMID:95275492; PMID:7755946
A:Accession: J51883
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-448 <RES>
A:Cross-references: EMBL:X74400; NID:g840862; PIDN:CAAS2411.1; PID:g940816
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 84.4%; Score 1993.5; DB 2; Length 448;
Best Local Similarity 84.2%; Pred. No. 1.7e-130;
Matches 377; Conservative 25; Mismatches 45; Indels 1; Gaps 1;

QY 1 MDHODPVSQVQATTAIAAATFTLFTTIGNALVTIAVLTSSRLAPQNLFLVSLAAADIL 60
DB 1 MDHODPVSQVQATTAIAAATFTLFTTIGNALVTIAVLTSSRLAPQNLFLVSLAAADIL 60
QY 61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
DB 61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
QY 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 180
DB 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 180
QY 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 180
DB 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 180
QY 181 FFAPCLIMILVYLRIYLAIRKSNRRGPRAKGGPGQSGSKQPRPHGALASAKLPALAS- 239
DB 181 FFAPCLIMILVYLRIYLAIRKSNRRGPRAKGGPGQSGSKQPRPHGALASAKLPALAS- 239
QY 240 VASAREVNGHSKSTGEKGETPEDTGTALPPSWAALPNSGQKQKGVCGASPEDAE 299

DB 241 LSSVGEANGHPKPREKEEBEETEDPEARALPEPTWSALPNSGQKQKGTSGATAEKXEE 300
QY 300 EEEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRQVTLGRGVGAIIGQWRRRAQ 359
DB 301 DEEBEECEPQTLPASASVCNPNLQOPQTSRYLATLRQVTLGRGVGAIIGQWRRRAQ 360
QY 360 LTRERKFTFVLAVVIGVFLCWPFPFSSYSLGICPKHCKVPHGLFQFPFMIYGCNSLN 419
DB 361 LTRERKFTFVLAVVIGVFLCWPFPFSSYSLGICPKHCKVPHGLFQFPFMIYGCNSLN 420
QY 420 PVITITNODFRRAFRRIICRPMTQTAM 447
DB 421 PVITITNODFRRAFRRIICRPMTQTAM 448

RESULT 3

A35642
alpha-2b-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C:Accession: A35642
R:Zeng, D.; Harrison, J.K.; D'Angelo, D.D.; Barber, C.M.; Tucker, A.L.; Lu, Z.; Lynch, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 3102-3106, 1990
A:Title: Molecular characterization of a rat alpha-2b-adrenergic receptor.
A:Reference number: A35642; PMID:90222177; PMID:2158103
A:Accession: A35642
A:Molecule type: mRNA
A:Residues: 1-453 <ZEN>
A:Cross-references: GB:M32061; NID:g202589; PIDN:AAA40635.1; PID:g202590
A>Note: 169-Phe was also found
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 84.0%; Score 1985.5; DB 2; Length 453;
Best Local Similarity 84.2%; Pred. No. 6.2e-130;
Matches 377; Conservative 24; Mismatches 46; Indels 1; Gaps 1;

QY 1 MDHODPVSQVQATTAIAAATFTLFTTIGNALVTIAVLTSSRLAPQNLFLVSLAAADIL 60
DB 6 MDHODPVSQVQATTAIAAATFTLFTTIGNALVTIAVLTSSRLAPQNLFLVSLAAADIL 65
QY 61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
DB 61 VATLIIPFSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 125
QY 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 180
DB 121 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 185
QY 126 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 185
DB 126 NSKRTPRRIKCIITLWMLIAAVISLPLIYKGDQGPQGRBPQCKLQEAAYIIASSISGS 185
QY 181 FFAPCLIMILVYLRIYLAIRKSNRRGPRAKGGPGQSGSKQPRPHGALASAKLPALAS- 239
DB 181 FFAPCLIMILVYLRIYLAIRKSNRRGPRAKGGPGQSGSKQPRPHGALASAKLPALAS- 239
QY 240 VASAREVNGHSKSTGEKGETPEDTGTALPPSWAALPNSGQKQKGVCGASPEDAE 299
DB 246 LSSVGEANGHPKPREKEEBEETEDPEARALPEPTWSALPNSGQKQKGTSGATAEKXEE 305
QY 300 EEEEBEECEPQAVPVSPASACSPPLQOPQGSRYLATLRQVTLGRGVGAIIGQWRRRAQ 359
DB 306 DEEBEECEPQTLPASASVCNPNLQOPQTSRYLATLRQVTLGRGVGAIIGQWRRRAQ 365
QY 360 LTRERKFTFVLAVVIGVFLCWPFPFSSYSLGICPKHCKVPHGLFQFPFMIYGCNSLN 419
DB 366 LTRERKFTFVLAVVIGVFLCWPFPFSSYSLGICPKHCKVPHGLFQFPFMIYGCNSLN 425
QY 420 PVITITNODFRRAFRRIICRPMTQTAM 447
DB 426 PVITITNODFRRAFRRIICRPMTQTAM 453

RESULT 4

S28221

alpha-2-C2 adrenergic receptor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
 C/Accession: S28221; JH0693
 R/Chen, W.M.; Chang, A.C.; Shie, B.J.; Chang, Y.H.; Chang, N.C.A.
 Biochim. Biophys. Acta 1171, 219-223, 1992
 A/Title: Molecular cloning and characterization of a mouse alpha(2)C2 adrenoceptor subty
 A/Reference number: S28221; MUID:93129625; PMID:1336396
 A/Accession: S28221
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-455 <CHR>
 A/Cross-references: EMBL:M94583
 A/Note: the authors translated the codon CCA for residue 161 as Phe, ACT for residue 337
 R/Christie, A.J.; Link, R.E.; Dunt, D.A.; Barsh, G.S.; Kobilka, B.K.
 Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992
 A/Title: Cloning and expression of the mouse homolog of the human alpha2-C2 adrenergic r
 A/Reference number: JH0693; MUID:92378586; PMID:1354956
 A/Accession: JH0693
 A/Molecule type: DNA
 A/Residues: 6-228,231-455 <CHR>
 A/Cross-references: GB:L00979; NID:g191547; PIDN:AAA37131.1; PID:g191548
 C/Superfamily: Vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein
 F/16-43/Domain: transmembrane #status predicted <TM1>
 F/55-81/Domain: transmembrane #status predicted <TM2>
 F/90-115/Domain: transmembrane #status predicted <TM3>
 F/134-158/Domain: transmembrane #status predicted <TM4>
 F/173-199/Domain: transmembrane #status predicted <TM5>
 F/377-402/Domain: transmembrane #status predicted <TM6>
 F/410-435/Domain: transmembrane #status predicted <TM7>

Query Match 82.6%; Score 1951.5; DB 2; Length 455;
 Best Local Similarity 83.6%; Pred. No. 1.4e-127;
 Matches 376; Conservative 22; Mismatches 49; Indels 3; Gaps 2;

QY 1 MDHDPYVQATATAIAAATFLILFTFGNALVLAIVTSRSLRAPONTFLVSLAADIL 60
 DB 6 MVHQEPYSVQATAIAASITFLILFTFGNALVLAIVTSRSLRAPONTFLVSLAADIL 65

QY 61 VATTILIPSLANELLGWYFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRLLEY 120
 DB 66 VATTILIPSLANELLGWYFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRLLEY 125

QY 121 NSKTRPRRICTIITWVLAIVSLPLIYKGDGPGQPKCKNOEMAYTIASSIGS 180
 DB 126 NSKTRPRRICTIITWVLAIVSLPLIYKGDGPGQPKCKNOEMAYTIASSIGS 185

QY 181 FPAFCLIMLVYLRITLAKSNRRGPRAGKGPQGGSKOPRPD--HGALASAKLPALA 238
 DB 186 FPAFCLIMLVYLRITLAKSNRRGPRAGKGPQGGSKOPRPD--HGALASAKLPALA 245

QY 239 S-VASAREVNGSHKSTKEKEGETPEDTGTALPPSMAALPNSGQKKEGVGASPEDEA 297
 DB 246 SPILSSVGEANGHPKPREKEGEPEDPEANALPPNMSALPRSTVQDQKKGTSATKGA 305

QY 298 EEEEEEEREPQAVPSPASACSPPIQQPGSGVYLTALRGQVLTGSGVGAIGQMMRRR 357
 DB 306 EEEEEEEREPQAVPSPASACSPPIQQPGSGVYLTALRGQVLTGSGVGAIGQMMRRR 365

QY 358 AOLTRERGTFTVLAIVGVPLCWPFPPFSYSLGAIKPKCKVPHGLFOFFFWIGYCNSS 417
 DB 366 TOLSRERGTFTVLAIVGVPLCWPFPPFSYSLGAIKPKCKVPHGLFOFFFWIGYCNSS 425

QY 418 LNPVIYTIFFNODPFRARFRIICRPMTQTAW 447
 DB 426 LNPVIYTIFFNODPFRARFRIICRPMTQTAW 455

RESULT 5
 153161
 alpha 2-adrenergic receptor, isolets of Langerhans - rat (fragment)
 C/Species: Rattus sp. (rat)

C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 30-May-1997
 C/Accession: 153161
 R/Mang, S.Y.; Pilkey, D.T.
 Diabetes 43, 127-136, 1994
 A/Title: Identification in islets of Langerhans of a new rat alpha 2-adrenergic receptor
 A/Reference number: 153161; MUID:94085695; PMID:8262309
 A/Accession: 153161
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-276 <RES>
 A/Cross-references: GB:S67316; NID:g456949
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: neurotransmitter receptor

Query Match 60.8%; Score 1437; DB 2; Length 276;
 Best Local Similarity 99.3%; Pred. No. 3e-92;
 Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 96 CTSSIVHLCAISLDRYMAVSRLLEYNSKTRPRRICTIITWVLAIVSLPLIYKGDG 155
 DB 1 CTSSIVHLCAISLDRYMAVSRLLEYNSKTRPRRICTIITWVLAIVSLPLIYKGDG 60

QY 156 POPRGRPOCKLNOEAWYTIASSIGSFPAFLIMLVYLRITLAKSNRRGPRAGKGPQ 215
 DB 61 POPRGRPOCKLNOEAWYTIASSIGSFPAFLIMLVYLRITLAKSNRRGPRAGKGPQ 120

QY 216 GESKQRPDHGALASAKLPALASVARSRRVNGHSGKSTGKEBETPEDTGTALPPSWA 275
 DB 121 GESKQRPDHGALASAKLPALASVARSRRVNGHSGKSTGKEBETPEDTGTALPPSWA 180

QY 276 ALPNSGGQKKEGVGASPEDBAEEREECEEPQAVPSPASACSPPIQQPGSRVLTAT 335
 DB 181 ALPNSGGQKKEGVGASPEDBAEEREECEEPQAVPSPASACSPPIQQPGSRVLTAT 240

QY 336 LRQGVLLGRGVGAIGQMMRRRAQLTREKRTFTVLA 371
 DB 241 LRQGVLLGRGVGAIGQMMRRRAQLTREKRTFTVLA 276

RESULT 6
 B40392
 alpha-2-adrenergic receptor (clone RG10) - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
 C/Accession: B40392
 R/Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
 J. Biol. Chem. 266, 10470-10478, 1991
 A/Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic rece
 A/Reference number: A40392; MUID:91244823; PMID:1645350
 A/Accession: B40392
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-450 <LAN>
 A/Cross-references: GB:M62372; NID:g206615; PIDN:AAA42034.1; PID:g206616
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 48.4%; Score 1143; DB 2; Length 450;
 Best Local Similarity 52.7%; Pred. No. 1e-71;
 Matches 244; Conservative 51; Mismatches 94; Indels 74; Gaps 14;

QY 6 PYVQATATAIAAATFLILFTFGNALVLAIVTSRSLRAPONTFLVSLAADILVATLI 65
 DB 27 PYVQATATAIAAATFLILFTFGNALVLAIVTSRSLRAPONTFLVSLAADILVATLI 86

QY 66 IPFSLANELLGWYFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRLLEYNSKRT 125
 DB 87 IPFSLANELLGWYFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRLLEYNSKRT 146

QY 126 PRRIKCIITWVLAIVSLPLI--YKGDGPGQPKCKNOEAWYTIASSIGSF 182
 DB 147 PRRIKCIITWVLAIVSLPLI--YKGDGPGQPKCKNOEAWYTIASSIGSF 206

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0Y      183  APCIMILVYRILYTLAKR-----SRRRPRRKGCGQSEKOPR---FDHGALASAKL  234
Db      207  APCIMILVYRILYTLAKRTRVPRVRREPDGASAPRGADRRPRNAPVPRRAGTAGAEA  266
0Y      235  PALASVASAREVNGHKSSTGEKEEGETPEDTGTRALPSMAALPNSGGQKEGVCASPE  294
Db      267  EPRPT-----QLNG-----APGE-----PAPT-----RPPDG-----  288
0Y      295  DEAE-EEEEEECEPOAVVPSPACSPDLPQPGSRVLTLR-GVYTLRGVATG--  350
Db      289  DAIIDLSSSSSHAEPRGQPGKPRG-----PRAKGTKASVYKRGDSLRRRRGGAAPG  343
0Y      351  -----GQWRN-----RAQLTRKRTFYLAVAVIGVFLCWPFFPFSSYLALCPKH  397
Db      344  ASGSGQCEERBAGAKASRMWRGRQNRKERTFYLAVAVIGVFLCWPFFFTYTLAV---G  400
0Y      398  CKVDHGLFOFPFWIGVGNLSINLVYITINQDPRRPRRIICR  440
Db      401  CPVDYQLNFNFVFWFGVNSLNEVYITLNNHPRRPAFKKILICR  443

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RESULT 7

alpha-2 adrenergic receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: 149481
R:Link, R.; Daunt, D.; Barsh, G.S.; Chruslinski, A.; Kobilka, B.
Mol. Pharmacol. 42, 16-27, 1992
A:Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and identification of an antagonist binding.
A:Reference number: 149480; PMID: 92342131; PMID: 1353249
A:Accession: 149481
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-450 <RES>
A:Cross-references: GB:M99377; NID:g191882; PIDD:AAA37213.1; PID:g191883
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match	48.0%	Score 1135	DB 2	length 450
Best Local Similarity	52.4%	Pred. No. 3.6e-71		
Matches 245	Conservative 41	Mismatches 98	Indels 84	Gaps 12
QY	6	PYSVQATPAIAAATFELLFTIFGNALVILAVTSRLAPONTFLVSLAADIIVATLLI	65	
Db	27	PYSIQVLTITLVLCLAGLIMLFVFGVNLVLIIVFTSRALKAPONTFLVSLASADIVATLIV	86	
QY	66	IPFSLANELLGWYPRRTWCEVYLLADVLPFCSSIVHLCATSLDYMVASRLVENSRT	125	
Db	87	IPFSLANEVWGVIWGWKWCCEIYLLADVLPCTSSIVHLCATSLDYMVSITQAIENLKR	146	
QY	126	PRRIKIIITLWVLIAAVISLPEPLI---YKDGQPGPGRPOCKLNOEAMYTIIASSIGSF	182	
Db	147	PRRIKAIITVFWVISAVISAPPPLISIEKKGAGGGQGPAPESCKINDQKMYVISISGSFF	206	
QY	183	APCLIMILVYRIYVILIAR---SNRGRPAKGPGGGSEKQPRPDHGCLASKLPAL	237	
Db	207	APCLIMILVYRIYQIARRTTRVPPSRKGPDPDCAAPPGGARRP-----	250	
QY	238	ASVASAREVNHGSKSTGKEGGETPEDIDGTALPSPMALPNSSGGQKEGVCGASPEDEA	297	
Db	251	-----NGLG-----PERGAGP---TGAEAP-----LPTQLNGARGEPAPAGPRGCD	289	
QY	298	E-----EEEEEECE-----PAVVPVSPASACSPPLAQPGGSRVYLTLRQVILG	343	
Db	290	ALDLSESSSSHAERPPGPRRRDRGPRKAGKTRASQVPRGDSLPR-----RQPGAG	341	
QY	344	-----RGVCAIGGQMMRRRAQLTRREKRFETVLAAYIVGVFLCWPFFFSYSGA	392	
Db	342	PGASGSGHGEGRGGAKASRM---RGRONREKRFTFLVAAYIVGVFVCMWFFFFFTYLLA	398	
QY	393	ICPHKCVPHGLFQPFPMWIGYCNSSLNDEVYITINODFRRAPRIILCR	440	

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Db
399 V---GCPVPSQLFNFFFWFEGVCNSSLNPVIYTI FNHDFRFRAPFKILCR 443

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RESULT

alpha-2A-adrenergic receptor - human
N:Alternate names: alpha-2C10 - adrenergic receptor
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #ext_change 29-Oct-1999
C:Accession: A34169; A40132; S14311
J:Fraser, C.M.; Arakawa, S.; McCombie, W.R.; Venter, J.C.
J: Biol. Chem. 264, 11754-11761, 1989
A:Title: Cloning, sequence analysis, and permanent expression of a human alpha2-adrenergic
cyclase attenuation and activation.
A:Reference number: A34169; MUID:89308571; PMID:2568356
A:Accession: A34169
A:Molecule type: DNA
A:Residues: 1-450 <FRA>
A:Cross-references: GB:M23533; NID:G178195; PIDN:AAA51665.1; PID:G178196
R:Kobilka, B.K.; Matsui, H.; Kobilka, T.S.; Yang-Feng, T.L.; Francke, U.; Caron, M.G.; Lander
Science 238, 650-656, 1987
A:Title: Cloning, sequencing, and expression of the gene coding for the human platelet al
A:Reference number: A40132; MUID:88042789; PMID:2823383
A:Accession: A40132
A:Molecule type: DNA
A:Residues: 1-103, 'T', 105-156, 'C', 158-367, 'L', 369-450 <KOB>
A:Cross-references: GB:M18415; NID:G178191; PIDN:AAA51664.1; PID:G178192
A:Note: the authors translated the codon TGT for residue 157 as Val, and CTC for residue
A:Note: part of this sequence was confirmed by protein sequencing
R:Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A:Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep
A:Reference number: S14308; MUID:91192139; PMID:1849485
A:Accession: S14311
A:Molecule type: DNA
A:Residues: 77-123, 'P', 125-209 <CHH>
C:Genetics:
A:Gene: GDB:ADRA2A; ADRA; ADRA2; ADRA2R
A:Cross-references: GDB:120538; OMIM:104210
A:Map position: 10q25-10q25
A:Insertions: #status absent
C:Superfamily: vertebrate rhodopsin
;Keywords: G protein-coupled receptor; transmembrane protein

[illegible]

Qy 347 GAIGQWRRRAQL---TREKRFVLAIVGVFLCMFPFFFSYSGALCPKIKVPHG 403
Db 352 SASGLP--RRRAGAGQRRKRFVLAIVGVFLCMFPFFFSYSGALCPKIKVPHG 406
Qy 404 LFOFFWIGYCNSSINPVIYITIFNDPFRARILLCR 440
Db 407 LKFFPFWGYCNSSINPVIYITIFNDPFRARILLCR 443

RESULT 9

A38316

alpha-2-adrenergic receptor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999

C:Accession: A38316

R:Gover: C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., E.J.; Lambird, L.E.

J:Bio1. Chem. 265, 17307-17317, 1990

A:Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2-ad

A:Reference number: A38316; MUID:91009167; PMID:2170371

A:Accession: A38316

A:Molecule type: DNA

A:Residues: 1-450 <GUY>

A:Cross-references: GB:J05652; NID:G164303; PIDN:AAA30984.1; PID:G164304

C:Superfamily: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 47.1%; Score 1114; DB 2; Length 450;
Best Local Similarity 52.0%; Pred. No. 1e-69;
Matches 237; Conservative 46; Mismatches 113; Indels 60; Gaps 9;

Qy 6 PYSVQATAAIAAATFTLFTFGNALVLAIVTSRSRAPQNLFLVSLAADIIVATLI 65
Db 27 PYSVQATLTLVCLAGLMLFTVFGVLIIVAFSTRALAKAPQNLFLVSLAADIIVATLV 86
Qy 66 IPEPLANELGMYFRRTWCVEYLAIDLFTCTSSIVHCAISLDRYMAVSRALEYSKRT 125
Db 87 IPEPLANELGMYFRRTWCVEYLAIDLFTCTSSIVHCAISLDRYMAVSRALEYSKRT 146
Qy 126 PRRIKCIITLWLAIVSLPPLI---YKDGQGPQRRPOCKLNQEMWYTLASSIGSF 182
Db 147 PRRIKCIITLWLAIVSLPPLI---YKDGQGPQRRPOCKLNQEMWYTLASSIGSF 206
Qy 183 APCIMILVLYRIYLIARSRNRGPRAKGPGQGESKQPRPDHGALASAKLPALASVAS 242
Db 207 APCIMILVLYRIYLIARSRNRGPRAKGPGQGESKQPRPDHGALASAKLPALASVAS 246
Qy 243 AREVNGHSKSTGEKEGETPDTGTRALPSMAALPNSGQKQKGVGASPEDEAEEREE 302
Db 247 ERRPENGKGPGRVGRVGAEE-----PLPVQANGAPGEPAPAGPRDADGDLLE 294
Qy 303 EEECEPQAVPVPSPASCPPLQOPQSGRVLTALRGVLLRGVGAIG----- 350
Db 295 ESSSEHAERPPGRSRERGRASK-ARASQVKGSLPRRGAPGAPGAPATGAGEER 353
Qy 351 -----GQWRRRAQLTREKRFVLAIVGVFLCMFPFFFSYSGALCPKIKVPHG 404
Db 354 GGVAKASRW---RGRONREKRFVLAIVGVFLCMFPFFFSYSGALCPKIKVPHG 407
Qy 405 FQFFWIGYCNSSINPVIYITIFNDPFRARILLCR 440
Db 408 FQFFWIGYCNSSINPVIYITIFNDPFRARILLCR 443

RESULT 10

I50829

alpha-2-adrenoceptor - cuckoo wrasse

C:Species: Labrus ocellatus (cuckoo wrasse)

C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999

C:Accession: I50829

R:Swenson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom, N.; Ala-Dotila, S.; Scheinin,

Br. J. Pharmacol. 110, 54-60, 1993

A:Title: Cloning and expression of a fish alpha-2-adrenoceptor.

A:Reference number: I50829; MUID:94035926; PMID:7693288

A:Accession: I50829
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-432 <SVB>
A:Cross-references: EMBL:U07743; NID:9467287; PIDN:AAA17386.1; PID:9467288
C:Superfamily: vertebrate rhodopsin

Query Match 46.6%; Score 1101; DB 2; Length 432;
Best Local Similarity 50.7%; Pred. No. 7.8e-69;
Matches 229; Conservative 62; Mismatches 101; Indels 60; Gaps 10;

Qy 7 YSVQATAAIAAATFTLFTFGNALVLAIVTSRSRAPQNLFLVSLAADIIVATLI 66
Db 27 YSLAIAISIALVSLFTLFTVGNILVIAVTSRALKAPQNLFLVSLAADIIVATLV 86
Qy 67 PFSIANELGMYFRRTWCVEYLAIDLFTCTSSIVHCAISLDRYMAVSRALEYSKRT 126
Db 87 PFSIANELGMYFRRTWCVEYLAIDLFTCTSSIVHCAISLDRYMAVSRALEYSKRT 146
Qy 127 PRRIKCIITLWLAIVSLPPLIYKQGPQRRPOCKLNQEMWYTLASSIGSFAPCL 186
Db 147 KRVCIITVYLIARSRNRGPRAKGPGQGESKQPRPDHGALASAKLPALASVASREV 205
Qy 187 IMILVLYRIYLIARSRNRGPRAKGPGQGESKQPRPDHGALASAKLPALASVASREV 246
Db 206 IMILVLYRIYLIARSRNRGPRAKGPGQGESKQPRPDHGALASAKLPALASVASREV 249
Qy 247 NGHSKST---GEKEEG--ETPEDTGTRALPSMAALPNSGQKQKGVGASPEDEAEER 300
Db 240 NGHSKST---GEKEEG--ETPEDTGTRALPSMAALPNSGQKQKGVGASPEDEAEER 300
Qy 301 EEECEPQAVPVPSPASCPPLQOPQSGRVLTALRGVLLRGVGAIGQWRRRAQL 360
Db 292 KQDQDQARAPPLKSSISK--QSAIRSV-----SNKVDLFASRRKRSSST 340
Qy 361 -----TREKRFVLAIVGVFLCMFPFFFSYSGALCPKIKVPHGIFQFFWIGY 413
Db 341 AEKVQAGREKRFVLAIVGVFLCMFPFFFSYSGALCPKIKVPHGIFQFFWIGY 399
Qy 414 CNSSLNPVIYITIFNDPFRARILLCRPWTOT 445
Db 400 CNSSLNPVIYITIFNDPFRARILLCRPWTOT 431

RESULT 11

JH0190

alpha-2-adrenergic receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997

C:Accession: JH0190

R:Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.

Mol. Cell. Biochem. 97, 161-172, 1990

A:Title: Molecular cloning, sequencing and expression of an alpha2-adrenergic receptor c

A:Reference number: JH0190; MUID:91125329; PMID:2177834

A:Accession: JH0190

A:Molecule type: mRNA

A:Residues: 1-450 <CHA>

A:Experimental source: brain

C:Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It mediat

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:34-59/Domain: hydrophobic <HDI>

F:71-96/Domain: hydrophobic <HII>

F:106-131/Domain: hydrophobic <III>

F:150-175/Domain: hydrophobic <HIV>

F:193-218/Domain: hydrophobic <HDV>

F:375-400/Domain: hydrophobic <HVI>

F:405-430/Domain: hydrophobic <VII>

Query Match 46.2%; Score 1091; DB 2; Length 450;
Best Local Similarity 52.5%; Pred. No. 4e-68;
Matches 238; Conservative 54; Mismatches 107; Indels 54; Gaps 13;

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QY 6 PYVQATAIAAATPILFTFTFGNALVILAVLTSSLRAPQNLPLVSLAADIIVATLI 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 PYSIQVTLTVCLAGLMLFTFRQNVILVITAFSTRALKAPQNLPLVSLASADIIIVATLV 86
QY 66 IPESLANELIGYVFRFTWCEVYIADLVLEFCTSSIVHLCAISIDRYWAVSRALEVNSKRT 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 IPESLANWVGWYFGKWCCEIYIADLVLEFCTSSIVHLCAISIDRYWSTQIAEIVLTKT 146
QY 126 PRRIKCIITVWILAAVSLPPLI---YKDDQGPQRRGRPOCKLNOEAWYIIASSIGSF 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 RRIKAIHCWCVIVSAVISFPPLISLEKKGAGGQGPAPBPSCKINQKXVYISSISGSF 206
QY 183 APCLMILVYLRITVLIAR-----SNRRGPRAKGGPQGESKOPR---PDHGALASATL 234
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 207 APCLMILVYLRITVLIARTRRVPSPRRGPDACAPPGCADRRPNLGFERRAGTNGEA 266
QY 235 PALASVASAEVNGHSGKSTGEKEGETPEDTGTALPSPWMAIPNSGQKQKGVGASPE 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 267 EPLPT-----QLNG---APGE-----PAPTRPR-----DGDALDLESSSS 299
QY 295 DEAEEREE-EEEECEPOAVVPSPASACSP-----PLQPGQSRVLTALRGQVILG--RGV 347
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 EHAERQGPCKPRGRPAKKTASQVKGEDSLPRKGPAAAGPGASGQ--GEERAGG 356
QY 348 AIGQWRRRAQUTREKRTFVLAVVIGVFLCWPFPFSSYSLGAIQPKGCKVPHGLFOF 407
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 357 AKASRW---RGRQNRKREKFTFLAVVIGFVVCWFPFFFTYLIIV---GCVPRQLTNF 410
QY 408 FFWIGCNSSINPVITYITFNODFRARFRILCR 440
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 411 FFWIGCNSSINPVITYITFNODFRARFRILCR 443

```

RESULT 12

```

A40392
Alpha-2-adrenergic receptor (clone RG10) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C:Accession: A40392
R:lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A:Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic rec
A:Reference number: A40392; MUID:91244623; PMID:1645350
A:Accession: A40392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-458 <LAN>
A:Cross-references: GB:M62371; NID:9206612; PIDN:AAA42033.1; PID:9206613
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

```

```

Query Match 45.9%; Score 1084.5; DB 2; Length 458;
Best Local Similarity 52.9%; Pred. No. 1.1e-67;
Matches 237; Conservative 46; Mismatches 108; Indels 57; Gaps 10;

QY 7 YSVQATAIAAATPILFTFTFGNALVILAVLTSSLRAPQNLPLVSLAADIIVATLI 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 46 YSAGAVAGLAAVGFLIVTAVGNLVIAVLTSTRALAPQNLPLVSLASADIIIVATLV 105
QY 67 PPSLANELIGYVFRFTWCEVYIADLVLEFCTSSIVHLCAISIDRYWAVSRALEVNSKRT 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 106 PPSLANELMAVYFGQWCGVYIADLVLEFCTSSIVHLCAISIDRYWSTQIAVEINLKRTP 165
QY 127 PRICIIITVWILAAVSLPPLI---YKDDQGPQRRGRPOCKLNOEAWYIIASSIGSF 184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166 RRVKATIVAVWLISAVISFPPLVSFYR---RPDGAAYPQCGINDETWYIILSSCIGSF 222
QY 185 CLIMILVYLRITVLIAR-----SNRRGPRAKGGPQGESKOPRPHGALASAK----- 233
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 223 CLINGIVARIRYAKLTKRTLSEKRG-APBDSFTTENGKAGANGHCAPPRTEV 281
QY 234 LPALASVASAEVNGHSGKSTGEKEGETPEDTGTALPSPWMAIPNSGQKQKGVGAS 293
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

Db 282 EPDESSAAERRRRGAVRGGRRREG-AEGDTGS-----ADPGPGILAAEQARTASR 333
QY 294 EDEAEEREEEECEPOAVVPSPASACSPPLQPGQSRVLTALRG-QVILGRGALGCG 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 334 -----SPG-----PGSLSPASRSVFFLSRRRRASSV 363
QY 353 WRRRAQUTREKRTFVLAVVIGVFLCWPFPFSSYSLGAIQPKGCKVPHGLFOFPFWIG 412
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 364 CRRVYAO-AEKREFTFLAVMGVFLCWPFPFSSYSLYICREACQLPPLPKFPFWIG 422
QY 413 YCNSSLNPVITYITFNODFRARFRILCR 440
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 423 YCNSSLNPVITYITFNODFRARFRILCR 450

```

RESULT 13

```

149480
Alpha-2 adrenergic receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: 149480
R:Link, R.; Daunt, D.; Barsh, G.S.; Chrusciel, A.; Kobilka, B.
Mol. Pharmacol. 42, 16-27, 1992
A:Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and id
in antagonist binding.
A:Reference number: 149480; MUID:92342131; PMID:1353249
A:Accession: 149480
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-458 <RES>
A:Cross-references: GB:M99376; NID:9191880; PIDN:AAA7212.1; PID:9191881
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

```

```

Query Match 45.9%; Score 1083.5; DB 2; Length 458;
Best Local Similarity 52.8%; Pred. No. 1.3e-67;
Matches 239; Conservative 46; Mismatches 101; Indels 67; Gaps 12;

QY 7 YSVQATAIAAATPILFTFTFGNALVILAVLTSSLRAPQNLPLVSLAADIIVATLI 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 46 YSAGAVAGLAAVGFLIVTAVGNLVIAVLTSTRALAPQNLPLVSLASADIIIVATLV 105
QY 67 PPSLANELIGYVFRFTWCEVYIADLVLEFCTSSIVHLCAISIDRYWAVSRALEVNSKRT 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 106 PPSLANELMAVYFGQWCGVYIADLVLEFCTSSIVHLCAISIDRYWSTQIAVEINLKRTP 165
QY 127 PRICIIITVWILAAVSLPPLI---YKDDQGPQRRGRPOCKLNOEAWYIIASSIGSF 184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166 RRVKATIVAVWLISAVISFPPLVSFYR---RPDGAAYPQCGINDETWYIILSSCIGSF 222
QY 185 CLIMILVYLRITVLIAR-----SNRRGPRAKGGPQGESKOPRPHGALASAK----- 233
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 223 CLINGIVARIRYAKLTKRTLSEKRG-APBDSFTTENGKAGANGHCAP 276
QY 234 -----LPALASVASAEVNGHSGKSTGEKEGETPEDTGTALPSPWMAIPNSGQKQKGV 288
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 277 PRTEVEPDESSAAERRRRGALRGRRREG-ABSDITS-----ADPGPGILAAE 328
QY 289 CGASPEDAEEREEEECEPOAVVPSPASACSPPLQPGQSRVLTALRG-QVILGRGV 347
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 329 RTASR-----SPG-----PGSLSPASRSVFFLSRRR 358
QY 348 AIGQWRRRAQUTREKRTFVLAVVIGVFLCWPFPFSSYSLGAIQPKGCKVPHGLFOF 407
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 359 ARSSVCRRKVAQ-AEKREFTFLAVMGVFLCWPFPFSSYSLYICREACQLPPLPKF 417
QY 408 FFWIGCNSSINPVITYITFNODFRARFRILCR 440
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 418 FFWIGCNSSINPVITYITFNODFRARFRILCR 450

```

RESULT 14

A48392

alpha 2C4 adrenoceptor subtype - mouse
N:Alternate names: alpha 2C4 isocceptor
C/Species: Mus musculus (house mouse)
C/Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C/Accession: A48392
R/Chang, Y.H.; Chang, N.C.; Chen, W.M.; Chang, A.C.
Biochem. Mol. Biol. Int. 29, 467-474, 1993
A/Title: Molecular characterization of a murine homologue of alpha 2C4 adrenoceptor sub
A/Reference number: A48392; MUID:93250567; PMID:8387367
A/Accession: A48392
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-458 <CH>
A/Cross-references: GB:M97516; NID:G191728; PIDN:AAA37183.1; PID:G191729
A/Experimental source: DBA/2, liver
A/Note: sequence extracted from NCBI backbone (NCBI:131475, NCBI:131476)
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor

Query Match 45.7%; Score 1080.5; DB 2; Length 458;
Best Local Similarity 51.6%; Pred. No. 2.2e-67;
Matches 236; Conservative 47; Mismatches 99; Indels 75; Gaps 12;
QY 7 YSVQATAIAAAITFLITFGNALVTLAVLTSRSLRAPONLFLVSLAADIIVATLII 66
DB 46 YSAGAVAGLAAVGFLIVFTVGNVLVIAVLTSRALRAPONLFLVSLASADILVATLVM 105
QY 67 PFSLANELGMYRRRTWCCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRALEYSKRTP 126
DB 106 PFSLANELMAYMYRGQWCGVYALDVLFTCTSSIVHLCAISLDRYMSVTQAVEYNLKRTP 165
QY 127 RRIKCIITLWLLIAVLSLPLI--YKGDGPQPRGRPOCKLNOBAYTILASISGSFPAP 184
DB 166 RRVATIVAAVWLISAVISFPLVSFYR--RPVAAVYQCGINDETWYILSSCISGSFPAP 222
QY 185 CLIMILVYLRITLYIAK-----RSNRKGRPAKGPQGESKOPRPHDGALASAKLPALAS 239
DB 223 CLIMGLVYARIVAKLRITLSEKGP--AGP--DGASPTTENG----- 263
QY 240 VASAREVNGH--SKSTGEKEGETPDTGTALPPSAALPNSGQKQKCVGASPEDE 296
DB 264 LGKAGNGHCAPRTEPEDESSAMERRRR-----AAVRGGR--RREGAEG----- 310
QY 297 AEEEBEEBEECEPQAVPSPASCSPLQOPGSRVATLRG-----QVLLG 343
DB 311 -----DTGSDGPGPGIAAQAKTASRSRPGGRISRASSRVEFFLS 354
QY 344 RGVGALGQWRRRAQLTREKRTFTFLAVVIGVFLCMFPFPFYSIGALCPKCKVPHG 403
DB 355 RRRARASSVCRKVAQ--AREKRTFTFLAVVIGVFLCMFPFPFYSIGALCPKCKVPHG 413
QY 404 LFOFFFWIGYCNSSLNPVITYITFNODPRRAFRILCR 440
DB 414 LFKFPFWIGYCNSSLNPVITYITFNODPRRSPKILFR 450

RESULT 15

A31237
alpha-2C-adrenergic receptor - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999
C/Accession: A31237; S14309; S14310
R/Regan, J.W.; Koblika, T.S.; Yang-Feng, T.L.; Caron, M.G.; Lefkowitz, R.J.; Koblika, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 6301-6305, 1988
A/Title: Cloning and expression of a human kidney cDNA for an alpha-2-adrenergic recept
A/Reference number: A31237; MUID:88320430; PMID:2842764
A/Accession: A31237
A/Molecule type: mRNA
A/Residues: 1-461 <RRG>
A/Cross-references: GB:U03853; NID:G178193; PIDN:AAA35513.1; PID:G178194
R/Chhajlani, V.; Rangeli, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep

A/Reference number: S14308; MUID:91192139; PMID:1849485
A/Accession: S14309
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 95-223 <CH>
A/Accession: S14310
A/Molecule type: DNA
A/Residues: 95-223 <CH2>
C/Genetics:
A/Gene: GDB:ADRA2C; ADRA2L2; ADRA2R2
A/Cross-references: GDB:120540; OMIM:104250
A/Map position: 4p16.3-4p15
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 45.7%; Score 1080; DB 2; Length 461;
Best Local Similarity 52.5%; Pred. No. 2.4e-67;
Matches 240; Conservative 41; Mismatches 104; Indels 72; Gaps 12;
QY 7 YSVQATAIAAAITFLITFGNALVTLAVLTSRSLRAPONLFLVSLAADIIVATLII 66
DB 46 YSAGAVAGLAAVGFLIVFTVGNVLVIAVLTSRALRAPONLFLVSLASADILVATLVM 105
QY 67 PFSLANELGMYRRRTWCCEVYALDVLFTCTSSIVHLCAISLDRYMAVSRALEYSKRTP 126
DB 106 PFSLANELMAYMYRGQWCGVYALDVLFTCTSSIVHLCAISLDRYMSVTQAVEYNLKRTP 165
QY 127 RRIKCIITLWLLIAVLSLPLI--YKGDGPQPRGR--POCKLNOBAYTILASISGSFP 182
DB 166 RRVATIVAAVWLISAVISFPLVSFYR--OPDGAAYPQCGINDETWYILSSCISGSFP 220
QY 183 APCIMILVYLRITLYIAKRSNRKGRPAKGPQGESKOPRPHDGALASAKLPALASVAS 242
DB 221 APCIMGLVYARIVAKLRITR-----TLSEKRAPVPGGAS 257
QY 243 AREVNGHSTGEKEGETPDTGT--RALPSW-----AALPNSG-----QOQ 284
DB 258 PTTENGGAAGAAR-----TGTARPRPTWRTAAQPRGAGAPLRGGRRAAGA 310
QY 285 KEVYCGASPEDAEABEEBEEBEECEPQAVPSPASCSPLQOPGSRVATLRG--QVLLG 343
DB 311 EGGAGGA-----DQGAGPGAAOSGALTAASRP--GPGGRISRASSRVEFFLS 357
QY 344 RGVGALGQWRRRAQLTREKRTFTFLAVVIGVFLCMFPFPFYSIGALCPKCKVPHG 403
DB 358 RRRARASSVCRKVAQ--AREKRTFTFLAVVIGVFLCMFPFPFYSIGALCPKCKVPHG 416
QY 404 LFOFFFWIGYCNSSLNPVITYITFNODPRRAFRILCR 440
DB 417 LFKFPFWIGYCNSSLNPVITYITFNODPRRSPKILFR 453

Search completed: February 6, 2004, 18:20:09
Job time: 17.4448 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:52:15 ; Search time 9.96656 Seconds
(without alignments)
2109.148 Million cell updates/sec

Title: US-09-692-077D-8

Perfect score: 2363
Sequence: 1 MDHQDPYSVQATTAIAAAT.....ODFRRAFRRLICREWTQTAW 447

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2351.5	99.5	450	1 A2AB_HUMAN	P18089 homo sapien
2	2077.5	87.9	448	1 A2AB_CAVPO	Q60475 cavia porce
3	1985.5	84.0	453	1 A2AB_RAT	P19328 rattus norv
4	1951.5	82.6	455	1 A2AB_MOUSE	P30545 mus musculu
5	1794	75.9	394	1 A2AB_RABRT	Q77830 cyctocologus
6	1777	75.2	388	1 A2AB_ORYAT	O19032 cyctocologus
7	1772.5	75.0	391	1 A2AB_ERLEU	O19012 erincaceus e
8	1758.5	74.4	389	1 A2AB_HORSE	O77721 equus cabal
9	1750	74.1	384	1 A2AB_ELEMA	O19014 elephas max
10	1749	74.0	386	1 A2AB_AMBHO	O18935 amblyomus
11	1745	73.8	392	1 A2AB_BOVIN	O77700 bos taurus
12	1741	73.7	390	1 A2AB_DUGDU	O77713 dugong dugo
13	1725.5	73.0	397	1 A2AB_TALEU	O19091 talpa europ
14	1724.5	73.0	389	1 A2AB_PROHA	O19054 procavia ca
15	1697.5	71.8	387	1 A2AB_MACPR	O19025 macroscelid
16	1603	67.8	384	1 A2AB_ECHTE	O77723 echinops te
17	1447	61.2	382	1 A2AB_DIDMA	O77715 didelphis m
18	1447	61.2	382	1 A2AB_DIDMA	O77715 didelphis m
19	1139	48.2	450	1 A2AA_RAT	P22909 rattus norv
20	1135	48.0	450	1 A2AA_MOUSE	O01338 mus musculu
21	1131	47.9	452	1 A2AA_BOVIN	Q28838 bos taurus
22	1128	47.7	450	1 A2AA_CAVPO	Q60474 cavia porce
23	1124	47.6	450	1 A2AA_HUMAN	P08913 homo sapien
24	1101	46.6	432	1 A2AR_LABOS	P18871 sus scrofa
25	1090	46.1	455	1 A2AC_MOUSE	Q91081 labrus o881
26	1083.5	45.9	458	1 A2AC_CAVPO	Q60476 cavia porce
27	1083.5	45.9	458	1 A2AC_MOUSE	Q01337 mus musculu
28	1077.5	45.6	462	1 A2AC_RAT	P22086 rattus norv
29	1062.5	45.0	469	1 A2AC_HUMAN	P18825 homo sapien
30	982.5	41.6	436	1 A2AC_CAVPO	P33405 didelphis m
31	689.5	29.2	484	1 OAR2_LOCM1	P33252 carassius a
32	685.5	29.0	484	1 OAR1_LOCM1	Q25321 locusta mig
33	665.5	28.2	477	1 OAR_HELV1	Q25186 heliothis v

34	652.5	27.6	601	1 OAR_DROME	P22270 drosophila
35	647	27.4	379	1 GRE2_BALAM	Q91127 balanus amp
36	641.5	27.1	479	1 OAR_BOMMO	Q17232 bombyx mori
37	615	26.0	416	1 SH1B_FUGRU	Q42384 fugu rubrip
38	603	25.5	638	1 OAR1_LYMST	Q77408 lymanea eta
39	599.5	25.4	476	1 GRE1_BALAM	Q93126 balanus amp
40	599	25.3	467	1 D4DR_HUMAN	P21917 homo sapien
41	594	25.1	463	1 D2DR_FUGRU	P53453 fugu rubrip
42	587.5	24.9	444	1 OAR_GAEEL	O02213 caenorhabdi
43	586.5	24.8	422	1 SH1A_RAT	P19327 rattus norv
44	586.5	24.8	436	1 D2DR_MEIGA	Q73810 meleagris g
45	586.5	24.8	444	1 D2DR_BOVIN	P20286 bos taurus

ALIGNMENTS

RESULT 1
A2AB_HUMAN STANDARD; PRT; 450 AA.
ID A2AB_HUMAN
AC P18089; O9BZKO; 01-NOV-1990 (Ref. 16, Created)
DT 28-FEB-2003 (Ref. 41, Last sequence update)
DT 28-FEB-2003 (Ref. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Subtype C2).
GN ADRA2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90311349; PubMed=2164221;
RA Lomasney J.W., Lorenz W., Allen L.F., King K., Regan J.W.,
RT Yang-Feng T.L., Caron M.G., Lefkowitz R.J.;
RT "Expansion of the alpha 2-adrenergic receptor family: cloning and
RT characterization of a human alpha 2-adrenergic receptor subtype, the
RT gene for which is located on chromosome 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5094-5098(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042469; PubMed=2172775;
RA Weinshank R.L., Zgombick J.M., Macchi M., Adam N., Lichthau H.,
RT Branchek T.A., Hartig P.R.;
RT "Cloning, expression, and pharmacological characterization of a human
RT alpha 2B-adrenergic receptor.";
RL Mol. Pharmacol. 38:681-688(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX Cayla C., Schack S., Bouloumie A., Devédjian J.C., Paris H.;
RT Submitted (UTL-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT 301-GLU--GLU-303.
RX MEDLINE=21265012; PubMed=11056163;
RA Small K.M., Brown K.M., Forbes S.L., Liggett S.B.;
RT "Polymorphic deletion of three intracellular acidic residues of the
RT alpha 2B-adrenergic receptor decreases G protein-coupled receptor
RT kinase-mediated phosphorylation and desensitization.";
RL J. Biol. Chem. 276:4917-4922(2001).
RN [5]
RP SEQUENCE OF 95-389 FROM N.A.
RX MEDLINE=91054503; PubMed=2173582;
RA Chang A.C., Ho T.F., Chang N.-C.A.;
RT "In vitro amplification by polymerase chain reaction of a partial
RT gene encoding the third subtype of alpha-2 adrenergic receptor in
RT humans.";
RL Biochem. Biophys. Res. Commun. 172:817-823(1990).
-I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIANE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
IS CLONIDINE > NORBENEPHRINE > EPINEPHRINE = OXYMETAZOLINE >
DOPAMINE > P-TYRAMINE = PHENYLEPHRINE > SEROTONIN > P-SYNEPHRINE /
P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >

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CC CHLORPROMAZINE > PHENTOLAMINE > MIANSERINE > SPIPERONE > PRAZOSIN
CC > ALPRENOLOL > PROPRANOLOL > FINDOLOL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: M34041; AAAS1666.1; -.
DR EMBL: M38742; AA62823.1; -.
DR EMBL: AF316895; AA61635.1; -.
DR EMBL: AF005900; AA62558.1; -.
DR PIR: A37223; A37223.
DR HSSP: P29274; 1MMH.
DR GeneW: HGNC:282; ADRA2B.
DR MIM: 104260; -.
DR GO: GO:0005887; C:Integral to plasma membrane; TAS.
DR GO: GO:0004938; F:alpha2-adrenergic receptor activity; TAS.
DR GO: GO:0007267; P:cell-cell signalling; TAS.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin...; TAS.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7cm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Multigene family;
KM Phosphorylation; Lipoprotein; Palmitate; Polymorphism.
FT DOMAIN 1 12
FT TRANSMEM 13 38
FT TRANSMEM 39 49
FT TRANSMEM 50 75
FT TRANSMEM 76 85
FT TRANSMEM 86 108
FT TRANSMEM 109 130
FT TRANSMEM 131 153
FT TRANSMEM 154 169
FT TRANSMEM 170 193
FT DOMAIN 194 372
FT TRANSMEM 373 396
FT TRANSMEM 397 405
FT TRANSMEM 406 429
FT TRANSMEM 430 450
FT TRANSMEM 451 474
FT DISULFID 485 164
FT LIPID 442 442
FT SITE 92 92
FT SITE 176 176
FT SITE 180 180
FT VARIANT 301 303
FT CONFLICT 362 363
FT SEQUENCE 450 AA; 49953 MW; 06E43857152A68ED CRC64;
Query Match 99.5%; Score 2351.5; DB 1; Length 450;
Best Local Similarity 99.3%; Pired 2.5e-130;
Matches 447; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 MDHODYSVOATTAATAATFTLFTLFTFNALVITAVLTSSRLAPQNTFLVSLAADTL 60
DB 1 MDHODYSVOATTAATAATFTLFTLFTFNALVITAVLTSSRLAPQNTFLVSLAADTL 60
QY 61 VATLTFPSLANELLGYWFRRTWCSEVYLAIDLFTCTSSIVHLCAISLDRYNAVSRLLEY 120

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DB 61 VATLTFPSLANELLGYWFRRTWCSEVYLAIDLFTCTSSIVHLCAISLDRYNAVSRLLEY 120
QY 121 NSKRTFRRIKCIITLTMWLAAYISLPLLYKDDQGPGRPOCKNOBAMWYLAISIS 180
DB 121 NSKRTFRRIKCIITLTMWLAAYISLPLLYKDDQGPGRPOCKNOBAMWYLAISIS 180
QY 181 FPAFCILMILVYRIYLIANKSRNRGRPRAKGGQSGESQPRPDHGLASATLPAASV 240
DB 181 FPAFCILMILVYRIYLIANKSRNRGRPRAKGGQSGESQPRPDHGLASATLPAASV 240
QY 241 ASAREVNGHSKSTGKEEGETPEDTSTRALPSWALPNSGQKQKGVCGASPEDDA--- 297
DB 241 ASAREVNGHSKSTGKEEGETPEDTSTRALPSWALPNSGQKQKGVCGASPEDDAEEB 300
QY 298 EEEEBEEDPEPQAVVSPASACSPLOQPGSRVLAATRGVTLGRGVATIGQWRRR 357
DB 298 EEEEBEEDPEPQAVVSPASACSPLOQPGSRVLAATRGVTLGRGVATIGQWRRR 357
QY 301 EEEEBEEDCEPQAVVSPASACSPLOQPGSRVLAATRGVTLGRGVATIGQWRRR 360
DB 301 EEEEBEEDCEPQAVVSPASACSPLOQPGSRVLAATRGVTLGRGVATIGQWRRR 360
QY 358 AOLTRERKFTFVAWVIGVFLCMPFPFSYSGAICPKHCKVPHGLPFFPMIGYCNSS 417
DB 361 AOLTRERKFTFVAWVIGVFLCMPFPFSYSGAICPKHCKVPHGLPFFPMIGYCNSS 420
QY 418 LNPVYITIFNQDPRRAFRRLICRPTQTAW 447
DB 421 LNPVYITIFNQDPRRAFRRLICRPTQTAW 450
RESULT 2
A2AB_CAVPO STANDARD; PRT; 448 AA.
ID A2AB_CAVPO
AC 060475;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-2001 (Rel. 40, Last annotation update)
DE 16-Oct-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
GN ADRA2B.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley;
RX MEDLINE=96152573; PubMed=8573196;
RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;
RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
RT and alpha 2C adrenoceptor subtypes. Radioligand binding and
RT functional coupling to a CAMP-responsive reporter gene.";
RL Biochem. Pharmacol. 51:291-300(1996).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U25723; AA67075.1; -.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7cm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Multigene family;
KM Phosphorylation; Lipoprotein; Palmitate.

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FT DOMAIN 1 12 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 13 38 1 (POTENTIAL).
 FT DOMAIN 39 49 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 50 75 2 (POTENTIAL).
 FT DOMAIN 76 85 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 86 108 3 (POTENTIAL).
 FT DOMAIN 109 130 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 131 153 4 (POTENTIAL).
 FT DOMAIN 154 168 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 169 192 5 (POTENTIAL).
 FT DOMAIN 193 370 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 371 394 6 (POTENTIAL).
 FT DOMAIN 395 403 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 404 427 7 (POTENTIAL).
 FT DOMAIN 428 448 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 85 163 BY SIMILARITY.
 FT LIPID 440 440 PALMITATE (POTENTIAL).
 FT DOMAIN 294 309 ASX/GLU-RICH (ACIDIC).
 FT SITE 92 92 IMPLICATED IN LIGAND BINDING (BY
 SIMILARITY).
 FT SITE 175 175 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT SITE 179 179 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT SEQUENCE 448 AA; 49597 MW; 8384F875E404777 CRC64;
 SQ
 Query Match 87.9%; Score 2077.5; DB 1; Length 448;
 Best Local Similarity 86.9%; Pred. No. 2.2e-114; Index 3; Gaps 3;
 Matches 399; Conservative 15; Mismatches 32; Indels 3; Gaps 3;
 QY 1 MOHODPSYQATAAIAATFTLLFTFGNALVLAVALTSRSRAPONTFLVSLAADI 60
 DB 1 MOHODPSYQATAAIAATFTLLFTFGNALVLAVALTSRSRAPONTFLVSLAADI 60
 QY 61 VATLLIPPSIANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
 DB 61 VATLLIPPSIANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYMAVSRALEY 120
 QY 121 NSKRTRRRIKCIITLWTLAAVSLPPLYIKGQGPORRPOCKLNQEMWYTLASIGS 180
 DB 121 NSKRTRRRIKCIITLWTLAAVSLPPLYIKGQGPORRPOCKLNQEMWYTLASIGS 180
 QY 181 FFAFCLIMLVLYRIYLAIRSNRGPRAKGPQSGESKOPRDHGGALASAKLPALAS- 239
 DB 181 FFAFCLIMLVLYRIYLAIRSNRGPRAKGPQSGESKOPRDHGGALASAKLPALAS- 239
 QY 180 FFAFCLIMLVLYRIYLAIRSNRGPRAKGPQSGESKOPRDHGGALASAKLPALAS- 239
 DB 180 FFAFCLIMLVLYRIYLAIRSNRGPRAKGPQSGESKOPRDHGGALASAKLPALAS- 239
 QY 240 VASAREVNHSGKSGKEGEGTPEDTGTRALPPSMAALPNSGGQKQKGVGASPEDAEAE 299
 DB 240 VASAREVNHSGKSGKEGEGTPEDTGTRALPPSMAALPNSGGQKQKGVGASPEDAEAE 299
 QY 240 LSGTGEANGHPKPTGKEGEGTSEDGARTLPSPMAALPTSGGQKKAVALADAEAEAE 299
 DB 240 LSGTGEANGHPKPTGKEGEGTSEDGARTLPSPMAALPTSGGQKKAVALADAEAEAE 299
 QY 300 EEEEEE-EECEPOAVPSPASACSPPLQOPGSRVLAALRGVLAIGGVARRRA 358
 DB 300 EEEEEE-EECEPOAVPSPASACSPPLQOPGSRVLAALRGVLAIGGVARRRA 358
 QY 300 EEEEEEDECEPOAAGLPSMCSPLQOPGSRVLAALRGVLAIGGVARRRA 359
 DB 300 EEEEEEDECEPOAAGLPSMCSPLQOPGSRVLAALRGVLAIGGVARRRA 359
 QY 359 QLTREGRFTVLAVVIGVFLCMFPFFFSYSGALCPKCKVHGHGFOPFFMIGYCNSSL 418
 DB 359 QLTREGRFTVLAVVIGVFLCMFPFFFSYSGALCPKCKVHGHGFOPFFMIGYCNSSL 418
 QY 360 QMTREGRFTVLAVVIGVFLCMFPFFFSYSGALCPKCKVHGHGFOPFFMIGYCNSSL 419
 DB 360 QMTREGRFTVLAVVIGVFLCMFPFFFSYSGALCPKCKVHGHGFOPFFMIGYCNSSL 419
 QY 419 NPVIYTIFFNODFFRARRILCRPMOTAW 447
 DB 419 NPVIYTIFFNODFFRARRILCRPMOTAW 447
 QY 420 NPVIYTIFFNODFFRARRILCRPMOTAW 448
 DB 420 NPVIYTIFFNODFFRARRILCRPMOTAW 448
 RESULT 3
 A2AB RAT STANDARD; PRT; 453 AA.
 AC P19328; Q63021;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
 GN ADRA2B.
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_Taxid=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=90222177; PubMed=2156103;
 RA Zeng D., Harrison J.K., D'Angelo D.D., Barber C.M., Tucker A.L.,
 RA Lu Z., Lynch K.R.;
 RT "Molecular characterization of a rat alpha 2B-adrenergic receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3102-3106(1990).
 RN [2]
 RP SEQUENCE OF 6-453 FROM N.A.
 RP STRAIN=Sabra; TISSUE=Kidney;
 RX MEDLINE=95275492; PubMed=7755946;
 RA le Joesec M., Cloix J.F., Pecquery R., Giudicelli Y., Dause J.P.;
 RT "Differential sodium regulation between salt-sensitive and salt-
 RT resistant Sabra rats is not due to any mutation in the renal alpha
 RT 2B-adrenoceptor gene.";
 RL Am. J. Hypertens. 8:177-182(1995).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL: M32061; AAA40635.1; -;
 DR EMBL: X74400; CA452411.1; -;
 DR PIR: A35642; A35642.
 DR HSSP: P29274; 1MMH.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1, 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE: PS02622; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 17
 FT TRANSMEM 18 42 1 (POTENTIAL).
 FT DOMAIN 43 54 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 55 80 2 (POTENTIAL).
 FT DOMAIN 81 90 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 91 113 3 (POTENTIAL).
 FT DOMAIN 114 135 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 136 158 4 (POTENTIAL).
 FT DOMAIN 159 174 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 175 198 5 (POTENTIAL).
 FT DOMAIN 199 375 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 376 399 6 (POTENTIAL).
 FT DOMAIN 400 408 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 409 432 7 (POTENTIAL).
 FT DOMAIN 433 453 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 90 169 BY SIMILARITY.
 FT LIPID 445 445 PALMITATE (POTENTIAL).
 FT DOMAIN 300 314 ASX/GLU-RICH (ACIDIC).
 FT SITE 97 97 IMPLICATED IN LIGAND BINDING (BY
 SIMILARITY).
 FT SITE 181 181 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT SITE 185 185 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT CONFLICT 132 132 C -> R (IN REF. 2).
 FT CONFLICT 162 163 DA -> EP (IN REF. 2).
 SQ SEQUENCE 453 AA; 50276 MW; BCA040FFFA310EB CRC64;

QY	298	EEEEEEBCECEQAVPVSPASACSPPLQOPQOSRVLATLRGVLLRGGVALLGGQWRRR	357
DB	306	EEDEEEVECECEQGTLPASPAASVFNPELPQOPQOSRVLATLRGVLLSKNVASGGQWRRR	365
QY	358	AQLTREKRPFTVLAVVIGVFLCWPPEFFPSYSIGALCPKHCXVPHGLPQPFPMWIGCNSS	417
DB	366	TQLSREKRPFTVLAVVIGVFWCWPPEFFPSYSIGALCPQCHKVPHGLPQPFPMWIGCNSS	425
QY	418	LNPVLYTTFNODFRRAFRRLCRPMTQTM	447
DB	426	LNPVLYTTFNODFRRAFRRLCRQMTQTM	455
RESULT 5			
A2AB	RABIT	STANDARD;	394 AA.
ID	_A2AB_RABIT		
AC	077830;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).		
GN	ADRA2B.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_Taxid=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Stanhope M.J., Madson O.J., Wadell V.G., Cleven G.C., de Jong W.W.,		
RA	Springer M.S., Madson O.O.M.;		
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBA databases.		
CC	-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-		
CC	INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G		
CC	PROTEINS.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/annouce		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; Y16189; CAAT6115.1; -		
DR	EMBL; Y15946; CAAT5899.2; -		
DR	HSSP; P29274; IMM.		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	Pfam; PF00001; 7cm 1; 1.		
DR	PRINTS; PR00237; GPCRHHODOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.		
FM	G-protein coupled receptor; Transmembrane; Glycoprotein.		
FT	NON_TER	1	
FT	TRANSMEM	<1	25
FT	DOMAIN	26	36
FT	TRANSMEM	37	62
FT	DOMAIN	63	72
FT	TRANSMEM	73	95
FT	DOMAIN	96	117
FT	TRANSMEM	118	140
FT	DOMAIN	141	156
FT	TRANSMEM	157	180
FT	DOMAIN	181	358
FT	TRANSMEM	359	382
FT	DOMAIN	383	391
FT	TRANSMEM	392	>394
FT	DISULFID	72	151
FT	DOMAIN	282	297
FT	NON_TER	394	394
QO	SEQUENCE	394 AA;	42906 MW; 5D520975AC6916A CRC64;

Query Match	Similarity	75-9% 88.8%	Score 1794	DB 1	Length 394
Best Local	Similarity	75-9% 88.8%	Pred. No. 6	3e-98	
Matches	350	Conservative	13	Mismatches	22
				Indels	2
				Gaps	2
QY	14	AIATAITFLITFTFGNALVTILAVLTSSRLAPQNLFLVLSLAADILVATLIIPPSLANE	73		
Db	1	AIATAITFLITFTFGNALVTILAVLTSSRLAPQNLFLVLSLAADILVATLIIPPSLANE	60		
QY	74	LLGWYFERTICEVYALADVIFCTSSIVHLCAISIDRYAVASRALEVNSKTPPRIKCI	133		
Db	61	LLGWYFERTICEVYALADVIFCTSSIVHLCAISIDRYAVASRALEVNSKTPPRIKCI	120		
QY	134	LTWVLIAAVISLPLIYKDGQPOPRGRPOCKLANOEAMVYIASSIGSFAPCLIMIVYL	193		
Db	121	LTWVLIAAVISLPLIYKDGQPOPRGRPOCKLANOEAMVYIASSIGSFAPCLIMIVYL	180		
QY	194	RIYLIAKSSNRGPPAKGPGQGESKQRPDPHGALASAKIIPALAS-VASAREVNGHSKS	252		
Db	181	RIYLIAKSSNRGPPAKGPGQGESKQRPDPHGALASAKIIPALAS-VASAREVNGHSKS	240		
QY	253	TGEKEGEGTPDGTFRALPSPMAALPNSGGQCKEVCASPEDEA-EEEEESECECPQA	311		
Db	241	TGEKEGEGTPDGTFRALPSPMAALPNSGGQCKEVCASPEDEA-EEEEESECECPQA	300		
QY	312	VPVSPASACSPPLQOPQGSRYLATIRGOVLLIGRVGAIGGQWRRRAOLTRKRTFYLA	371		
Db	301	VPVSPASACSPPLQOPQGSRYLATIRGOVLLIGRVGAIGGQWRRRAOLTRKRTFYLA	360		
QY	372	VVIGVFVLCWEPFPFSSYSLAICPHCKCVPRGLF	405		
Db	361	VVIGVFVLCWEPFPFSSYSLAICPHCKCVPRGLF	394		

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RESULT 6
A2AB ORYAE
ID _A2AB ORYAE STANDARD; PRT; 388 AA.
AC 019032;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Oryzcterus afer (Aardvark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Tubulidentata; Orycteropodidae; Oryzcterus.
OX NCBI_TaxID=9818;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97357151, PubMed=9214502;
RA Springer M.S., Clevon G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
RA Amline H.M., Stanhope M.J.;
RT "Endemic African mammals shake the phylogenetic tree.";
RL Nature 388:61-64(1997).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; Y12522; CAAT73122.2; ALT SEQ.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2; 1.

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KW G-protein coupled receptor; Transmembrane; Multigene family;
 KM Phosphorylation; Lipoprotein; Palmitate.
 FT NON TER 1 1
 FT TRANSSEM <1 25
 FT TRANSSEM 26 36
 FT TRANSSEM 37 62
 FT TRANSSEM 63 72
 FT TRANSSEM 73 95
 FT TRANSSEM 96 117
 FT TRANSSEM 118 140
 FT TRANSSEM 141 156
 FT TRANSSEM 157 180
 FT TRANSSEM 181 352
 FT TRANSSEM 353 376
 FT TRANSSEM 377 385
 FT TRANSSEM 386 >388
 FT TRANSSEM 72 151
 FT TRANSSEM 280 291
 FT TRANSSEM 79 79
 FT TRANSSEM 163 163
 FT TRANSSEM 167 167
 FT TRANSSEM 388 388
 FT TRANSSEM 42429 MM; 1810DC767B3897 CRC64;
 SQ SEQUENCE 388 AA; 42429 MM; 1810DC767B3897 CRC64;
 Query Match 75.2%; Score 1777; DB 1; Length 388;
 Best Local Similarity 87.8%; Pred. No. 6e-97;
 Matches 345; Conservative 15; Mismatches 27; Indels 6; Gaps 4;
 14 AIAAATFLITFTFGNALVILAVTSRSLAPQNFIVSLAADIIVATLIIIPSLANE 73
 1 AIAAVITFLITFTFGNALVILAVTSRSLAPQNFIVSLAADIIVATLIIIPSLANE 60
 74 LIGWYFRRTWCVEYIALDVLFCTSSIVHLCASIDRYAWASRALEVNSKTPRIKCTI 133
 61 LIGWYFRRTWCVEYIALDVLFCTSSIVHLCASIDRYAWASRALEVNSKTPRIKCTI 120
 134 LITWLLAAVITSLPPLIYKDGQPGRGRPOCKLQNGEAWYIIASSIGSFAPCLIMILVYL 193
 121 LITWLLAAVITSLPPLIYKDGQPGRGRPOCKLQNGEAWYIIASSIGSFAPCLIMILVYL 180
 194 RITYLAKSNRRGPRAKGPGQSGSKQPRPDHGALASAKIPAL-ASVARSREVNHSKS 252
 181 RITYLAKSNRRGPRAKGPGQSGSKQPRPDHGALASAKIPAL-ASVARSREVNHSKS 239
 253 TSEKEGERTPEPTGTRALPDSWALPNSGQGGKSGVCGASPEDEAEEREEECCEPOAV 312
 240 TSEK-EGKTPEDPGLTLPSPMPAPNPGEGQKEGICGTSPEEFA--EEEREECEPOA 295
 313 PVSPASACGPILOQPGQSRVATLGRGVTLGRGVATGGQWRRRAQLTREKFTFVLAV 372
 296 PASSASACGPILOQPGQSRVATLGRGVTLGRGVATGGQWRRRAQLTREKFTFVLAV 355
 373 VIGVAVLTCMPPEPFYSYSGATCPKCKVPHGLF 405
 356 VIGVAVLTCMPPEPFYSYSGATCPKCKVPHGLF 388
 RESULT 7
 A2AB_ERIEU STANDARD; PRT; 391 AA.
 ID A2AB_ERIEU STANDARD; PRT; 391 AA.
 AC 019012;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADRA2B.
 OS Eriaceae europaeus (Western European heidehog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Eriaceae; Eriaceae; Eriaceae.
 NCBI_TaxID=3365;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97357151; PubMed=9214502;
 RA Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
 RA Amrine H.M., Stachow M.J.;
 RL "Endemic African mammals shake the phylogenetic tree";
 CC Nature 388:61-64(1997).
 CC - FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; Y12521; CAJ73121.1; --
 DR HSSP; P23274; 1MMH.
 DR InterPro; IPR00276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
 DR PROSITE; PS00262; G PROTEIN RECP F1.2; 1.
 KM G-protein coupled receptor; Transmembrane; Multigene family;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT NON TER 1 1
 FT TRANSSEM <1 25
 FT TRANSSEM 26 36
 FT TRANSSEM 37 62
 FT TRANSSEM 63 72
 FT TRANSSEM 73 95
 FT TRANSSEM 96 117
 FT TRANSSEM 118 140
 FT TRANSSEM 141 156
 FT TRANSSEM 157 180
 FT TRANSSEM 181 352
 FT TRANSSEM 353 376
 FT TRANSSEM 377 385
 FT TRANSSEM 386 >388
 FT TRANSSEM 72 151
 FT TRANSSEM 280 294
 FT TRANSSEM 79 79
 FT TRANSSEM 163 163
 FT TRANSSEM 167 167
 FT TRANSSEM 391 391
 FT TRANSSEM 42919 MM; F21PA2757B1EIDA CRC64;
 SQ SEQUENCE 391 AA; 42919 MM; F21PA2757B1EIDA CRC64;
 Query Match 75.0%; Score 1772.5; DB 1; Length 391;
 Best Local Similarity 88.0%; Pred. No. 1.1e-96;
 Matches 346; Conservative 14; Mismatches 30; Indels 3; Gaps 2;
 14 AIAAATFLITFTFGNALVILAVTSRSLAPQNFIVSLAADIIVATLIIIPSLANE 73
 1 AIAAVITFLITFTFGNALVILAVTSRSLAPQNFIVSLAADIIVATLIIIPSLANE 60
 74 LIGWYFRRTWCVEYIALDVLFCTSSIVHLCASIDRYAWASRALEVNSKTPRIKCTI 133
 61 LIGWYFRRTWCVEYIALDVLFCTSSIVHLCASIDRYAWASRALEVNSKTPRIKCTI 120
 134 LITWLLAAVITSLPPLIYKDGQPGRGRPOCKLQNGEAWYIIASSIGSFAPCLIMILVYL 193
 121 LITWLLAAVITSLPPLIYKDGQPGRGRPOCKLQNGEAWYIIASSIGSFAPCLIMILVYL 180
 194 RITYLAKSNRRGPRAKGPGQSGSKQPRPDHGALASAKIPAL-ASVARSREVNHSKS 252

Db 181 RYLIARSHRCGRAPGAPGKESKOTGASLCPASSAKLPNIVSRVAAREANRHSKS 240
 QY 253 TGEKEGETEDTSTRALPSSMALPNSGOGKEGVCASPEDAESEEESECEPOAV 312
 Db 241 TGEKEGETEDTSTRALPSSMALPNSGOGKEGVCASPEDAESEEESECEPOAV 298
 QY 313 PVSFASACSPPLQPGQSRVLTATRGVLLGRGVGAIIGQWRRRAQLTREKFTFYLA 372
 Db 299 PVSFASACSPPLQPGQSRVLTATRGVLLGRGVGAIIGQWRRRAQLTREKFTFYLA 358
 QY 373 VIGFVLCWPFPPFFSYSLGAIICPKCKVPHGLF 405
 Db 359 VIGFVLCWPFPPFFSYSLGAIICPKCKVPHGLF 391

RESULT 8
 A2AB_HORSE STANDARD; PRT; 389 AA.
 ID A2AB_HORSE STANDARD; PRT; 389 AA.
 AC 077721;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN Equus caballus (Horse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP MEDLINE=9834573; PubMed=9667998;
 RA Stanhope M.J., Madsen O.J., Waddell V.G., Clevens G.C., de Jong W.W.,
 RA Springer M.S.;
 RT "Highly congruent molecular support for a diverse superordinal clade
 of endemic African mammals";
 RL Mol. Phylogenet. Evol. 9:501-508 (1998).
 [2]
 RP REVISIONS.
 RA Madsen O.J.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; Y15945; CAA75898.2; -;
 DR HSSP; P29274; 1MMH.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KM G-protein coupled receptor; Transmembrane; Multigene family.
 FT NON_TER 1 1
 FT TRANSMEM <1 25
 FT DOMAIN 26 36 1 (POTENTIAL).
 FT TRANSMEM 37 62 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 63 72 2 (POTENTIAL).
 FT TRANSMEM 73 95 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 96 117 3 (POTENTIAL).
 FT TRANSMEM 118 140 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 141 156 4 (POTENTIAL).
 FT TRANSMEM 157 180 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 181 363 5 (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 364 387 6 (POTENTIAL).
 FT DOMAIN 388 >389 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 72 151 BY SIMILARITY.
 FT DOMAIN 281 302 POLY-GU.
 FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
 SIMILARITY).
 FT SITE 163 163 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
 (BY SIMILARITY).
 FT NON_TER 389 389
 SQ SEQUENCE 389 AA; 42257 MW; 992179431679B0FD CRC64;
 Query Match 74.4%; Score 1758.5; DB 1; Length 389;
 Best Local Similarity 88.7%; Pred. No. 7.2e-96;
 Matches 346; Conservative 11; Mismatches 24; Indels 9; Gaps 3;
 QY 14 AIAAATFLLFTFGNALVILAVTSRSRAPONLEFVSLAADIIVATLIPSLANE 73
 Db 1 AIAAATFLLFTFGNALVILAVTSRSRAPONLEFVSLAADIIVATLIPSLANE 60
 QY 74 LIGWYFRRTWCERYIALDVLFCSTSIYHICAIISLDHYAVSRLENSKTRPRICII 133
 Db 61 LIGWYFRRTWCERYIALDVLFCSTSIYHICAIISLDHYAVSRLENSKTRPRICII 120
 QY 134 LTVWLIANAIVSLPLIYKGGQGPGRPOCKNOBAMYLIIASIGSFAPCLIMILVYL 193
 Db 121 LTVWLIANAIVSLPLIYKGGQGPGRPOCKNOBAMYLIIASIGSFAPCLIMILVYL 180
 QY 194 RYLIARSHRCGRAPGAPGKESKOTGASLCPASSAKLPNIVSRVAAREANRHSKS 252
 Db 181 RYLIARSHRCGRAPGAPGKESKOTGASLCPASSAKLPNIVSRVAAREANRHSKS 240
 QY 253 TGEKEGETEDTSTRALPSSMALPNSGOGKEGVCASPEDAESEEESECEPOAV 312
 Db 241 TGEKEGETEDTSTRALPSSMALPNSGOGKEGVCASPEDAESEEESECEPOAV 298
 QY 313 PVSFASACSPPLQPGQSRVLTATRGVLLGRGVGAIIGQWRRRAQLTREKFTFYLA 372
 Db 299 PVSFASACSPPLQPGQSRVLTATRGVLLGRGVGAIIGQWRRRAQLTREKFTFYLA 358
 QY 373 VIGFVLCWPFPPFFSYSLGAIICPKCKVPHGLF 405
 Db 359 VIGFVLCWPFPPFFSYSLGAIICPKCKVPHGLF 391

RESULT 9
 A2AB_ELEMA STANDARD; PRT; 384 AA.
 ID A2AB_ELEMA STANDARD; PRT; 384 AA.
 AC 019014;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN Elephas maximus (Indian elephant).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
 OX NCBI_TaxID=9783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97357151; PubMed=9214502;
 RA Springer M.S., Clevens G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
 RA Amrine H.M., Stanhope M.J.;
 RT "Endemic African mammals shake the phylogenetic tree";
 RL Nature 388:61-64 (1997).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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Query Match	Similarity	74.0%	Score 1749	DB 1	Length 386
Best Local Similarity	87.8%	Pred. No. 2.6e-95			
Matches 345	Conservative	7	Mismatches 33	Indels 8	Gaps 3

QY	14	AI	AA	IT	FL	IT	FG	NM	LV	IL	AV	TS	RS	LA	PQ	PL	VS	LA	AD	IL	VA	TI	IP	SL	NE	
Db	1	AAAA	IT	FL	IT	FG <td>NM <td>LV <td>IL <td>AV <td>TS <td>RS <td>LA <td>PQ <td>PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	NM <td>LV <td>IL <td>AV <td>TS <td>RS <td>LA <td>PQ <td>PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	LV <td>IL <td>AV <td>TS <td>RS <td>LA <td>PQ <td>PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	IL <td>AV <td>TS <td>RS <td>LA <td>PQ <td>PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	AV <td>TS <td>RS <td>LA <td>PQ <td>PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td>	TS <td>RS <td>LA <td>PQ <td>PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td>	RS <td>LA <td>PQ <td>PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td>	LA <td>PQ <td>PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td></td></td>	PQ <td>PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td></td>	PL <td>VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td></td>	VS <td>LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td></td>	LA <td>AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td></td>	AD <td>IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td></td>	IL <td>VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td></td>	VA <td>TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td></td>	TI <td>IP <td>SL <td>NE <td>60</td> </td></td></td>	IP <td>SL <td>NE <td>60</td> </td></td>	SL <td>NE <td>60</td> </td>	NE <td>60</td>	60	
QY	74	LL	GW	YF	RR	TC	EV	LA	LD	VL	FC	TS	SY	HL	CA	IS	LD	R	W	AV	S	R	A	E	N	S
Db	61	LL	GW	YF	RR	TC	EV	LA	LD	VL	FC	TS	SY	HL	CA	IS	LD	R	W	AV	S	R	A	E	N	S
QY	134	LT	WM	LI	AV	IS	PL	IT	YK	GD	GP	GR	PO	CR	PO	CL	NO	EA	Y	T	LA	SS	IG	SF	AP	CL
Db	121	LT	WM	LI	AA	IS	PL	IT	YK	GD	GP	GR	PO	CR	PO	CL	NO	EA	Y	T	LA	SS	IG	SF	AP	CL
QY	194	RI	YL	IA	RS	NR	GR	PA	NG	PG	GS	KO	RP	DH	GA	LA	SA	KU	PL	AS	VA	S	A	R	E	V
Db	181	RI	YL	IA	RS	NR	GR	PA	NG	PG	GS	KO	RP	DH	GA	LA	SA	KU	PL	AS	VA	S	A	R	E	V
QY	253	TG	EE	GT	LD	PD	VT	SL	TP	PS	WP	AL	PN	SD	GQ	KE	GV	CE	TS	P	---	---	---	---	---	---
Db	241	TG	EE	GT	LD	PD	VT	SL	TP	PS	WP	AL	PN	SD	GQ	KE	GV	CE	TS	P	---	---	---	---	---	---
QY	313	PV	SP	AS	AS	PP	LG	QO	GS	RV	AT	TT	AG	VL	RG	VA	IG	QO	W	RR	AA	OL	T	R	E	K
Db	294	PV	SP	AS	AS	PP	LG	QO	GS	RV	AT	TT	AG	VL	RG	VA	IG	QO	W	RR	AA	OL	T	R	E	K
QY	373	VIG	VF	LC	MP	PF	FS	YS	LG	AI	CP	KR	CK	PH	GL	F	405									
Db	354	VIG	VF	LC	MP	PF	FS	YS	LG	AI	CP	KR	CK	PH	GL	F	386									

RESULT 11	ID	A2AB	BOVIN	STANDARD	PRT	392	AA
AC	077700						
DT	15-JUL-1999						
DT	16-OCT-2001						
DT	28-FEB-2003						
DE	Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).						
GN	ADRA2B						
OS	Bos taurus (bovine).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;						
OX	Bovidae; Bovinae; Bos.						
NCBI	NCBI_TaxID=9913;						
RP	SEQUENCE FROM N.A.						
RA	MEDLINE=98334573; PubMed=9667998;						
RX	Stanhope M.J., Madson O.J., Maddell V.G., Clevon G.C., de Jong W.W.,						
RT	Springer M.S.;						
RT	"Highly congruent molecular support for a diverse superordinal clade						
RT	of endemic African mammals.";						
RL	Mol. Phylogenet. Evol. 9:501-508(199						

DR	PRINTS: PR00237; GPCRHHODOSP.
DR	PROSITE: PS00237; G_PROTEIN_REEP_F1_1; 1.
DR	PROSITE: PS00262; G_PROTEIN_REEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Multigene family.
FT	NON_TER 1 1
FT	TRANSMEM <1 25 1 (POTENTIAL).
FT	DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 37 62 2 (POTENTIAL).
FT	DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 73 95 3 (POTENTIAL).
FT	DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 118 140 4 (POTENTIAL).
FT	DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 157 180 5 (POTENTIAL).
FT	DOMAIN 181 356 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 357 380 6 (POTENTIAL).
FT	DOMAIN 381 >392 EXTRACELLULAR (POTENTIAL).
FT	DISULFID 72 151 BY SIMILARITY.
FT	DOMAIN 283 292 POLY-GLIU.
FT	SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
FT	SITE 163 163 SIMILARITY).
FT	SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
FT	(BY SIMILARITY).
FT	IMPLICATED IN CATECHOL AGONIST BINDING
FT	(BY SIMILARITY).
FT	NON TER 392 392
FT	SEQUENCE 392 AA; 42839 MW; 471596A7446475E0 CRC64;
Query Match	73.8%; Score 1745; DB 1; Length 392;
Best Local Similarity	87.1%; Pred. No.4.4e-95;
Matches 343; Conservative	12; Mismatches 35; Indels 4; Gaps 3
QY	14 AIAAAITFLIFETFGNALVTLAVTSRSRAPQNLPLVSLAADIVATLIIPEPSLANE 73
DB	1 AIAAVITFLIIFTFGNALVTLAVTSRLAPQLPLVSLAADIVATLIIPEPSLANE 60
QY	74 LLGYTFPRTCCEVYLADVLCFTSSIVHLCAISLDRAWANSALEFNASKTPRIKCTI 133
DB	61 LLGWYEFRTICEVYALADVLCFTSSIVHLCASIDRWAVNSRALEFNASKTPRIKEPII 120
QY	134 LTWMLIAVISLPPIYKGDDGPORGRRPOCKDNEAYTIILASSIGSFPAFLMILVYL 193
DB	121 LIWMLIAVISLPPIYKGGDGPDLARPCKDNEAYTIILASSIGSFPAFLMILVYL 180
QY	194 RIYLLAKRSNRGRPRKAGPCGSGESKOPRPHGALSASAKLPALAS-VASAREVNGSHK- 251
DB	181 RIYLLAKRSNHRGRPRKAGCPERSRKQHVPVGEVSDSKAKIPTLASQLATGEANGSCQP 240
QY	252 STEKEBGETPEBDGTTRALLPPSWMALPNSSGOQKEGVCGASPEDFAEEEBEEECPEQA 311
DB	241 RPGEKGDETEAEAGTPTALPPSPWPAIPKSGOGKEGVCGSSPEBEA--EEEEEECEPEQA 298
QY	312 VPVSASASCSPLOOPOSRYLATLRGVLLARGVALIGGOMWRRAQTREKRPTFYLA 371
DB	299 LPASPASCSPPLOOPOSRYLATLRGVLLARGVGITAGGAQMWRRTLSREKPTFYLA 358
QY	372 VVIGVFVLCMPFFFSYSIGAICPKCHKCVPRGLF 405
DB	359 VVIGVFVLCMPFFFSYSIGAICQHCVRHGFLF 392
RESULT 12	
A2AB_DUGDU	
ID_A2AB_DUGDU	STANDARD; PRT; 390 AA.
AC 077713;	
DT 15-JUL-1999 (Rel. 38, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 28-FEB-2003 (Rel. 41, Last annotation update)	
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).	
GN ADRA2B.	
OS Dugong dugon (Dugong).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Sirenia; Dugongidae; Dugong.	

OX NCBI_TaxID=29137;
 RN SEQUENCE FROM N.A.
 RA Stanhope M.J., Madsen O.J., Waddell V.G., Clevon G.C., de Jong W.W.,
 RA Springer M.S., Madsen O.O.M.,
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: Y15947; CAA75900.2; -.
 CC HSSP: P29274; IMM.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHOPOSN.
 CC PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
 CC PROSITE: PS00262; G_PROTEIN_REC_P1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Multigene family.
 CC
 CC NON TER 1 1
 CC TRANSSEM 26 25 1 (POTENTIAL).
 CC DOMAIN 26 36 2 (POTENTIAL).
 CC TRANSSEM 37 62 2 (POTENTIAL).
 CC DOMAIN 63 72 2 (POTENTIAL).
 CC TRANSSEM 73 95 3 (POTENTIAL).
 CC DOMAIN 96 117 4 (POTENTIAL).
 CC TRANSSEM 118 140 4 (POTENTIAL).
 CC DOMAIN 141 156 5 (POTENTIAL).
 CC TRANSSEM 157 180 5 (POTENTIAL).
 CC DOMAIN 181 354 6 (POTENTIAL).
 CC TRANSSEM 355 378 6 (POTENTIAL).
 CC DOMAIN 379 >390 6 (POTENTIAL).
 CC TRANSSEM 281 291 6 (POTENTIAL).
 CC DOMAIN 72 151 6 (POTENTIAL).
 CC DISULFID 72 151 6 (POTENTIAL).
 CC NON TER 390 390 6 (POTENTIAL).
 CC SEQUENCE 390 AA; 42562 MW; 779F849267F9314 CRC64;
 SQ
 Query Match 73.7%; Score 1741; DB 1; Length 390;
 Best Local Similarity 86.5%; Pred. No. 7.5e-95;
 Matches 340; Conservative 13; Mismatches 36; Indels 4; Gaps 3;

OY 373 VIGVFLCWFPEPFSYSGALCPKHKVPHGLF 405
 DB 358 VIGVFLCWFPEPFSYSGALCPKHKVPHGLF 390
 RESULT 13
 A2AB_TALEU STANDARD; PRT; 397 AA.
 ID A2AB_TALEU
 AC 019051;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2b adrenergic receptor (Alpha-2b adrenoreceptor) (Fragment).
 GN A2AB.
 OS Talpa europaea (European mole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.
 OX NCBI_TaxID=9375;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97357151; PubMed=9214502;
 RA Springer M.S., Clevon G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
 RA Martine H.M., Stanhope M.J.,
 RT "Indemic African mammals shake the phylogenetic tree";
 RL Nature 388:61-64(1997).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: Y15520; CAA73120.1; -.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHOPOSN.
 CC PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
 CC PROSITE: PS00262; G_PROTEIN_REC_P1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Multigene family;
 CC Phosphorylation; Lipoprotein; Palmitate.
 CC
 CC NON TER 1 1
 CC TRANSSEM 26 25 1 (POTENTIAL).
 CC DOMAIN 26 36 2 (POTENTIAL).
 CC TRANSSEM 37 62 2 (POTENTIAL).
 CC DOMAIN 63 72 2 (POTENTIAL).
 CC TRANSSEM 73 95 3 (POTENTIAL).
 CC DOMAIN 96 117 4 (POTENTIAL).
 CC TRANSSEM 118 140 4 (POTENTIAL).
 CC DOMAIN 141 156 5 (POTENTIAL).
 CC TRANSSEM 157 180 5 (POTENTIAL).
 CC DOMAIN 181 361 6 (POTENTIAL).
 CC TRANSSEM 362 385 6 (POTENTIAL).
 CC DOMAIN 386 394 7 (POTENTIAL).
 CC TRANSSEM 395 >397 7 (POTENTIAL).
 CC DISULFID 72 151 7 (POTENTIAL).
 CC DOMAIN 282 300 7 (POTENTIAL).
 CC SITE 79 79 7 (POTENTIAL).
 CC SITE 163 163 7 (POTENTIAL).
 CC SITE 167 167 7 (POTENTIAL).
 CC SITE 167 167 7 (POTENTIAL).
 CC NON TER 397 397 7 (POTENTIAL).
 CC SEQUENCE 397 AA; 43620 MW; 9C3812515ADC3E84 CRC64;

Query Match 73.0%; Score 1725.5; DB 1; Length 397;
 Best Local Similarity 84.6%; Pred. No. 6.1e-94;
 Matches 336; Conservative 16; Mismatches 40; Indels 5; Gaps 2;

QY 14 AIAAATFTLFTFGNALVTLAVLTSRSLAPQNLPLVSLAADIIVATLIIPEPSLANE 73
 FT |||||
 DB 1 AIAAATFTLFTFGNALVTLAVLTSRSLAPQNLPLVSLAADIIVATLIIPEPSLANE 60
 FT |||||

QY 74 LLAGYFRRRTWCEVYALADVLCFTSSIVHLCALSIDRWMAVSRALRYNSKRTPRIRICII 133
 FT |||||
 DB 61 LLAGYFRRRTWCEVYALADVLCFTSSIVHLCALSIDRWMAVSRALRYNSKRTPRIRICII 120
 FT |||||

QY 134 LTVWLLAAVLSLPLIYKGDGQPPRGRPOCKLQNEAWYIIASSISGFAPCLIMILVYL 193
 FT |||||
 DB 121 LTVWLLAAVLSLPLIYKGDGQPPRGRPOCKLQNEAWYIIASSISGFAPCLIMILVYL 180
 FT |||||

QY 194 RIVYIARSRNRGRPRAGGPGQGESKOPRPHGALASAKI.PALAS.-VASAREVNGHSKS 252
 FT |||||
 DB 181 RIVYIARSRNRGRPRAGGPGQGESKOPRPHGALASAKI.PALAS.-VASAREVNGHSKS 240
 FT |||||

QY 253 TGEKEGETPEDTGTTRALPPSMALPNSGQOKGVCASPDEBAE-----EEEEEECE 308
 FT |||||
 DB 241 TGEKEGETPEDTGTTRALPPSMALPNSGQOKGVCASPDEBAE-----EEEEEECE 300
 FT |||||

QY 309 POAVPVSPASACSPPLQOPQGSRYLATLRGVLLGRVGAIGQWMRRRAQLTREKRTF 368
 FT |||||
 DB 301 POAVPVSPASACSPPLQOPQGSRYLATLRGVLLGRVGAIGQWMRRRAQLTREKRTF 360
 FT |||||

QY 369 VLAIVIGVFLCWPFPFFSYSLGAIICPHKCVPHGLF 405
 FT |||||
 DB 361 VLAIVIGVFLCWPFPFFSYSLGAIICPHKCVPHGLF 397
 FT |||||

RESULT 14
 A2AB_PROHA STANDARD; PRT; 389 AA.
 ID A2AB_PROHA STANDARD; PRT; 389 AA.
 AC O19054;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADRA2B.
 OS *Procavia capensis habessinica* (Abyssinian hyrax).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Hyracoidea; Procaviidae; Procavia.
 OC NCBI_TaxID=9814;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97357151; PubMed=9214502;
 RA Springer M.S., Cleven G.C., Madson O.J., de Jong W.W., Maddell V.G.,
 RA Amrine H.M., Stanhope M.J.;
 RT "Endemic African mammals shake the phylogenetic tree.";
 RL Nature 388:61-64 (1997).
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: Y13523; CAA73123.1; -.
 DR HSSP; P29274; 1MMH.
 DR InterPro; IPR00276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 KM Phosphorylation; Lipoprotein; Palmitate.
 FT NON TER 1 1
 FT TRANSMEM 26 25
 FT DOMAIN 36 36
 FT TRANSMEM 37 62
 FT DOMAIN 63 72
 FT TRANSMEM 73 95
 FT DOMAIN 96 117
 FT TRANSMEM 118 140
 FT DOMAIN 141 156
 FT TRANSMEM 157 180
 FT DOMAIN 181 353
 FT TRANSMEM 354 377
 FT DOMAIN 378 386
 FT TRANSMEM 387 389
 FT DOMAIN 281 292
 FT DISULFID 72 151
 FT SITE 79 79
 FT SITE 163 163
 FT SITE 167 167
 FT SITE 167 167
 FT NON TER 389 389
 SQ SEQUENCE 389 AA; 42528 MM; 4F2089EAL40876E1 CRC64;

Query Match 73.0%; Score 1724.5; DB 1; Length 389;
 Best Local Similarity 86.5%; Pred. No. 6.9e-94;
 Matches 340; Conservative 9; Mismatches 39; Indels 5; Gaps 3;

QY 14 AIAAATFTLFTFGNALVTLAVLTSRSLAPQNLPLVSLAADIIVATLIIPEPSLANE 73
 FT |||||
 DB 1 AIAAATFTLFTFGNALVTLAVLTSRSLAPQNLPLVSLAADIIVATLIIPEPSLANE 60
 FT |||||

QY 74 LLAGYFRRRTWCEVYALADVLCFTSSIVHLCALSIDRWMAVSRALRYNSKRTPRIRICII 133
 FT |||||
 DB 61 LLAGYFRRRTWCEVYALADVLCFTSSIVHLCALSIDRWMAVSRALRYNSKRTPRIRICII 120
 FT |||||

QY 134 LTVWLLAAVLSLPLIYKGDGQPPRGRPOCKLQNEAWYIIASSISGFAPCLIMILVYL 193
 FT |||||
 DB 121 LTVWLLAAVLSLPLIYKGDGQPPRGRPOCKLQNEAWYIIASSISGFAPCLIMILVYL 180
 FT |||||

QY 194 RIVYIARSRNRGRPRAGGPGQGESKOPRPHGALASAKI.PALAS.-VASAREVNGHSKS 252
 FT |||||
 DB 181 RIVYIARSRNRGRPRAGGPGQGESKOPRPHGALASAKI.PALAS.-VASAREVNGHSKS 240
 FT |||||

QY 253 TGEKEGETPEDTGTTRALPPSMALPNSGQOKGVCASPDEBAE-----EEEEEECE 312
 FT |||||
 DB 241 TGEKEGETPEDTGTTRALPPSMALPNSGQOKGVCASPDEBAE-----EEEEEECE 296
 FT |||||

QY 313 PVSPASACSPPLQOPQGSRYLATLRGVLLGRVGAIGQWMRRRAQLTREKRTFVLAV 372
 FT |||||
 DB 297 PVSPASACSPPLQOPQGSRYLATLRGVLLGRVGAIGQWMRRRAQLTREKRTFVLAV 356
 FT |||||

QY 373 VIGVFLCWPFPFFSYSLGAIICPHKCVPHGLF 405
 FT |||||
 DB 357 VIGVFLCWPFPFFSYSLGAIICPHKCVPHGLF 389
 FT |||||

RESULT 15
 A2AB_MACPR STANDARD; PRT; 387 AA.
 ID A2AB_MACPR STANDARD; PRT; 387 AA.
 AC O19025;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
 GN ADRA2B.
 OS *Macroselides proboscideus* (short-eared elephant shrew).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Macroscelidae; Macroscelididae; Macroscelides.

NCBI_TaxID=29082;
 OX NCB1
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97357151; PubMed=9214502;
 RX Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
 RA Amrine H.M., Stanhope M.J.;
 RT "Endemic African mammals shake the phylogenetic tree."
 RL Nature 368:61-64(1997).
 RN REVISIONS TO 148 AND 255.
 RP Springer M.S., Cleven G.C., Madsen O., de Jong W.W., Waddell V.G.,
 RA Amrine H.M., Stanhope M.J.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL: Y12524; CAA73124.2; -
 DR HSSP: P29274; 1MMH.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT NON TER 1 1
 FT TRANSMEM 1 25
 FT DOMAIN 26 36
 FT TRANSMEM 37 62
 FT DOMAIN 63 72
 FT TRANSMEM 73 95
 FT DOMAIN 96 117
 FT TRANSMEM 118 140
 FT DOMAIN 141 156
 FT TRANSMEM 157 180
 FT TRANSMEM 181 351
 FT TRANSMEM 352 375
 FT DOMAIN 376 384
 FT TRANSMEM 385 387
 FT DOMAIN 388 288
 FT DISULFD 72 151
 FT SITE 79 79
 FT SITE 163 163
 FT SITE 167 167
 FT NON TER 387 387
 FT SEQUENCE 387 AA; 42587 MW; B74AD5F0EB23BD5A CRC64;
 Query Match 71.8%; Score 1697.5; DB 1; Length 387;
 Best Local Similarity 85.0%; Pred. No. 2.6e-92;
 Matches 335; Conservative 13; Mismatches 37; Indels 9; Gaps 4;
 OY 14 AIAAATFLILFTFGNALVILAVLTSSRLAPQNLFLVSLAADIIVATLIIPFSLANE 73
 DB 1 AIAAVITFLILFTIGNLVILAVLTSSRLAPQNLFLVSLAADIIVATLIIPFSLANE 60
 OY 74 ILGYVFRRTWCEVTLADVLFCTSSIVHLCAISLDRYAVSRALVNSKRTPRRIKCI 133
 DB 61 ILGYVFRHTWCXVIALDVLFCTSSIVHLCAISLDRYAVSRALVNSKRTPRRIKCI 120

OY 134 LTVWLIAAVISLPPLIYKDGQFQPRGRPOCKLNOEAWYILASSIGSFAPCLIMILVYL 193
 DB 121 LTVWLIAAASLPPLIYKDGQFQPRGRPOCKLNOEAWYILASSIGSFAPCLIMILVYL 180
 OY 194 RIVLIANK-SNRGPRKAGPGGEGSKQPRPDHIGALASAKLPAIAS-VASAREVNCHSK 251
 DB 181 RIVLIARKSSRRKPRKAGPREGESKQPLRPVGSVSARPPALISPLAVTGEANGHSK 240
 OY 252 STGEKEBETPEPDGTALPPSWAALPNSGQKREGVCGASPEDEAESEEESECEPQA 311
 DB 241 PTGER--ETPEDLVSPASPSPSPALINSGRGKEGVCSTSPDEEA----EEEECCPEEA 293
 OY 312 VPVSPASACSPLOPOGSRVLTATLRQVLLIGRGVAGIIGQWARRRRAQLTRERKFTVLA 371
 DB 294 VPASPALACSPSLOPQGSRYLTATLRQVLLIGRGVGTARQGMWRRRAQLTRERKFTVLA 353
 OY 372 VVIGVFLCWPFPPFSYSIGAIQPHCKVPRGLF 405
 DB 354 VVIGVFLCWPFPPFSYSIGAIQPHCKVPRGLF 387

Search completed: February 6, 2004, 18:18:04
 Job time : 10.9666 secs

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OM protein - protein search, using SW model

Run on: February 6, 2004, 18:11:25 ; Search time 32.8896 Seconds
(without alignments)
3507.169 Million cell updates/sec

Title: US-09-692-077D-8
Perfect score: 2363
Sequence: 1 MDHODPYSVQATAIAAIAIT.....QDFRRARFRILCRPWTQTAW 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2120	89.7	451	6	Q8HY8
2	2003.5	84.8	453	11	Q925E4
3	1961.5	83.0	448	11	Q925K7
4	1956.5	82.8	448	11	Q925K6
5	1868.5	79.1	401	6	Q8MK45
6	1866.5	79.0	393	6	Q9GL11
7	1844.5	78.1	389	6	Q9GL07
8	1843.5	78.0	391	6	Q9GL06
9	1842.5	77.8	387	6	Q9GL17
10	1838.5	77.8	399	6	Q8MID0
11	1833.5	77.6	395	11	Q8KI09
12	1829.5	77.4	397	11	Q8KI06
13	1826	77.3	390	6	Q9GL12
14	1820.5	77.0	393	6	Q8MIR1
15	1818.5	76.7	389	6	Q9GK25
16	1812.5	76.7	389	6	Q9GK25

17	1811.5	76.7	399	6	Q8MK51	Q8mk51 lama guanic
18	1808	76.5	392	11	Q8KI03	Q8ki03 marmota mon
19	1799.5	76.2	389	11	Q8KI01	Q8ki01 echinops chr
20	1799	76.1	390	6	Q9SN89	Q9sn89 tapozous s
21	1798.5	76.1	393	11	Q9UTW2	Q9utw2 cavia porce
22	1798	76.1	398	6	Q8SQ92	Q8sq92 natalus str
23	1797.5	76.1	393	11	Q8KI02	Q8ki02 trichys fas
24	1797.5	76.1	399	6	Q8MIB3	Q8mib3 lepus craws
25	1795.5	76.0	395	11	Q8KIR6	Q8kir6 anomalurus
26	1794.5	75.9	393	6	Q9GL16	Q9gl16 hyppopotamu
27	1793	75.9	388	6	Q8SQ93	Q8sq93 nycteris gr
28	1792.5	75.9	389	11	Q8CG78	Q8cg78 chinchilla
29	1791.5	75.8	395	6	Q9SN91	Q9sn91 conacia bid
30	1791	75.8	388	6	Q8SQ91	Q8sq91 nycteris th
31	1790.5	75.8	391	6	Q8SQ00	Q8sq00 emballonura
32	1785	75.5	388	6	Q9GL18	Q9gl18 diceros dic
33	1783.5	75.5	389	6	Q9SN94	Q9sn94 hipposidero
34	1782.5	75.4	389	11	Q8KI08	Q8ki08 bathyergus
35	1777	75.2	392	6	Q9GL35	Q9gl35 balaenopter
36	1774.5	75.1	395	6	Q8SQ94	Q8sq94 noctilio al
37	1773	75.0	392	11	Q8K4Y3	Q8k4y3 sciurus vul
38	1772.5	75.0	391	6	Q8HY23	Q8hy23 physter ca
39	1772.5	75.0	395	11	Q8KI07	Q8ki07 myoxus glis
40	1772	75.0	392	6	Q9SN90	Q9sn90 tadarda br
41	1770.5	74.9	391	11	Q8KIR1	Q8kir1 massoutiera
42	1769.5	74.9	391	6	Q8MIR5	Q8mir5 hylomyx sui
43	1763	74.6	406	11	Q8KIN6	Q8kin6 thomomys ta
44	1760	74.5	394	6	Q8SQ01	Q8sq01 desmodus ro
45	1759.5	74.5	391	11	Q8KIR7	Q8kir7 aplodontia

ALIGNMENTS

RESULT 1	
Q8HY8	PRELIMINARY; PRT; 451 AA.
ID	Q8HY8
AC	Q8HY8
DT	01-MAR-2003 (TREMBLrel_23, Created)
DT	01-MAR-2003 (TREMBLrel_23, Last sequence update)
DT	01-MAR-2003 (TREMBLrel_23, Last annotation update)
DE	Alpha-2B adrenoceptor.
OS	Tupaia belangeri (Northern tree shrew).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
OX	NCBI_TaxID=37347;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Heilbronner U., van Kampen M., Isovich E., Pluegge G.;
RT	"Phalamic alpha-2B adrenoceptors under chronic stress: persistent
RT	upregulation in the paraventricular nucleus.";
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY150333; AAN72436.1;
SQ	SEQUENCE 451 AA; 50356 MW; 3172403011F3BC60 CRC64;

Query Match	89.7%; Score 2120; DB 6; Length 451;
Best Local Similarity	90.7%; Pred. No. 2.3e-161;
Matches 409; Conservative	8; Mismatches 30; Indels 4; Gaps 2;
QY	1 MDHODPYSVQATAIAAIAITFLIFTFGNALVTIAVTSRSLRAPONTLFLVSLAADIL 60
DB	1 MHOEPYVQATAIAAIAVITFLIFTFGNALVTIAVTSRSLRAPONTLFLVSLAADIL 60
QY	61 VATLIIFPSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYAVASRALEY 120
DB	61 VATLIIFPSLANELLGWYFRRTWCEVYALDVLFCTSSIVHLCAISLDRYAVASRALEY 120
QY	121 NSKRTPRKICITITLWVLAIAVISLPLIYKGGQPPRRPQCKLNOEMAYITLASSIGS 180
DB	121 NSKRTPRKICITITLWVLAIAVISLPLIYKGGQPPRRPQCKLNOEMAYITLASSIGS 180
QY	181 FPAAPCLIMLVIRIYIARSNRGRGKAGPQGGSKPRPDHGALSAKLPALA-S 239
DB	181 FPAAPCLIMLVIRIYIARSNRGRGKAGPQGGSKPRPDHGALSAKLPALA-S 239


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Db      181  FPAACLMILVLRILYLAIRAKSNRGRPRVKGPFWGGSKQPRFVPGRASAKLPTLASS 240
Qy      240  VASAREVNGSHSGTGEKEGETPEDTGTALPESNALPNSGGQKRGVAGSPEDAE 299
Db      241  LATGEANGHSGKPPGNREDGETPEDPGTRVLPESMALASSGQKRGVAREABEEREE 300
Qy      300  EEEEEEE---CEPOAVPSPASACSPPLQPGSGRVATLARGVTLGRVGAIGGQWRR 356
Db      301  EEEEEEEGCEPPEVPSPASVCSPPLOQPGSRVATLARGVTLGRVGAASGQWRR 360
Qy      357  RAQLTREKRFVLAIVIGFVLCMPFFPSYSIGALCPKCKPFGHLFOFFWIGYCN 416
Db      361  RAHLREKRFVLAIVIGFVLCMPFFPSYSIGALCPCHKVPHGLFOFFWIGYCN 420

RESULT 2
ID      0925E4  PRELIMINARY;  PRT;  453 AA.
AC      0925E4;
DT      01-DEC-2001 (TReMBLrel. 19, Created)
DT      01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      Alpha2B-adrenergic receptor.
NG.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley;
RA      Schaak S., Cusack D., Paris H.;
RT      "Cloning and characterization of the rat alpha2B-adrenergic receptor
RT      gene promoter."
RL      Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR      EMBL; AF368899; AAK53388.1; -.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCR_RHODOPS.
DR      PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR      PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
KW      G-protein coupled receptor; Receptor; Transmembrane.
SQ      SEQUENCE 453 AA; 50369 MW; CBA69CE23EACB511 CRC64;

Query Match      84.8%; Score 2003.5; DB 11; Length 453;
Best Local Similarity 84.6%; Pred. No. 4,7e-152;
Matches 379; Conservative 25; Mismatches 43; Indels 1; Gaps 1;

Qy      1  MDHDPYSVQTAATAAATFLILFTFGNALVTLAVTSRSRAPONLFLVSLAADIL 60
Db      6  MDHDPYSVQTAATAAATFLILFTFGNALVTLAVTSRSRAPONLFLVSLAADIL 65
Qy      61  VATLIIPSLANELLGWYFRRTWCCEVYALDVLFCTSSIVHLCAISLDRYWAVSRLEY 120
Db      66  VATLIIPSLANELLGWYFRRTWCCEVYALDVLFCTSSIVHLCAISLDRYWAVSRLEY 125
Qy      121  NSKRTPRRIKCIILVWMLIAAVISLPPLIYKGDGPORGRPOCKLNOEAYIIASSIGS 180
Db      126  NSKRTPRRIKCIILVWMLIAAVISLPPLIYKGDGPORGRPOCKLNOEAYIIASSIGS 185
Qy      181  FPAACLMILVLRILYLAIRAKSNRGRPRVKGPFWGGSKQPRFVPGRASAKLPTLAS- 239
Db      186  FPAACLMILVLRILYLAIRAKSNRGRPRVKGPFWGGSKQPRFVPGRASAKLPTLAS- 245
Qy      240  VASAREVNGSHSGTGEKEGETPEDTGTALPESNALPNSGGQKRGVAGSPEDAE 299
Db      246  LSSVGEANGHSPKPREKEGETPEDPEARALPPTWSALFRSGQKKGTSATAEEDGE 305

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Qy      300  EEEEECEPOAVVSPASACSPPLQPGSGRVATLARGVTLGRVGAIGGQWRRRAQ 359
Db      306  DEEEVECEPOTLSPASVSCNPNLOPOTSRVATLARGVTLGRVGAIGGQWRRRTQ 365
Qy      360  LTREKRFVLAIVIGFVLCMPFFPSYSIGALCPKCKVPHGLFOFFWIGYCNSSLN 419
Db      366  LSREKRFVLAIVIGFVLCMPFFPSYSIGALCPCHKVPHGLFOFFWIGYCNSSLN 425
Qy      420  PVIYTFVNODRRARFRILCRPWTQTM 447
Db      426  PVIYTFVNODRRARFRILCRPWTQTM 453

RESULT 3
ID      0925K7  PRELIMINARY;  PRT;  448 AA.
AC      0925K7;
DT      01-DEC-2001 (TReMBLrel. 19, Created)
DT      01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      Adrenergic receptor alpha 2B.
NG.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ISS;
RA      Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA      Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT      "High-Throughput Sequence Identification of Gene Coding Variants
RT      within Alcohol-Related QTLs."
RL      Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR      EMBL; AF332049; AAK56078.1; -.
DR      MGD; MGI:87935; Adra2b.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCR_RHODOPS.
DR      PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR      PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
KW      G-protein coupled receptor; Receptor; Transmembrane.
SQ      SEQUENCE 448 AA; 50018 MW; 1B5ED9456CDB2B73 CRC64;

Query Match      83.0%; Score 1961.5; DB 11; Length 448;
Best Local Similarity 83.9%; Pred. No. 1.1e-148;
Matches 376; Conservative 22; Mismatches 49; Indels 1; Gaps 1;

Qy      1  MDHDPYSVQTAATAAATFLILFTFGNALVTLAVTSRSRAPONLFLVSLAADIL 60
Db      1  MVHGEPYSVQTAATAAATFLILFTFGNALVTLAVTSRSRAPONLFLVSLAADIL 60
Qy      61  VATLIIPSLANELLGWYFRRTWCCEVYALDVLFCTSSIVHLCAISLDRYWAVSRLEY 120
Db      61  VATLIIPSLANELLGWYFRRTWCCEVYALDVLFCTSSIVHLCAISLDRYWAVSRLEY 120
Qy      121  NSKRTPRRIKCIILVWMLIAAVISLPPLIYKGDGPORGRPOCKLNOEAYIIASSIGS 180
Db      121  NSKRTPRRIKCIILVWMLIAAVISLPPLIYKGDGPORGRPOCKLNOEAYIIASSIGS 180
Qy      181  FPAACLMILVLRILYLAIRAKSNRGRPRVKGPFWGGSKQPRFVPGRASAKLPTLAS- 239
Db      181  FPAACLMILVLRILYLAIRAKSNRGRPRVKGPFWGGSKQPRFVPGRASAKLPTLAS- 240
Qy      240  VASAREVNGSHSGTGEKEGETPEDTGTALPESNALPNSGGQKRGVAGSPEDAE 299
Db      241  LSSVGEANGHSPKPREKEGETPEDPEARALPPTWSALFRSGQKKGTSATAEKGAEE 300
Qy      300  EEEEECEPOAVVSPASACSPPLQPGSGRVATLARGVTLGRVGAIGGQWRRRAQ 359

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Db 301 DEBEVECEBQTLSPASPAVFNPLQOPQTSRYLATLRGQVLLSKVNVASGQMMRRRTQ 360
QY LTRKKRFTFLAVAVIGVFLCMFPFPFSSYLGAIICPKHCKVPHGLFQFPFMIGYCNSSLN 419
Db 361 LSRKKRFTFLAVAVIGVFLCMFPFPFSSYLGAIICPKHCKVPHGLFQFPFMIGYCNSSLN 420
QY 420 PVIYTI FNODFRAPRRILCRPWTOTAM 447
Db 421 PVIYTI FNODFRAPRRILCRPWTOTAM 448

RESULT 4
Q925K6 PRELIMINARY; PRT; 448 AA.
ID Q925K6
AC Q925K6; PRELIMINARY; PRT; 448 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adrennergic receptor alpha 28.
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1] _SEQUENCE FROM N.A.
RC STRAIN=ILS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Caniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-Throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF332050; AAK56079.1; -.
DR MGI; MGI:87935; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 448 AA; 4998 MW; B37BEE21B0EC4625 CRC64;

Query Match 82.8%; Score 1956.5; DB 11; Length 448;
Best Local Similarity 83.7%; Pred. No. 2.7e-148;
Matches 375; Conservative 22; Mismatches 50; Indels 1; Gaps 1;

QY 1 MHODEYSVOATAIAAIFLFTIFGNALVILAVTSRSLRAPQNLFLVSLAADI 60
Db 1 MHODEYSVOATAIAAIFLFTIFGNALVILAVTSRSLRAPQNLFLVSLAADI 60
QY 61 VATLLIPFSLANELLGYWFRRTWCSEYVLLDVLFTSSIVHLCAISLDRYMAVSRAL 120
Db 61 VATLLIPFSLANELLGYWFRRTWCSEYVLLDVLFTSSIVHLCAISLDRYMAVSRAL 120
QY 121 NSKRTFRRIKCIITLWMLAAVLSLPLLYKGDQGPQPRGPOCKLNOEAWYILASSIG 180
Db 121 NSKRTFRRIKCIITLWMLAAVLSLPLLYKGDQGPQPRGPOCKLNOEAWYILASSIG 180
QY 121 NSKRTFRRIKCIITLWMLAAVLSLPLLYKGDQGPQPRGPOCKLNOEAWYILASSIG 180
Db 121 NSKRTFRRIKCIITLWMLAAVLSLPLLYKGDQGPQPRGPOCKLNOEAWYILASSIG 180
QY 181 PFAPCLIMLVLYRIYLIKRSNRGRBRAGKGPQGESKOPRPHDGLASATLPLAS- 239
Db 181 PFAPCLIMLVLYRIYLIKRSNRGRBRAGKGPQGESKOPRPHDGLASATLPLAS- 239
QY 240 VASAREVNGSKSTGKEGETPEDTCTRALPPSMAALPNSGQGEKGVCGASPEDAE 299
Db 240 VASAREVNGSKSTGKEGETPEDTCTRALPPSMAALPNSGQGEKGVCGASPEDAE 299
QY 300 EEEVECEBQTLSPASPAVFNPLQOPQTSRYLATLRGQVLLSKVNVASGQMMRRRTQ 359
Db 301 DEBEVECEBQTLSPASPAVFNPLQOPQTSRYLATLRGQVLLSKVNVASGQMMRRRTQ 360
QY 360 LTRKKRFTFLAVAVIGVFLCMFPFPFSSYLGAIICPKHCKVPHGLFQFPFMIGYCNSSLN 419

Db 361 LSRKKRFTFLAVAVIGVFLCMFPFPFSSYLGAIICPKHCKVPHGLFQFPFMIGYCNSSLN 420
QY 420 PVIYTI FNODFRAPRRILCRPWTOTAM 447
Db 421 PVIYTI FNODFRAPRRILCRPWTOTAM 448

RESULT 5
Q8MK45 PRELIMINARY; PRT; 401 AA.
ID Q8MK45
AC Q8MK45; PRELIMINARY; PRT; 401 AA.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alpha 2B adrennergic receptor (Fragment).
GN ADRA2B.
OS Tapirus terrestris (Lowland tapir) (Brazilian tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9801;
[1] _SEQUENCE FROM N.A.
RX MEDLINE=21608557; PubMed=11743200;
RA Murphy W.J., Eizirik E., O'Brien S.J., Madsen O., Scally M.,
RA Douady C.J., Teeling E., Ryder O.A., Stanhope M.J., de Jong W.W.,
RA Springer M.S.;
RT "Resolution of the early placental mammal radiation using Bayesian
RT phylogenetics";
RL Science 294:2348-2351 (2001).
DR EMBL; AJ115939; CAC87003.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 401
SQ SEQUENCE 401 AA; 43835 MW; 8D01F4C2548BFB6 CRC64;

Query Match 79.1%; Score 1868.5; DB 6; Length 401;
Best Local Similarity 89.8%; Pred. No. 2.5e-141;
Matches 360; Conservative 12; Mismatches 20; Indels 9; Gaps 2;

QY 14 AIAAATPILFTIFGNALVILAVTSRSLRAPQNLFLVSLAADI 73
Db 1 AIAAATPILFTIFGNALVILAVTSRSLRAPQNLFLVSLAADI 73
QY 74 LGGWYFRRTWCSEYVLLDVLFTSSIVHLCAISLDRYMAVSRALYNSKRTFRRIKCI 133
Db 74 LGGWYFRRTWCSEYVLLDVLFTSSIVHLCAISLDRYMAVSRALYNSKRTFRRIKCI 133
QY 134 LTVWLAAVLSLPLLYKGDQGPQPRGPOCKLNOEAWYILASSIGSFAPCLIMLVYL 193
Db 134 LTVWLAAVLSLPLLYKGDQGPQPRGPOCKLNOEAWYILASSIGSFAPCLIMLVYL 193
QY 194 RYLIKRSNRGRBRAGKGPQGESKOPRPHDGLASATLPLAS- VASAREVNGSKS 252
Db 194 RYLIKRSNRGRBRAGKGPQGESKOPRPHDGLASATLPLAS- VASAREVNGSKS 252
QY 253 TGRKEGETPEDTCTRALPPSMAALPNSGQGEKGVCGASPEDAE-----EEEEEE 304
Db 253 TGRKEGETPEDTCTRALPPSMAALPNSGQGEKGVCGASPEDAE-----EEEEEE 304
QY 305 EEEVECEBQTLSPASPAVFNPLQOPQTSRYLATLRGQVLLSKVNVASGQMMRRRTQ 364
Db 301 EEEVECEBQTLSPASPAVFNPLQOPQTSRYLATLRGQVLLSKVNVASGQMMRRRTQ 360
QY 365 RFTFLAVAVIGVFLCMFPFPFSSYLGAIICPKHCKVPHGLF 405
Db 361 RFTFLAVAVIGVFLCMFPFPFSSYLGAIICPKHCKVPHGLF 401

RESULT 6
 Q9GL11 PRELIMINARY; PRT; 393 AA.
 ID Q9GL11
 AC Q9GL11
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Alpha adrenergic receptor 2B (Fragment).
 GN AAR2B
 OS Nycticebus coucang (Slow loris).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
 OC NCBI_TaxId=9470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082081; PubMed=11214318;
 RA Madden O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
 RA Amrine H., Stanhope M., de Jong W., Springer M.,
 RT "Parallel adaptive radiations in two major clades of placental
 mammals".
 RL Nature 409:610-614(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ251186; CAC16695.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 393 AA; 42990 MW; 713D3D10EE08714A CEC64;
 Query Match 79.0%; Score 1866.5; DB 6; Length 393;
 Best Local Similarity 91.9%; Pred. No. 3.6e-14;
 Matches 361; Conservative 11; Mismatches 20; Indels 1; Gaps 1;
 QY 14 AIAAAITFLIFLTIFGNALVLIATVTSRLAPQNLFLVSLAAADILVATLITPISLANE 73
 DB 1 AIAAAITFLIFLTIFGNALVLIATVTSRLAPQNLFLVSLAAADILVATLITPISLANE 60
 QY 74 LIGWYFRRTWCEVYIADLVFECTSIYHLCASIDRWAVSRALEYNSKTPRRIKCI 133
 DB 61 LIGWYFRRTWCEVYIADLVFECTSIYHLCASIDRWAVSRALEYNSKTPRRIKCI 120
 QY 134 LTVMLIAAVISLPPLLYKDGQPPRGRPOCKLQNEAWYIIASSIGSFAPCLIMILVYL 193
 DB 121 LTVMLIAAVISLPPLLYKDGQPPRGRPOCKLQNEAWYIIASSIGSFAPCLIMILVYL 180
 QY 194 RYLIAKRSNRGRPRAGKGGPGGEGSKQPPDHGALASKLPALAS-VASAREVNGHSKS 252
 DB 181 RYLIAKRSNRGRPRAGKGGPGGEGSKQPPDHGALASKLPALAS-VASAREVNGHSKS 240
 QY 253 TGEKEGETPEDTGTALPSSWALPNSGOGQEGVCGASPEDEAEEEEEECEPOAV 312
 DB 241 TGEKEGETPEDTGTALPSSWALPNSGOGQEGVCGASPEDEAEEEEEECEPOAV 300
 QY 313 PVSPASACSPPLQPOGSRVLTATLRGQVLLGRGVGAIGGQWRRRAOULTREKRTFTVLAV 372
 DB 301 PVSPASACSPPLQPOGSRVLTATLRGQVLLGRGVGAIGGQWRRRAOULTREKRTFTVLAV 360
 QY 373 VIGFVLCWFPFFPSYSIGAICPKHCKVPHGLF 405
 DB 361 VIGFVLCWFPFFPSYSIGAICPKHCKVPHGLF 393
 RESULT 7
 Q9GL07 PRELIMINARY; PRT; 389 AA.
 ID Q9GL07
 AC Q9GL07
 DT 01-MAR-2001 (TREMblrel. 16, Created)

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Alpha adrenergic receptor 2B (Fragment).
 GN AAR2B
 OS Phoca vitulina (Harbor seal).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
 OC NCBI_TaxId=9720;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082081; PubMed=11214318;
 RA Madden O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
 RA Amrine H., Stanhope M., de Jong W., Springer M.,
 RT "Parallel adaptive radiations in two major clades of placental
 mammals".
 RL Nature 409:610-614(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ251176; CAC16696.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 389 AA; 42278 MW; E42F177873FE47FF CEC64;
 Query Match 78.1%; Score 1844.5; DB 6; Length 389;
 Best Local Similarity 90.8%; Pred. No. 2e-139;
 Matches 356; Conservative 10; Mismatches 23; Indels 3; Gaps 2;
 QY 14 AIAAAITFLIFLTIFGNALVLIATVTSRLAPQNLFLVSLAAADILVATLITPISLANE 73
 DB 1 AIAAAITFLIFLTIFGNALVLIATVTSRLAPQNLFLVSLAAADILVATLITPISLANE 60
 QY 74 LIGWYFRRTWCEVYIADLVFECTSIYHLCASIDRWAVSRALEYNSKTPRRIKCI 133
 DB 61 LIGWYFRRTWCEVYIADLVFECTSIYHLCASIDRWAVSRALEYNSKTPRRIKCI 120
 QY 134 LTVMLIAAVISLPPLLYKDGQPPRGRPOCKLQNEAWYIIASSIGSFAPCLIMILVYL 193
 DB 121 LTVMLIAAVISLPPLLYKDGQPPRGRPOCKLQNEAWYIIASSIGSFAPCLIMILVYL 180
 QY 194 RYLIAKRSNRGRPRAGKGGPGGEGSKQPPDHGALASKLPALAS-VASAREVNGHSKS 253
 DB 181 RYLIAKRSNRGRPRAGKGGPGGEGSKQPPDHGALASKLPALAS-VASAREVNGHSKS 238
 QY 254 TGEKEGETPEDTGTALPSSWALPNSGOGQEGVCGASPEDEAEEEEEECEPOAV 313
 DB 239 TGEKEGETPEDTGTALPSSWALPNSGOGQEGVCGASPEDEAEEEEEECEPOAV 297
 QY 314 VSPASACSPPLQPOGSRVLTATLRGQVLLGRGVGAIGGQWRRRAOULTREKRTFTVLAV 373
 DB 298 VSPASACSPPLQPOGSRVLTATLRGQVLLGRGVGAIGGQWRRRAOULTREKRTFTVLAV 357
 QY 374 VIGFVLCWFPFFPSYSIGAICPKHCKVPHGLF 405
 DB 358 VIGFVLCWFPFFPSYSIGAICPKHCKVPHGLF 389
 RESULT 8
 Q9GL06 PRELIMINARY; PRT; 391 AA.
 ID Q9GL06
 AC Q9GL06
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Alpha adrenergic receptor 2B (Fragment).
 GN AAR2B
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082081; PubMed=11214318;
 RA Maden O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
 RA Amrine H., Stanhope M., de Jong W., Springer M.,
 RT "Parallel adaptive radiations in two major clades of placental
 mammals";
 RL Nature 409:610-614(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ251177; CAC16697.1; -
 DR InterPro; IPR000276; GPCR_Rhodpn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 391 391
 SQ SEQUENCE 391 AA; 42846 MW; 76A4F0FA3ECT4F16 CRC64;
 Query Match 78.0%; Score 1843.5; DB 6; Length 391;
 Best Local Similarity 90.6%; Pred. No. 2.5e-139;
 Matches 356; Conservative 12; Mismatches 22; Indels 3; Gaps 2;
 QY 14 AIAAAITFLILFTFGNALVTLAVLTSRSLRAPONLFLVSLAADIIVATLITPFSLANE 73
 DB 1 AIAAVITFLILFTFGNSLVTLAVLTSRSLRAPONLFLVSLAADIIVATLITPFSLANE 60
 QY 74 LIGWYFRRTMCEVYLADVLFCSTSIYVHCAISLDYVMAVSRALEYSKRTPRICIT 133
 DB 61 LIGWYFRRTMCEVYLADVLFCSTSIYVHCAISLDYVMAVSRALEYSKRTPRICIT 120
 QY 134 LTVWLIAAVSLPLIYKDGDPGRGRPOCKLQNEAMYLIIASSIGSFAPCLIMILVYL 193
 DB 121 LTVWLIAAVSLPLIYKDGDPGRGRPOCKLQNEAMYLIIASSIGSFAPCLIMILVYL 180
 QY 194 RYLIARSRNRGRPRAGGCGQSGKOPRPHGALASAKLPALAS-VASAREVNGHSKST 252
 DB 181 RYLIARSRNRGRPRAGGCGQSGKOPRPHGALASAKLPALAS-VASAREVNGHSKST 240
 QY 253 TGEKEGETPEDTGTALPPSMALPNSGOGQKEGVGASPEDAESEEESECEPOAV 312
 DB 241 TGEKEGETPEDTGTALPPSMALPNSGOGQKEGVGASPEDAESEEESECEPOAV 298
 QY 313 PVPASACSPPLQPOGSRVLTATLRGVLLGRGVALIGOMWRRRAQLTREKRTFVLAV 372
 DB 299 PVPASACSPPLQPOGSRVLTATLRGVLLGRGVALIGOMWRRRAQLTREKRTFVLAV 356
 QY 373 VIGFVLCMPFPFSSYSIGAICPHKCVPHGLF 405
 DB 359 VIGFVLCMPFPFSSYSIGAICPHKCVPHGLF 391
 RESULT 9
 Q9GL17 PRELIMINARY; PRT; 387 AA.
 ID Q9GL17
 AC Q9GL17
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Alpha adrenergic receptor 2B (Fragment).
 GN AAR2B.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Placentalia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082081; PubMed=11214318;
 RA Maden O., Scally M., Douady C., Kao D., Debry R., Adkins R.,

RA Amrine H., Stanhope M., de Jong W., Springer M.,
 RT "Parallel adaptive radiations in two major clades of placental
 mammals";
 RL Nature 409:610-614(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ251174; CAC16689.1; -
 DR InterPro; IPR000276; GPCR_Rhodpn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 387 387
 SQ SEQUENCE 387 AA; 42546 MW; 2C1CD5D4B43F8D9B CRC64;
 Query Match 78.0%; Score 1842.5; DB 6; Length 387;
 Best Local Similarity 90.6%; Pred. No. 2.9e-139;
 Matches 355; Conservative 12; Mismatches 20; Indels 5; Gaps 2;
 QY 14 AIAAAITFLILFTFGNALVTLAVLTSRSLRAPONLFLVSLAADIIVATLITPFSLANE 73
 DB 1 AIAAVITFLILFTFGNSLVTLAVLTSRSLRAPONLFLVSLAADIIVATLITPFSLANE 60
 QY 74 LIGWYFRRTMCEVYLADVLFCSTSIYVHCAISLDYVMAVSRALEYSKRTPRICIT 133
 DB 61 LIGWYFRRTMCEVYLADVLFCSTSIYVHCAISLDYVMAVSRALEYSKRTPRICIT 120
 QY 134 LTVWLIAAVSLPLIYKDGDPGRGRPOCKLQNEAMYLIIASSIGSFAPCLIMILVYL 193
 DB 121 LTVWLIAAVSLPLIYKDGDPGRGRPOCKLQNEAMYLIIASSIGSFAPCLIMILVYL 180
 QY 194 RYLIARSRNRGRPRAGGCGQSGKOPRPHGALASAKLPALAS-VASAREVNGHSKST 253
 DB 181 RYLIARSRNRGRPRAGGCGQSGKOPRPHGALASAKLPALAS-VASAREVNGHSKST 238
 QY 254 TGEKEGETPEDTGTALPPSMALPNSGOGQKEGVGASPEDAESEEESECEPOAV 313
 DB 239 TGEKEGETPEDTGTALPPSMALPNSGOGQKEGVGASPEDAESEEESECEPOAV 295
 QY 314 VVPASACSPPLQPOGSRVLTATLRGVLLGRGVALIGOMWRRRAQLTREKRTFVLAV 373
 DB 296 VVPASACSPPLQPOGSRVLTATLRGVLLGRGVALIGOMWRRRAQLTREKRTFVLAV 355
 QY 374 VIGFVLCMPFPFSSYSIGAICPHKCVPHGLF 405
 DB 356 VIGFVLCMPFPFSSYSIGAICPHKCVPHGLF 387
 RESULT 10
 Q8MID0 PRELIMINARY; PRT; 399 AA.
 ID Q8MID0
 AC Q8MID0
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha 2B adrenergic receptor (Fragment).
 GN ADR2B.
 OS Manis tetradactyla (Long-tailed pangolin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Pholidota; Manidae; Manis.
 OX NCBI_TaxID=73815;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maden O., Williams D., Ursing B.M., Arnason U., de Jong W.M.,
 RT "Molecular evolution of the alpha 2B adrenergic receptor";
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ505820; CAD44321.1; -
 DR InterPro; IPR000276; GPCR_Rhodpn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 399

SO SEQUENCE 399 AA; 43888 MW; 910ECAPB10659EDD CRC64;

Query Match

Best Local Similarity 89.5%; Pred. No. 6.3e-139;

Matches 359; Conservative 10; Mismatches 21; Indels 11; Gaps 3;

QY 14 AIAAATFTLFTFGNALVTLAVLTSSRLAPQNLFLVSLAADIIVATLIIIPSLANE 73
 DB 1 AIAAATFTLFTFGNALVTLAVLTSSRLAPQNLFLVSLAADIIVATLIIIPSLANE 60
 QY 74 LLGWYFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALRYNSKRTPRKICII 133
 DB 61 LLGWYFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALRYNSKRTPRKICII 120
 QY 134 LTVMLIAAVISLPLIYKGDGPQGRPOCKNOEMWYLLASISGFAPCLIMILVYL 193
 DB 121 LTVMLIAAVISLPLIYKGDGPQGRPOCKNOEMWYLLASISGFAPCLIMILVYL 180
 QY 194 RYLIAKSRNRGRPRAGKGPGEESKOPRPHGALASAKI PALASVASAREVNGHSKST 253
 DB 181 RYLIAKSRNRGRPRAGKGPGEESKOPRPHGALASAKI PALASVASAREVNGHSKST 238
 QY 254 GEKEGETPEDDTGTALPSSMALPNSGQCKEVCAGASPEDEA-----EEEEEEEE 306
 DB 239 GEKEGETPEDDTGTALPSSMALPNSGQCKEVCAGASPEDEA-----EEEEEEEE 298
 QY 307 CERQAVPSPASACSPLOQPOGSRVLTALRGVGLRGVGAIGQWRRRAQLTREK 364
 DB 299 CERQAVPSPASACSPLOQPOGSRVLTALRGVGLRGVGAIGQWRRRAQLTREK 358
 QY 365 RFTFVLAVVIGVFLCMFPFPPSYSLGAIICPKCKVPHGLF 405
 DB 359 RFTFVLAVVIGVFLCMFPFPPSYSLGAIICPKCKVPHGLF 399

RESULT 11
 Q8KIU9 PRELIMINARY; PRT; 395 AA.
 ID Q8KIU9;
 AC Q8KIU9;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Alpha 2B adrenergic receptor (Fragment).
 GN A2B.
 OS Erythron dorsatum (North American porcupine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Erethizontidae;
 OC Erethizon.
 OC NCBI_TaxID=34844;
 RN SEQUENCE FROM N.A.
 RP Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., Stanhope M.,
 RA Catzeffis F., de Jong W.W., Douzery E.J.P.,
 RT "Rodent phylogeny and a timescale for the evolution of Glires:
 evidence from an extensive taxon sampling using three nuclear genes."
 RT Mol. Biol. Evol. 0:0-0(2002).
 RL EMBL; AJ427270; CAD20308.1;
 DR EMBL; AJ427270; GPCR_Rhodopsin.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR000237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 395
 FT NON_TER 395
 SO SEQUENCE 395 AA; 43157 MW; 9E46A1E10EB41FB CRC64;

Query Match
 Best Local Similarity 90.1%; Pred. No. 1.6e-138;

Matches 356; Conservative 13; Mismatches 23; Indels 3; Gaps 2;
 QY 14 AIAAATFTLFTFGNALVTLAVLTSSRLAPQNLFLVSLAADIIVATLIIIPSLANE 73
 DB 1 AIAAATFTLFTFGNALVTLAVLTSSRLAPQNLFLVSLAADIIVATLIIIPSLANE 60
 QY 74 LLGWYFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALRYNSKRTPRKICII 133
 DB 61 LLGWYFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALRYNSKRTPRKICII 120
 QY 134 LTVMLIAAVISLPLIYKGDGPQGRPOCKNOEMWYLLASISGFAPCLIMILVYL 193
 DB 121 LTVMLIAAVISLPLIYKGDGPQGRPOCKNOEMWYLLASISGFAPCLIMILVYL 180
 QY 194 RYLIAKSRNRGRPRAGKGPGEESKOPRPHGALASAKI PALASVASAREVNGHSKST 252
 DB 181 RYLIAKSRNRGRPRAGKGPGEESKOPRPHGALASAKI PALASVASAREVNGHSKST 240
 QY 253 TGEKEGETPEDDTGTALPSSMALPNSGQCKEVCAGASPEDEA-----EEEEEEEECEPQ 310
 DB 241 TGEKEGETPEDDTGTALPSSMALPNSGQCKEVCAGASPEDEA-----EEEEEEEECEPQ 300
 QY 311 AVPSPASACSPLOQPOGSRVLTALRGVGLRGVGAIGQWRRRAQLTREK 370
 DB 301 AVPSPASACSPLOQPOGSRVLTALRGVGLRGVGAIGQWRRRAQLTREK 360
 QY 371 AVTGVFLCMFPFPPSYSLGAIICPKCKVPHGLF 405
 DB 361 AVTGVFLCMFPFPPSYSLGAIICPKCKVPHGLF 395

RESULT 12
 Q8KIU6 PRELIMINARY; PRT; 397 AA.
 ID Q8KIU6;
 AC Q8KIU6;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Alpha 2B adrenergic receptor (Fragment).
 GN A2B.
 OS Castor canadensis (Beaver).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Castoridae; Castor.
 OC NCBI_TaxID=51336;
 RN SEQUENCE FROM N.A.
 RP Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., Stanhope M.,
 RA Catzeffis F., de Jong W.W., Douzery E.J.P.,
 RT "Rodent phylogeny and a timescale for the evolution of Glires:
 evidence from an extensive taxon sampling using three nuclear genes."
 RT Mol. Biol. Evol. 0:0-0(2002).
 RL EMBL; AJ427260; CAD20298.1;
 DR EMBL; AJ427260; GPCR_Rhodopsin.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR000237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 397
 FT NON_TER 397
 SO SEQUENCE 397 AA; 43571 MW; BE4F239E4236A12B CRC64;

Query Match
 Best Local Similarity 89.7%; Pred. No. 3.3e-138;
 Matches 356; Conservative 10; Mismatches 26; Indels 5; Gaps 3;
 QY 14 AIAAATFTLFTFGNALVTLAVLTSSRLAPQNLFLVSLAADIIVATLIIIPSLANE 73
 DB 1 AIAAATFTLFTFGNALVTLAVLTSSRLAPQNLFLVSLAADIIVATLIIIPSLANE 60
 QY 74 LLGWYFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALRYNSKRTPRKICII 133
 DB 61 LLGWYFRRTWCEVYALADVLTCTSSIVHLCAISLDRYMAVSRALRYNSKRTPRKICII 120

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QY 134 LTVMLIAVLSLPLIYKDGQGPGRGRPOCKLNOEAWYLIASSIGSFAPCLIMILVYL 193
DB 121 LTVMLIAVLSLPLIYKDGQGPGRGRPOCKLNOEAWYLIASSIGSFAPCLIMILVYL 180
QY 194 RYIYIAKSNRGRPRAGKPGQGSKQPRPD-HGAGALASATLPAAL-ASVASAREVNGHSK 251
DB 181 RYIYIAKSNRGRPRAGKPGQGSKQPRPD-HGAGALASATLPAAL-ASVASAREVNGHSK 240
QY 252 STGKEGEPEDPTDTRALPSPMALPNSGQKQKGVGASPE---DEAESEEESEEC 308
DB 241 PGKEKEBETPEDPTDTRALPSPMALPNSGQKQKGVGASPESEEESEEESEEC 300
QY 309 PQAIVPSPASACSPPLQOPQGSRYLATLRGQVLLGRGVAIGGQWRRRAQLTREKRTF 368
DB 301 PQAIVPSPASACSPPLQOPQGSRYLATLRGQVLLGRGVAIGGQWRRRAQLTREKRTF 360
QY 369 VLAIVGVFLCWPFPFSSYSLGAIICPHCKVPHGLF 405
DB 361 VLAIVGVFLCWPFPFSSYSLGAIICPHCKVPHGLF 397
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RESULT 13

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QY 09GL19 PRELIMINARY; PRT; 390 AA.
ID 09GL19
AC 09GL19/
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Cynocephalus variegatus.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.
OX NCBI_TaxID=9457;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082081; PubMed=11214318;
RA Maden O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer M.;
RT "Parallel adaptive radiations in two major clades of placental
RT mammals.";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ251182; CAC16685.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 390
SQ SEQUENCE 390 AA; 42428 MW; C99055D3EC60E2C6 CRC64;
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Query Match 77.3%; Score 1826; DB 6; Length 390;

Best Local Similarity 90.1%; Pred. No. 6; 1e-138;

Matches 354; Conservative 9; Mismatches 26; Indels 4; Gaps 2;

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QY 14 AIAAAITFLIFTFGNALVILAVLTSRSLAPONLFLVSLAADIIVATLIPFSLANE 73
DB 1 AIAAAITFLIFTFGNALVILAVLTSRSLAPONLFLVSLAADIIVATLIPFSLANE 60
QY 74 LIGWYRRRTWCEVYALADVLCFTSSIVHLCAISLDRYWAVSRALVENSRTPRIRICII 133
DB 61 LIGWYRRRTWCEVYALADVLCFTSSIVHLCAISLDRYWAVSRALVENSRTPRIRICII 120
QY 134 LTVMLIAVLSLPLIYKDGQGPGRGRPOCKLNOEAWYLIASSIGSFAPCLIMILVYL 193
DB 121 LTVMLIAVLSLPLIYKDGQGPGRGRPOCKLNOEAWYLIASSIGSFAPCLIMILVYL 180
QY 194 RYIYIAKSNRGRPRAGKPGQGSKQPRPDHGAGALASAKLPAALAS-VASAREVNGHSK 252
```

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DB 181 RYIYIAKSNRGRPRAGKPGQGSKQPRPDHGAGALASAKLPAALASPLASAGENGSKP 240
QY 253 TGEKEBETPEDPTDTRALPSPMALPNSGQKQKGVGASPEDEAESEEESEEC 312
DB 241 TGEKEBETPEDPTDTRALPSPMALPNSGQKQKGVGASPEDEAESEEESEEC 297
QY 313 PVPSPASACSPPLQOPQGSRYLATLRGQVLLGRGVAIGGQWRRRAQLTREKRTF 372
DB 298 PVPSPASACSPPLQOPQGSRYLATLRGQVLLGRGVAIGGQWRRRAQLTREKRTF 357
QY 373 VIGVFLCWPFPFSSYSLGAIICPHCKVPHGLF 405
DB 358 VIGVFLCWPFPFSSYSLGAIICPHCKVPHGLF 390
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RESULT 14

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QY 09GL12 PRELIMINARY; PRT; 395 AA.
ID 09GL12
AC 09GL12/
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Manis sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Pholidota; Manidae; Manis.
OX NCBI_TaxID=49127;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082081; PubMed=11214318;
RA Maden O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer M.;
RT "Parallel adaptive radiations in two major clades of placental
RT mammals.";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ251185; CAC16694.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 395
SQ SEQUENCE 395 AA; 43427 MW; 2663DA564356D84 CRC64;
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Query Match 77.0%; Score 1820.5; DB 6; Length 395;

Best Local Similarity 89.9%; Pred. No. 1; 7e-137;

Matches 357; Conservative 10; Mismatches 23; Indels 7; Gaps 3;

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QY 14 AIAAAITFLIFTFGNALVILAVLTSRSLAPONLFLVSLAADIIVATLIPFSLANE 73
DB 1 AIAAAITFLIFTFGNALVILAVLTSRSLAPONLFLVSLAADIIVATLIPFSLANE 60
QY 74 LIGWYRRRTWCEVYALADVLCFTSSIVHLCAISLDRYWAVSRALVENSRTPRIRICII 133
DB 61 LIGWYRRRTWCEVYALADVLCFTSSIVHLCAISLDRYWAVSRALVENSRTPRIRICII 120
QY 134 LTVMLIAVLSLPLIYKDGQGPGRGRPOCKLNOEAWYLIASSIGSFAPCLIMILVYL 193
DB 121 LTVMLIAVLSLPLIYKDGQGPGRGRPOCKLNOEAWYLIASSIGSFAPCLIMILVYL 180
QY 194 RYIYIAKSNRGRPRAGKPGQGSKQPRPDHGAGALASAKLPAALASVASAREVNGHSK 253
DB 181 RYIYIAKSNRGRPRAGKPGQGSKQPRPDHGAGALASAKLPAALASVASAREVNGHSK 238
QY 254 GKEKEBETPEDPTDTRALPSPMALPNSGQKQKGVGASPEDEAESEEESEEC 310
DB 239 GKEKEBETPEDPTDTRALPSPMALPNSGQKQKGVGASPEDEAESEEESEEC 298
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Job time : 33.8896 secs

QY 311 AVPSASACSPPLQOQSGSRVATLRGQVLLGRGVGAI - GGQWRRRAQITREKRTF 368
 DB 299 ALPSASACSPPLQOQSGSRVATLRGQVLLGRGVGAAVSGQWRRRAQITREKRTF 358
 QY 369 VLAVVIGFVLCWPFPPFSYSLGAIQPKHCKVPHGLF 405
 DB 359 VLAVVIGFVLCWPFPPFSYSLGAIQPKHCKVPHGLF 395

RESULT 15

Q8MIE1 PRELIMINARY; PRT; 393 AA.
 AC 08MIE1;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha 2B adrenergic receptor (Fragment).
 GN ADRA2B.
 OS Lama guanicoe pacos (Alpaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OC NCBI_TaxID=30538;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maden O., Willemssen D., Ursing B.M., Arnason U., de Jong W.W.;
 RT "Molecular evolution of the alpha 2B adrenergic receptor."
 RL Submitted (AUG-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ505821; CAD44322.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_P1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_P1_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 393 393
 FT NON_TER 43268 MM; E2F24F89B92801E5 CRC64;
 SQ SEQUENCE 393 AA; 43268 MM; E2F24F89B92801E5 CRC64;

Query Match 77.0%; Score 1818.5; DB 6; Length 393;
 Best Local Similarity 89.6%; Pred. NO. 2.5e-137;
 Matches 352; Conservative 10; Mismatches 30; Indels 1; Gaps 1;

QY 14 AIAAATPLILFTIFGNALVILAVLTSRSLAPQNTFLVSLAADIIVATLIPSLANE 73
 DB 1 AIAAATPLILFTIFGNALVILAVLTSRSLAPQNTFLVSLAADIIVATLIPSLANE 60
 QY 74 LLGWYFRRTWCEVTLADVLTCTSSIVHLCATSLDRYMAVSRALEYNKRTPRRIKCI 133
 DB 61 LLGWYFRRTWCEVTLADVLTCTSSIVHLCATSLDRYMAVSRALEYNKRTPRRIKCI 120
 QY 134 LTVWLLIAAVISLPPLIYKDGQOPQPRGRPOCKLQNEAWYIIASSIGSFAPCLIMIVYL 193
 DB 121 LTVWLLIAAVISLPPLIYKDGQOPQPRGRPOCKLQNEAWYIIASSIGSFAPCLIMIVYL 180
 QY 194 RIYLIAKRSNRGRPRAGKGGPGQGESKOPPDHGGALASAKL PALAS -VASAREVNGSHKS 252
 DB 181 RIYLIAKRSNRGRPRAGKGGPGQGESKOPPDHGGALASAKL PALAS -VASAREVNGSHKS 240
 QY 253 TGEKEGEPEDTGTALPESWAALPNSGQKEGVCASPEDEAESEEECEPEQAV 312
 DB 241 TGEKDEGETPEDGTALPESWAALPNSGQKEGVCASPEDEAESEEECEPEQAV 300
 QY 313 PVSAPASCSPLLOQPGSRVATLRGQVLLGRGVGAIQPKHCKVPHGLF 405
 DB 301 PVSAPASCSPLLOQPGSRVATLRGQVLLGRGVGAIQPKHCKVPHGLF 395
 QY 373 VIGVFVLCWPFPPFSYSLGAIQPKHCKVPHGLF 405
 DB 361 VIGVFVLCWPFPPFSYSLGAIQPKHCKVPHGLF 393